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(21) International Application Number: PCT/US97/07657 (22) International Filing Date: 5 May 1997 (05.05.97) (30) Priority Data: 08/705,484 29 August 1996 (29.08.96) US 08/743,699 6 November 1996 (06.11.96) US PCT/US96/18003 6 November 1996 (06.11.96) WO (34) Countries for which the regional or international application was filed: KE et al. (71) Applicants: DOWELANCO [US/US]; 9330 Zionsville Road, Indianapolis, IN 46268-1054 (US). WISCONSIN ALUMNI RESEARCH FOUNDATION [US/US]; 614 North Walnut Street, P.O. Box 7365, Madison, WI 53707-7365 (US).		(72) Inventors: ENSIGN, Jerald, C.; 1810 Camelot Drive, Madison, WI 53705 (US). BOWEN, David, J.; 5668 Highway A, Oregon, WI 53575 (US). PETELL, James; 1427 Hunters Glen, Zionsville, IN 46077 (US). FATIG, Raymond; 30 Clay Court, Zionsville, IN 46077 (US). SCHOONOVER, Sue; 7142 Marstella, Brownsburg, IN 46112 (US). FFRENCH-CONSTANT, Richard, H.; 1006 University Bay Drive, Madison, WI 53705 (US). ROCHELEAU, Thomas, A.; 3100 Buena Vista Street, Madison, WI 53704 (US). BLACKBURN, Michael, B.; 2127 Luann Lane, Madison, WI 53713 (US). HEY, Timothy, D.; 1653 Catalina Way, Zionsville, IN 46077 (US). MERLO, Donald, J.; 11845 Durbin Drive, Carmel, IN 46032 (US). ORR, Gregory, L.; 1028 Saratoga Circle, Indianapolis, IN 46280 (US). ROBERTS, Jean, L.; 26035 State Road 19, Arcadia, IN 46030 (US). STRICKLAND, James, A.; 780 Mt. Zion Road, Lebanon, IN 46052 (US). GUO, Lining; 7 Nelson Circle, Brownsburg, IN 46112 (US). CICHE, Todd, A.; 1609 Chadbourne Avenue, Madison, WI 53705 (US). SUKHAPINDA, Kitisri; 4748 Ashwood Court, Zionsville, IN 46077 (US). (74) Agent: BORUCKI, Andrea, T.; DowElanco, 9330 Zionsville Road, Indianapolis, IN 46268-1054 (US). (81) Designated States: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, UZ, VN, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i>
(54) Title: INSECTICIDAL PROTEIN TOXINS FROM <i>PHOTORHABDUS</i> (57) Abstract Proteins from the genus <i>Photorhabdus</i> are toxic to insects upon exposure. <i>Photorhabdus luminescens</i> (formerly <i>Xenorhabdus luminescens</i>) have been found in mammalian clinical samples and as a bacterial symbiont of entomopathogenic nematodes of genus <i>Heterorhabditis</i> . These protein toxins can be applied to, or genetically engineered into, insect larvae food and plants for insect control.		

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INSECTICIDAL PROTEIN TOXINS FROM PHOTORHABDUS

Cross-reference to Related Application

5 This patent application is a continuation-in-part of U.S. Patent Application Serial Number 08/743,699 filed on November 6, 1996, which is a continuation-in-part of U.S. Patent Application Serial Number 08/705,484 filed on August 28, 1996, which is a continuation-in-part of U.S. Patent Application Serial
10 Number 08/608,423 filed February 28, 1996, which is a continuation-in-part of U.S. Patent Application Serial Number 08/395,947 filed February 28, 1995, which was a continuation-in-part of U.S. Patent Application Serial Number 08/063,615 filed May 18, 1993. This application is also a continuation-in-part of provisional U.S.
15 Patent Application Serial Number 60/007,255 filed November 6, 1995.

Field of the Invention

20 The present invention relates to toxins isolated from bacteria and the use of said toxins as insecticides.

Background of the Invention

25 Many insects are widely regarded as pests to homeowners, to picnickers, to gardeners, and to farmers and others whose investments in agricultural products are often destroyed or diminished as a result of insect damage to field crops. Particularly in areas where the growing season is short, significant insect damage can mean the loss of all profits to
30 growers and a dramatic decrease in crop yield. Scarce supply of particular agricultural products invariably results in higher costs to food processors and, then, to the ultimate consumers of food plants and products derived from those plants.

35 Preventing insect damage to crops and flowers and eliminating the nuisance of insect pests have typically relied on strong organic pesticides and insecticides with broad toxicities. These synthetic products have come under attack by the general population as being too harsh on the environment and on those exposed to such agents. Similarly in non-agricultural settings, homeowners would
40 be satisfied to have insects avoid their homes or outdoor meals without needing to kill the insects.

The extensive use of chemical insecticides has raised environmental and health concerns for farmers, companies that

produce the insecticides, government agencies, public interest groups, and the public in general. The development of less intrusive pest management strategies has been spurred along both by societal concern for the environment and by the development of biological tools which exploit mechanisms of insect management. Biological control agents present a promising alternative to chemical insecticides.

Organisms at every evolutionary development level have devised means to enhance their own success and survival. The use of biological molecules as tools of defense and aggression is known throughout the animal and plant kingdoms. In addition, the relatively new tools of the genetic engineer allow modifications to biological insecticides to accomplish particular solutions to particular problems.

One such agent, *Bacillus thuringiensis* (Bt), is an effective insecticidal agent, and is widely commercially used as such. In fact, the insecticidal agent of the Bt bacterium is a protein which has such limited toxicity, it can be used on human food crops on the day of harvest. To non-targeted organisms, the Bt toxin is a digestible non-toxic protein.

Another known class of biological insect control agents are certain genera of nematodes known to be vectors of transmission for insect-killing bacterial symbionts. Nematodes containing insecticidal bacteria invade insect larvae. The bacteria then kill the larvae. The nematodes reproduce in the larval cadaver. The nematode progeny then eat the cadaver from within. The bacteria-containing nematode progeny thus produced can then invade additional larvae.

In the past, insecticidal nematodes in the *Steinernema* and *Heterorhabditis* genera were used as insect control agents. Apparently, each genus of nematode hosts a particular species of bacterium. In nematodes of the *Heterorhabditis* genus, the symbiotic bacterium is *Photorhabdus luminescens*.

Although these nematodes are effective insect control agents, it is presently difficult, expensive, and inefficient to produce, maintain, and distribute nematodes for insect control.

It has been known in the art that one may isolate an insecticidal toxin from *Photorhabdus luminescens* that has activity only when injected into Lepidopteran and Coleopteran insect larvae. This has made it impossible to effectively exploit the insecticidal properties of the nematode or its bacterial symbiont. What would be useful would be a more practical, less labor-intensive wide-area delivery method of an insecticidal toxin which would retain its

biological properties after delivery. It would be quite desirable to discover toxins with oral activity produced by the genus *Photorhabdus*. The isolation and use of these toxins are desirable due to efficacious reasons. Until applicants' discoveries, these toxins had not been isolated or characterized.

Summary of the Invention

The native toxins are protein complexes that are produced and secreted by growing bacteria cells of the genus *Photorhabdus*, of interest are the proteins produced by the species *Photorhabdus luminescens*. The protein complexes, with a molecular size of approximately 1,000 kDa, can be separated by SDS-PAGE gel analysis into numerous component proteins. The toxins contain no hemolysin, lipase, type C phospholipase, or nuclease activities. The toxins exhibit significant toxicity upon exposure administration to a number of insects.

The present invention provides an easily administered insecticidal protein as well as the expression of toxin in a heterologous system.

The present invention also provides a method for delivering insecticidal toxins that are functional active and effective against many orders of insects.

Objects, advantages, and features of the present invention will become apparent from the following specification.

Brief Description of the Drawings

Fig. 1 is an illustration of a match of cloned DNA isolates used as a part of sequence genes for the toxin of the present invention.

Fig. 2 is a map of three plasmids used in the sequencing process.

Fig. 3 is a map illustrating the inter-relationship of several partial DNA fragments.

Fig. 4 is an illustration of a homology analysis between the protein sequences of TcbA_{ij} and TcaB_{ij} proteins.

Fig. 5 is a phenogram of *Photorhabdus* strains. Relationship of *Photorhabdus* Strains was defined by rep-PCR.

The upper axis of Fig. 5 measures the percentage similarity of strains based on scoring of rep-PCR products (i.e., 0.0 [no similarity] to 1.0 [100% similarity]). At the right axis, the numbers and letters indicate the various strains tested; 14=W-14,

Hm=Hm, H9=H9, WX-7, 1=WX-1, 2=WX-2, 88=HP88, NC-1=NC-1, 4=WX-4, 9=WX-9, 8=WX-8, 10=WX-10, WIR=WIR, 3=WX-3, 11=WX-11, 5=WX-5, 6=WX-6, 12=WX-12, 14=WX-14, 15=WX-15, Hb=Hb, B2=B2, 48 through 52=ATCC 43948 through ATCC 43952. Vertical lines separating horizontal lines indicate the degree of relatedness (as read from the extrapolated intersection of the vertical line with the upper axis) between strains or groups of strains at the base of the horizontal lines (e.g., strain W-14 is approximately 60% similar to strains H9 and Hm).

Fig. 6 is an illustration of the genomic maps of the W-14 Strain.

Fig. 6A is an illustration of the tca and tcb loci and primary gene products.

Fig. 7 is a phenogram of *Photothabdus* strains as defined by rep-PCR. The upper axis of Fig. 7 measures the percentage similarity of strains based on scoring of rep-PCR products (i.e., 0.0 [no similarity] to 1.0 [100% similarity]). At the right axis, the numbers and letters indicate the various strains tested. Vertical lines separating horizontal lines indicate the degree of relatedness (as read from the extrapolated intersection of the vertical line with the upper axis) between strains or groups of strains at the base of the horizontal lines (e.g., strain Indicis is approximately 30% similar to strains MP1 and HB Oswego). Note that the *Photothabdus* strains on the phenogram are as follows: 14 = W-14; Hm = Hm; H9 = H9; 7 = WX-7; 1 = WX-1; 2 = WX-2; 88 = HP88; NC1 = NC-1; 4 = WX-4; 9 = WX-9; 8 = WX-8; 10 = WX-10; 30 = W30; WIR = WIR; 3 = WX-3; 11 = WX-11; 5 = WX-5; 6 = WX-6; 12 = WX-12; 15 = WX-15; 14 = WX-14; Hb = Hb; B2 = B2; 48 = ATCC 43948; 49 = ATCC 43949; 50 = ATCC 43950; 51 = ATCC 43951; 52 = ATCC 43952.

Detailed Description of the Invention

The present inventions are directed to the discovery of a unique class of insecticidal protein toxins from the genus *Photothabdus* that have oral toxicity against insects. A unique feature of *Photothabdus* is its bioluminescence. *Photothabdus* may be isolated from a variety of sources. One such source is nematodes, more particularly nematodes of the genus *Heterorhabditis*. Another such source is from human clinical samples from wounds, see Farmer et al. 1989 J. Clin. Microbiol. 27

pp. 1594-1600. These saprophytic strains are deposited in the American Type Culture Collection (Rockville, MD) ATCC #s 43948, 43949, 43950, 43951, and 43952, and are incorporated herein by reference. It is possible that other sources could harbor
5 *Photorhabdus* bacteria that produce insecticidal toxins. Such sources in the environment could be either terrestrial or aquatic based.

The genus *Photorhabdus* is taxonomically defined as a member of the Family *Enterobacteriaceae*, although it has certain traits
10 atypical of this family. For example, strains of this genus are nitrate reduction negative, yellow and red pigment producing and bioluminescent. This latter trait is otherwise unknown within the *Enterobacteriaceae*. *Photorhabdus* has only recently been described as a genus separate from the *Xenorhabdus* (Boemare et al., 1993 Int.
15 J. Syst. Bacteriol. 43, 249-255). This differentiation is based on DNA-DNA hybridization studies, phenotypic differences (e.g., presence (*Photorhabdus*) or absence (*Xenorhabdus*) of catalase and bioluminescence) and the Family of the nematode host (*Xenorhabdus*; *Steinernematidae*, *Photorhabdus*; *Heterorhabditidae*). Comparative,
20 cellular fatty-acid analyses (Janse et al. 1990, Lett. Appl. Microbiol 10, 131-135; Suzuki et al. 1990, J. Gen. Appl. Microbiol., 36, 393-401) support the separation of *Photorhabdus* from *Xenorhabdus*.

In order to establish that the strain collection disclosed
25 herein was comprised of *Photorhabdus* strains, the strains were characterized based on recognized traits which define *Photorhabdus* and differentiate it from other *Enterobacteriaceae* and *Xenorhabdus* species. (Farmer, 1984 Bergey's Manual of Systemic Bacteriology Vol. 1 pp.510-511; Akhurst and Boemare 1988, J. Gen. Microbiol. 134
30 pp. 1835-1845; Boemare et al. 1993 Int. J. Syst. Bacteriol. 43 pp. 249-255, which are incorporated herein by reference). The traits studied were the following: gram stain negative rods, organism size, colony pigmentation, inclusion bodies, presence of catalase, ability to reduce nitrate, bioluminescence, dye uptake,
35 gelatin hydrolysis, growth on selective media, growth temperature, survival under anerobic conditions and motility. Fatty acid analysis was used to confirm that the strains herein all belong to the single genus *Photorhabdus*.

Currently, the bacterial genus *Photorhabdus* is comprised of a
40 single defined species, *Photorhabdus luminescens* (ATCC Type strain #29999, Poinar et al., 1977, Nematologica 23, 97-102). A variety of related strains have been described in the literature (e.g., Akhurst et al. 1988 J. Gen. Microbiol., 134, 1835-1845; Boemare

et al. 1993 *Int. J. Syst. Bacteriol.* 43 pp. 249-255; Putz et al. 1990, *Appl. Environ. Microbiol.*, 56, 181-186). Numerous *Photorhabdus* strains have been characterized herein. Because there is currently only one species (*luminescens*) defined within the genus *Photorhabdus*, the *luminescens* species traits were used to characterize the strains herein. As can be seen in Fig. 5, these strains are quite diverse. It is not unforeseen that in the future there may be other *Photorhabdus* species that will have some of the attributes of the *luminescens* species as well as some different characteristics that are presently not defined as a trait of *Photorhabdus luminescens*. However, the scope of the invention herein is to any *Photorhabdus* species or strains which produce proteins that have functional activity as insect control agents, regardless of other traits and characteristics.

Furthermore, as is demonstrated herein, the bacteria of the genus *Photorhabdus* produce proteins that have functional activity as defined herein. Of particular interest are proteins produced by the species *Photorhabdus luminescens*. The inventions herein should in no way be limited to the strains which are disclosed herein. These strains illustrate for the first time that proteins produced by diverse isolates of *Photorhabdus* are toxic upon exposure to insects. Thus, included within the inventions described herein are the strains specified herein and any mutants thereof, as well as any strains or species of the genus *Photorhabdus* that have the functional activity described herein.

There are several terms that are used herein that have a particular meaning and are as follows:

By "functional activity" it is meant herein that the protein toxin(s) function as insect control agents in that the proteins are orally active, or have a toxic effect, or are able to disrupt or deter feeding, which may or may not cause death of the insect. When an insect comes into contact with an effective amount of toxin delivered via transgenic plant expression, formulated protein compositions(s), sprayable protein composition(s), a bait matrix or other delivery system, the results are typically death of the insect, or the insects do not feed upon the source which makes the toxins available to the insects.

By the use of the term "genetic material" herein, it is meant to include all genes, nucleic acid, DNA and RNA.

By "homolog" it is meant an amino acid sequence that is identified as possessing homology to a reference W-14 toxin polypeptide amino acid sequence.

5 By "homology" it is meant an amino acid sequence that has a similarity index of at least 33% and/or an identity index of at least 26% to a reference W-14 toxin polypeptide amino acid sequence, as scored by the GAP algorithm using the B10sum 62 protein scoring matrix (Wisconsin Package Version 9.0, Genetics Computer Group
10 (GCG), Madison, WI).

By "identity" is meant an amino acid sequence that contains an identical residue at a given position, following alignment with a reference W-14 toxin polypeptide amino acid sequence by the GAP
15 algorithm.

The protein toxins discussed herein are typically referred to as "insecticides". By insecticides it is meant herein that the protein toxins have a "functional activity" as further defined
20 herein and are used as insect control agents.

By the use of the term "oligonucleotides" it is meant a macromolecule consisting of a short chain of nucleotides of either RNA or DNA. Such length could be at least one nucleotide, but
25 typically are in the range of about 10 to about 12 nucleotides. The determination of the length of the oligonucleotide is well within the skill of an artisan and should not be a limitation herein. Therefore, oligonucleotides may be less than 10 or greater than 12.

30 By the use of the term "Photorhabdus toxin" it is meant any protein produced by a *Photorhabdus* microorganism strain which has functional activity against insects, where the *Photorhabdus* toxin could be formulated as a sprayable composition, expressed by a
35 transgenic plant, formulated as a bait matrix, delivered via baculovirus, or delivered by any other applicable host or delivery system.

40 By the use of the term "toxic" or "toxicity" as used herein it is meant that the toxins produced by *Photorhabdus* have "functional activity" as defined herein.

By "truncated peptide" it is meant herein to include any peptide that is fragment(s) of the peptides observed to have functional activity.

- 5 By "substantial sequence homology" is meant either: a DNA fragment having a nucleotide sequence sufficiently similar to another DNA fragment to produce a protein having similar biochemical properties; or a polypeptide having an amino acid sequence sufficiently similar to another polypeptide to exhibit similar biochemical properties.

10

Fermentation broths from selected strains reported in Table 20 were used to determine the following: breadth of insecticidal toxin production by the *Photorhabdus* genus, the insecticidal spectrum of these toxins, and to provide source material to purify the toxin complexes. The strains characterized herein have been shown to have oral toxicity against a variety of insect orders. Such insect orders include but are not limited to *Coleoptera*, *Homoptera*, *Lepidoptera*, *Diptera*, *Acarina*, *Hymenoptera* and *Dictyoptera*.

20

As with other bacterial toxins, the rate of mutation of the bacteria in a population causes many related toxins slightly different in sequence to exist. Toxins of interest here are those which produce protein complexes toxic to a variety of insects upon exposure, as described herein. Preferably, the toxins are active against *Lepidoptera*, *Coleoptera*, *Homoptera*, *Diptera*, *Hymenoptera*, *Dictyoptera* and *Acarina*. The inventions herein are intended to capture the protein toxins homologous to protein toxins produced by the strains herein and any derivative strains thereof, as well as any protein toxins produced by *Photorhabdus*. These homologous proteins may differ in sequence, but do not differ in function from those toxins described herein. Homologous toxins are meant to include protein complexes of between 300 kDa to 2,000 kDa and are comprised of at least two (2) subunits, where a subunit is a peptide which may or may not be the same as the other subunit.

30

Various protein subunits have been identified and are taught in the Examples herein. Typically, the protein subunits are between about 18 kDa to about 230 kDa; between about 160 kDa to about 230 kDa; 100 kDa to 160 kDa; about 80 kDa to about 100 kDa; and about 50 kDa to about 80 kDa.

40

As discussed above, some *Photorhabdus* strains can be isolated from nematodes. Some nematodes, elongated cylindrical parasitic worms of the phylum *Nematoda*, have evolved an ability to exploit insect larvae as a favored growth environment. The insect larvae

provide a source of food for growing nematodes and an environment in which to reproduce. One dramatic effect that follows invasion of larvae by certain nematodes is larval death. Larval death results from the presence of, in certain nematodes, bacteria that produce an insecticidal toxin which arrests larval growth and inhibits feeding activity.

Interestingly, it appears that each genus of insect parasitic nematode hosts a particular species of bacterium, uniquely adapted for symbiotic growth with that nematode. In the interim since this research was initiated, the name of the bacterial genus *Xenorhabdus* was reclassified into the *Xenorhabdus* and the *Photorhabdus*. Bacteria of the genus *Photorhabdus* are characterized as being symbionts of *Heterorhabditus* nematodes while *Xenorhabdus* species are symbionts of the *Steinernema* species. This change in nomenclature is reflected in this specification, but in no way should a change in nomenclature alter the scope of the inventions described herein.

The peptides and genes that are disclosed herein are named according to the guidelines recently published in the Journal of Bacteriology "Instructions to Authors" p. i-xii (Jan. 1996), which is incorporated herein by reference. The following peptides and genes were isolated from *Photorhabdus* strain W-14.

Table 1
Peptide/Gene Nomenclature
Toxin Complex

1 Peptide Name	2 Peptide Sequence ID No.*	3 Gene Name	4 Gene Sequence ID No.*
<u>tca genomic region</u>			
TcaA	34 ^c	tcaA	33
TcaA _i	pro-peptide	tcaA	-
TcaA _{ii}	[15] ^a , 34 ^c	tcaA	-
TcaA _{iii}	[4] ^a , 35 ^c	tcaA	-
TcaA _{iv}	[62] ^a	tcaA	-
TcaB	[3] ^a , (19, 20) ^b , 26 ^c	tcaB	25
TcaB _i	[3] ^a , (19, 20) ^b , 28 ^c	tcaB	27
TcaB _{ii}	[5] ^a , 30 ^c	tcaB	29
TcaC	[2] ^a , 32 ^c	tcaC	31
<u>tcb genomic region</u>			
TcbA	12 ^c , [16] ^a , (21, 22, 23, 24) ^b	tcbA	11
TcbA _i	pro-peptide	tcbA	-
TcbA _{ii}	[1] ^a , (21, 22, 23, 24) ^b , 53 ^c	tcbA	52
TcbA _{iii}	[40] ^a , 55 ^c	tcbA	54
<u>tcc genomic region</u>			
TccA	[8] ^a , 57 ^c	tccA	56
TccB	[7] ^a , 59 ^c	tccB	58
TccC	61 ^c	tccC	60
<u>tcd genomic region</u>			
TcdA	(17, 18, 37, 38, 39, 42, 43) ^b , 47 ^c	tcdA	(36) ^d , 46
TcdA _i	pro-peptide	tcdA	-
TcdA _{ii}	[13] ^a , (17, 18, 37, 38, 39) ^b , 49 ^c	tcdA	48
TcdA _{iii}	[41] ^a , (42, 43) ^b , 51 ^c	tcdA	50
TcdB	[14] ^a	tcdB	-

^aSequence ID No.'s in brackets are peptide N-termini;

^bNumbers in parentheses are N-termini of internal peptide tryptic fragments

^cdeduced from gene sequence

^dinternal gene fragment

The sequences listed above are grouped by genomic region. More specifically, the *Photorhabdus luminescence* bacteria (W-14) has at least four distinct genomic regions- tca, tcb, tcc and tcd. As can be seen in Table 1, peptide products are produced from these distinct genomic regions. Furthermore, as illustrated in the Examples, specifically Examples 15 and 21, individual gene products produced from three genomic regions are associated with insect activity. There is also considerable homology between these four genomic regions.

As is further illustrated in the Examples, the *tcbA* gene was expressed in *E. coli* as two possible biological active protein fragments (*TcbA* and *TcbA_{ii/iii}*). The *tcdA* gene was also expressed in *E. coli*. As illustrated in Example 16, when the native unprocessed *TcbA* toxin was treated with the endogeneous metalloproteases or insect gut contents containing proteases, the *TcbA* protein toxin was processed into smaller subunits that were less than the size of the native peptides and Southern Corn Rootworm activity increased. The smaller toxin peptides remained associated as part of a toxin complex. It may be desirable in some situations to increase activation of the toxin(s) by proteolytic processing or using truncated peptides. Thus, it may be more desirable to use truncated peptide(s) in some applications, i.e., commercial transgenic plant applications.

In addition to the W-14 strain, there are other species within the *Photorhabdus* genus that have functional activity which is differential (specifically see Tables 20 and 36). Even though there is differential activity, the amino acid sequences in some cases have substantial sequence homology. Moreover, the molecular probes indicate that some genes contained in the strains are homologous to the genes contained in the W-14 strain. In fact all of the strains illustrated herein have one or more homologs of W-14 toxin genes. The antibody data in Example 26 and the N-terminal sequence data in Example 25 further support the conclusion that there is homology and identity (based on amino acid sequence) between the protein toxin(s) produced by these strains. At the molecular level, the W-14 gene probes indicated that the homologs or the W-14 genes themselves (Tables 37, 38, and 39) are dispersed throughout the *Photorhabdus* genus. Further, it is possible that new toxin genes exist in other strains which are not homologous to W-14, but maintain overall protein attributes (see specifically Examples 14 and 25).

Even though there is homology or identity between toxin genes produced by the *Photorhabdus* strains, the strains themselves are quite diverse. Using polymerase chain reaction technology further discussed in Example 22, most of the strains illustrated herein are quite distinguishable. For example as can be seen in Figs. 5, the percentage relative similarity of some of the strains, such as HP88 and NC-1, was about 0.8, which indicates that the strains are similar, while HP88 and Hb was about 0.1, which indicates substantial diversity. Therefore, even though the insect toxin genes or gene products that the strains produce are the same or similar, the strains themselves are diverse.

In view of the data further disclosed in the Examples and discussions herein, it is clear that a new and unique family of insecticidal protein toxin(s) has been discovered. It has been further illustrated herein that these toxin(s) widely exist within bacterial strains of the *Photorhabdus* genus. It may also be the case that these toxin genes widely exist within the family *Enterobacteraceae*. Antibodies prepared as described in Example 21 or gene probes prepared as described in Example 25 may be used to further screen for bacterial strains within the family *Enterobacteraceae* that produce the homologous toxin(s) that have functional activity. It may also be the case that specific primer sets exist that could facilitate the identification of new genes within the *Photorhabdus* genus or family *Enterobacteraceae*.

As stated above, the antibodies may be used to rapidly screen bacteria of the genus *Photorhabdus* or the family *Enterobacteraceae* for homologous toxin products as illustrated in Example 26. Those skilled in the art are quite familiar with the use of antibodies as an analysis or screening tool (see US Patent No. 5,430,137, which is incorporated herein by reference). Moreover, it is generally accepted in the literature that antibodies are elicited against 6 to 20 amino acid residue segments that tend to occupy exposed surface of polypeptides (Current Protocols in Immunology, Coligan et al, National Institutes of Health, John Wiley & Sons, Inc.). Usually the amino acid consist of contiguous amino acid residues, however, in certain cases they may be formed by non-contiguous amino acids that are constrained by specific conformation. The amino acid segments recognized by antibodies are highly specific and commonly referred to epitopes. The amino acid fragment can be generated by chemical and/or enzymatic cleavage of the native protein, by automated, solid-phase peptide synthesis, or by production from genetic engineering organisms. Polypeptide fragments can be isolated by a variety and/or combination of HPLC and FPLC chromatographic methods known in the art. Selection of polypeptide fragment can be aided by the use of algorithms, for example Kyte and Doolittle, 1982, Journal of Molecular Biology 157: 105-132 and Chou and Fasman, 1974, Biochemistry 13: 222-245, that predict those sequences most likely to exposed on the surface of the protein. For preparation of immunogen containing the polypeptide fragment of interest, in general, polypeptides are covalently coupled using chemical reactions to carrier proteins such as keyhole limpet hemocyanin via free amino (lysine), sulfhydryl (cysteine), phenolic (tyrosine) or carboxylic (aspartate or glutamate) groups. Immunogen with an adjuvant is injected in animals, such as mice or rabbits, or

chickens to elicit an immune response against the immunogen. Analysis of antibody titer in antisera of inject animals against polypeptide fragment can be determined by a variety of immunological methods such as ELISA and Western blot. Alternatively, monoclonal antibodies can be prepared using spleen cells of the injected animal for fusion with tumor cells to produce immortalized hybridomas cells producing a single antibody species. Hybridomas cells are screened using immunological methods to select lines that produce a specific antibody to the polypeptide fragment of interest. Purification of antibodies from different sources can be performed by a variety of chromatographic HPLC or FPLC methods.

The toxins described herein are quite unique in that the toxins have functional activity, which is key to developing an insect management strategy, it is possible to delay or circumvent the protein degradation process by injecting a protein directly into an organism, avoiding its digestive tract. In such cases, the protein administered, non-specifically degraded, or eliminated by the immune system in higher organisms. Injection into insects of an insecticidal toxin has potential application only in the laboratory, and then only on large insects which are easily injected. The observation that the insecticidal protein toxins herein described exhibits their toxic activity after oral ingestion or contact with the toxins permits the development of an insect management plan based solely on the ability to incorporate the protein toxins into the insect diet. Such a plan could result in the production of insect baits.

The *Photobacterium* toxins may be administered to insects in a purified form. The toxins may also be delivered in amounts from about 1 to about 100 mg / liter of broth. This may vary upon formulation condition, conditions of the inoculum source, techniques for isolation of the toxin, and the like. The toxins may be administered as an exudate secretion or cellular protein host. Bacteria are typically the hosts in which proteins are expressed. Eukaryotic hosts could include but are not limited to plants, insects and yeast. Alternatively, the toxins may be produced in bacteria or transgenic plants in the field or in the insect by a baculovirus vector. Typically the toxins will be introduced to the insect by incorporating one or more of the toxins into the insects' feed.

Complete lethality to feeding insects is useful but is not required to achieve useful toxicity. If the insects avoid the toxin or cease feeding, that avoidance will be useful in some applications, even if the effects are sublethal. For example, if insect resistant transgenic crop plants are desired, a reluctance of insects to feed on the plants is as useful as lethal toxicity to the insects since the ultimate objective is protection of the plants rather than killing the insect.

There are many other ways in which toxins can be incorporated into an insect's diet. As an example, it is possible to adulterate the larval food source with the toxic protein by spraying the food with a protein solution, as disclosed herein. Alternatively, the purified protein could be genetically engineered into an otherwise harmless bacterium, which could then be grown in culture, and either applied to the food source or allowed to reside in the soil in an area in which insect eradication was desirable. Also, the protein could be genetically engineered directly into an insect food source. For instance, the major food source of many insect larvae is plant material.

By incorporating genetic material that encodes the insecticidal properties of the *Photobacterium* toxins into the genome of a plant eaten by a particular insect pest, the adult or larvae would die after consuming the food plant. Numerous members of the monocotyledonous and dictyledenous genera have been transformed. Transgenic agronomic crops as well as fruits and vegetables are of commercial interest. Such crops include but are not limited to maize, rice, soybeans, canola, sunflower, alfalfa, sorghum, wheat, cotton, peanuts, tomatoes, potatoes, and the like. Several techniques exist for introducing foreign genetic material into plant cells, and for obtaining plants that stably maintain and express the introduced gene. Such techniques include acceleration of genetic material coated onto microparticles directly into cells (U.S. Patents 4,945,050 to Cornell and 5,141,131 to DowElanco). Plants may be transformed using *Agrobacterium* technology, see U.S. Patent 5,177,010 to University of Toledo, 5,104,310 to Texas A&M, European Patent Application 0131624B1, European Patent Applications 120516, 159418B1 and 176,112 to Schilperoot, U.S. Patents 5,149,645, 5,469,976, 5,464,763 and 4,940,838 and 4,693,976 to Schilperoot, European Patent Applications 116718, 290799, 320500 all to MaxPlanck, European Patent Applications 604662 and 627752 to Japan Tobacco, European Patent Applications 0267159, and 0292435 and U.S. Patent 5,231,019 all to Ciba Geigy, U.S. Patents 5,463,174 and 4,762,785 both to Calgene, and U.S. Patents 5,004,863 and

5,159,135 both to Agriacetus. Other transformation technology includes whiskers technology, see U.S. Patents 5,302,523 and 5,464,765 both to Zeneca. Electroporation technology has also been used to transform plants, see WO 87/06614 to Boyce Thompson Institute, 5,472,869 and 5,384,253 both to Dekalb, WO9209696 and WO9321335 both to PGS. All of these transformation patents and publications are incorporated by reference. In addition to numerous technologies for transforming plants, the type of tissue which is contacted with the foreign genes may vary as well. Such tissue would include but would not be limited to embryogenic tissue, callus tissue type I and II, hypocotyl, meristem, and the like. Almost all plant tissues may be transformed during dedifferentiation using appropriate techniques within the skill of an artisan.

Another variable is the choice of a selectable marker. The preference for a particular marker is at the discretion of the artisan, but any of the following selectable markers may be used along with any other gene not listed herein which could function as a selectable marker. Such selectable markers include but are not limited to aminoglycoside phosphotransferase gene of transposon Tn5 (Aph II) which encodes resistance to the antibiotics kanamycin, neomycin and G418, as well as those genes which code for resistance or tolerance to glyphosate; hygromycin; methotrexate; phosphinothricin (bialaphos); imidazolinones, sulfonylureas and triazolopyrimidine herbicides, such as chlorosulfuron; bromoxynil, dalapon and the like.

In addition to a selectable marker, it may be desirable to use a reporter gene. In some instances a reporter gene may be used without a selectable marker. Reporter genes are genes which are typically not present or expressed in the recipient organism or tissue. The reporter gene typically encodes for a protein which provides for some phenotypic change or enzymatic property. Examples of such genes are provided in K. Weising et al. Ann. Rev. Genetics, 22, 421 (1988), which is incorporated herein by reference. A preferred reporter gene is the glucuronidase (GUS) gene.

Regardless of transformation technique, the gene is preferably incorporated into a gene transfer vector adapted to express the *Photorhabdus* toxins in the plant cell by including in the vector a plant promoter. In addition to plant promoters, promoters from a variety of sources can be used efficiently in plant cells to express foreign genes. For example, promoters of bacterial origin, such as the octopine synthase promoter, the nopaline synthase

promoter, the mannopine synthase promoter; promoters of viral origin, such as the cauliflower mosaic virus (35S and 19S), reengineered 35S, known as 35T (see PCT/US96/16582, WO 97/13402 published April 17, 1997, which is incorporated herein by reference) and the like may be used. Plant promoters include, but are not limited to ribulose-1,6-bisphosphate (RUBP) carboxylase small subunit (ssu), beta-conglycinin promoter, phaseolin promoter, ADH promoter, heat-shock promoters and tissue specific promoters. Promoters may also contain certain enhancer sequence elements that may improve the transcription efficiency. Typical enhancers include but are not limited to Adh-intron 1 and Adh-intron 6. Constitutive promoters may be used. Constitutive promoters direct continuous gene expression in all cells types and at all times (e.g., actin, ubiquitin, CaMV 35S). Tissue specific promoters are responsible for gene expression in specific cell or tissue types, such as the leaves or seeds (e.g., zein, oleosin, napin, ACP) and these promoters may also be used. Promoters may also be active during a certain stage of the plants' development as well as active in plant tissues and organs. Examples of such promoters include but are not limited to pollen-specific, embryo specific, corn silk specific, cotton fiber specific, root specific, seed endosperm specific promoters and the like.

Under certain circumstances it may be desirable to use an inducible promoter. An inducible promoter is responsible for expression of genes in response to a specific signal, such as: physical stimulus (heat shock genes); light (RUBP carboxylase); hormone (Em); metabolites; and stress. Other desirable transcription and translation elements that function in plants may be used. Numerous plant-specific gene transfer vectors are known to the art.

In addition, it is known that to obtain high expression of bacterial genes in plants it is preferred to reengineer the bacterial genes so that they are more efficiently expressed in the cytoplasm of plants. Maize is one such plant where it is preferred to reengineer the bacterial gene(s) prior to transformation to increase the expression level of the toxin in the plant. One reason for the reengineering is the very low G+C content of the native bacterial gene(s) (and consequent skewing towards high A+T content). This results in the generation of sequences mimicking or duplicating plant gene control sequences that are known to be highly A+T rich. The presence of some A+T-rich sequences within the DNA of the gene(s) introduced into plants (e.g., TATA box regions normally found in gene promoters) may result in aberrant

transcription of the gene(s). On the other hand, the presence of other regulatory sequences residing in the transcribed mRNA (e.g., polyadenylation signal sequences (AAUAAA), or sequences complementary to small nuclear RNAs involved in pre-mRNA splicing) may lead to RNA instability. Therefore, one goal in the design of reengineered bacterial gene(s), more preferably referred to as plant optimized gene(s), is to generate a DNA sequence having a higher G+C content, and preferably one close to that of plant genes coding for metabolic enzymes. Another goal in the design of the plant optimized gene(s) is to generate a DNA sequence that not only has a higher G+C content, but by modifying the sequence changes, should be made so as to not hinder translation.

An example of a plant that has a high G+C content is maize. The table below illustrates how high the G+C content is in maize. As in maize, it is thought that G+C content in other plants is also high.

Table 2
Compilation of G+C Contents of Protein Coding Regions
of Maize Genes

Protein Class ^a	Range %G+C	Mean %G+C ^b
Metabolic Enzymes (40)	44.4-75.3	59.0 (8.0)
Storage Proteins		
Group I (23)	46.0-51.9	48.1 (1.3)
Group II (13)	60.4-74.3	67.5 (3.2)
Group I + II (36)	46.0-74.3	55.1 (9.6) ^c
Structural Proteins (18)	48.6-70.5	63.6 (6.7)
Regulatory Proteins (5)	57.2-68.9	62.0 (4.9)
Uncharacterized Proteins (9)	41.5-70.3	64.3 (7.2)
All Proteins (108)	44.4-75.3	60.8 (5.2)

^a Number of genes in class given in parentheses.

^b Standard deviations given in parentheses.

^c Combined groups mean ignored in calculation of overall mean.

For the data in Table 2, coding regions of the genes were extracted from GenBank (Release 71) entries, and base compositions were calculated using the MacVector™ program (IBI, New Haven, CT). Intron sequences were ignored in the calculations. Group I and II storage protein gene sequences were distinguished by their marked difference in base composition.

Due to the plasticity afforded by the redundancy of the genetic code (i.e., some amino acids are specified by more than one codon), evolution of the genomes of different organisms or classes or organisms has resulted in differential usage of redundant codons. This "codon bias" is reflected in the mean base composition of protein coding regions. For example, organisms with relatively low G+C contents utilize codons having A or T in the third position of redundant codons, whereas those having higher G+C contents utilize codons having G or C in the third position. It is thought that the presence of "minor" codons within a gene's mRNA may reduce the absolute translation rate of that mRNA, especially when the relative abundance of the charged tRNA corresponding to the minor codon is low. An extension of this is that the diminution of translation rate by individual minor codons would be at least additive for multiple minor codons. Therefore, mRNAs having high relative contents of minor codons would have correspondingly low translation rates. This rate would be reflected by the synthesis of low levels of the encoded protein.

In order to reengineer the bacterial gene(s), the codon bias of the plant is determined. The codon bias is the statistical codon distribution that the plant uses for coding its proteins. After determining the bias, the percent frequency of the codons in the gene(s) of interest is determined. The primary codons preferred by the plant should be determined as well as the second and third choice of preferred codons. The amino acid sequence of the protein of interest is reverse translated so that the resulting nucleic acid sequence codes for the same protein as the native bacterial gene, but the resulting nucleic acid sequence corresponds to the first preferred codons of the desired plant. The new sequence is analyzed for restriction enzyme sites that might have been created by the modification. The identified sites are further modified by replacing the codons with second or third choice preferred codons. Other sites in the sequence which could affect the transcription or translation of the gene of interest are the exon:intron 5' or 3' junctions, poly A addition signals, or RNA polymerase termination signals. The sequence is further analyzed and modified to reduce the frequency of TA or GC doublets. In

addition to the doublets, G or C sequence blocks that have more than about four residues that are the same can affect transcription of the sequence. Therefore, these blocks are also modified by replacing the codons of first or second choice, etc. with the next preferred codon of choice. It is preferred that the plant optimized gene(s) contains about 63% of first choice codons, between about 22% to about 37% second choice codons, and between 15% and 0% third choice codons, wherein the total percentage is 100%. Most preferred the plant optimized gene(s) contain about 63% of first choice codons, at least about 22% second choice codons, about 7.5% third choice codons, and about 7.5% fourth choice codons, wherein the total percentage is 100%. The method described above enables one skilled in the art to modify gene(s) that are foreign to a particular plant so that the genes are optimally expressed in plants. The method is further illustrated in application PCT/US96/16582, WO 97/13402 published April 17, 1997.

Thus, in order to design plant optimized gene(s) the amino acid sequence of the toxins are reverse translated into a DNA sequence, utilizing a nonredundant genetic code established from a codon bias table compiled for the gene DNA sequence for the particular plant being transformed. The resulting DNA sequence, which is completely homogeneous in codon usage, is further modified to establish a DNA sequence that, besides having a higher degree of codon diversity, also contains strategically placed restriction enzyme recognition sites, desirable base composition, and a lack of sequences that might interfere with transcription of the gene, or translation of the product mRNA.

It is theorized that bacterial genes may be more easily expressed in plants if the bacterial genes are expressed in the plastids. Thus, it may be possible to express bacterial genes in plants, without optimizing the genes for plant expression, and obtain high express of the protein. See U.S. Patent Nos. 4,762,785; 5,451,513 and 5,545,817, which are incorporated herein by reference.

One of the issues regarding commercial exploiting transgenic plants is resistance management. This is of particular concern with *Bacillus thuringiensis* toxins. There are numerous companies commercially exploiting *Bacillus thuringiensis* and there has been much concern about *Bt* toxins becoming resistant. One strataegy for insect resistant management would be to combine the toxins produced by *Photorhabdus* with toxins such as *Bt*, vegetative insect proteins (Ciba Geigy) or other toxins. The combinations could be formulated

for a sprayable application or could be molecular combinations. Plants could be transformed with *Photorhabdus* genes that produce insect toxins and other insect toxin genes such as *Bt* as with other insect toxin genes such as *Bt*.

5 European Patent Application 0400246A1 describes transformation of 2 *Bt* in a plant, which could be any 2 genes. Another way to produce a transgenic plant that contains more than one insect resistant gene would be to produce two plants, with each plant containing an insect resistant gene. These plants would be
10 backcrossed using traditional plant breeding techniques to produce a plant containing more than one insect resistant gene.

In addition to producing a transformed plant containing plant optimized gene(s), there are other delivery systems where it may be desirable to reengineer the bacterial gene(s). Along the same
15 lines, a genetically engineered, easily isolated protein toxin fusing together both a molecule attractive to insects as a food source and the insecticidal activity of the toxin may be engineered and expressed in bacteria or in eukaryotic cells using standard, well-known techniques. After purification in the laboratory such a
20 toxic agent with "built-in" bait could be packaged inside standard insect trap housings.

Another delivery scheme is the incorporation of the genetic material of toxins into a baculovirus vector. Baculoviruses infect particular insect hosts, including those desirably targeted with
25 the *Photorhabdus* toxins. Infectious baculovirus harboring an expression construct for the *Photorhabdus* toxins could be introduced into areas of insect infestation to thereby intoxicate or poison infected insects.

Transfer of the insecticidal properties requires nucleic acid sequences encoding the coding the amino acid sequences for the
30 *Photorhabdus* toxins integrated into a protein expression vector appropriate to the host in which the vector will reside. One way to obtain a nucleic acid sequence encoding a protein with insecticidal properties is to isolate the native genetic material
35 which produces the toxins from *Photorhabdus*, using information deduced from the toxin's amino acid sequence, large portions of which are set forth below. As described below, methods of purifying the proteins responsible for toxin activity are also disclosed.

40 Using N-terminal amino acid sequence data, such as set forth below, one can construct oligonucleotides complementary to all, or a section of, the DNA bases that encode the first amino acids of the toxin. These oligonucleotides can be radiolabeled and used as

molecular probes to isolate the genetic material from a genomic genetic library built from genetic material isolated from strains of *Photorhabdus*. The genetic library can be cloned in plasmid, cosmid, phage or phagemid vectors. The library could be transformed into *Escherichia coli* and screened for toxin production by the transformed cells using antibodies raised against the toxin or direct assays for insect toxicity.

This approach requires the production of a battery of oligonucleotides, since the degenerate genetic code allows an amino acid to be encoded in the DNA by any of several three-nucleotide combinations. For example, the amino acid arginine can be encoded by nucleic acid triplets CGA, CGC, CGG, CGT, AGA, and AGG. Since one cannot predict which triplet is used at those positions in the toxin gene, one must prepare oligonucleotides with each potential triplet represented. More than one DNA molecule corresponding to a protein subunit may be necessary to construct a sufficient number of oligonucleotide probes to recover all of the protein subunits necessary to achieve oral toxicity.

From the amino acid sequence of the purified protein, genetic materials responsible for the production of toxins can readily be isolated and cloned, in whole or in part, into an expression vector using any of several techniques well-known to one skilled in the art of molecular biology. A typical expression vector is a DNA plasmid, though other transfer means including, but not limited to, cosmids, phagemids and phage are also envisioned. In addition to features required or desired for plasmid replication, such as an origin of replication and antibiotic resistance or other form of a selectable marker such as the *bar* gene of *Streptomyces hygroscopicus* or *viridochromogenes*, protein expression vectors normally additionally require an expression cassette which incorporates the cis-acting sequences necessary for transcription and translation of the gene of interest. The cis-acting sequences required for expression in prokaryotes differ from those required in eukaryotes and plants.

A eukaryotic expression cassette requires a transcriptional promoter upstream (5') to the gene of interest, a transcriptional termination region such as a poly-A addition site, and a ribosome binding site upstream of the gene of interest's first codon. In bacterial cells, a useful transcriptional promoter that could be included in the vector is the T7 RNA Polymerase-binding promoter. Promoters, as previously described herein, are known to efficiently promote transcription of mRNA. Also upstream from the gene of interest the vector may include a nucleotide sequence encoding a

signal sequence known to direct a covalently linked protein to a particular compartment of the host cells such as the cell surface.

Insect viruses, or baculoviruses, are known to infect and adversely affect certain insects. The affect of the viruses on insects is slow, and viruses do not stop the feeding of insects. Thus viruses are not viewed as being useful as insect pest control agents. Combining the *Photographus* toxins genes into a baculovirus vector could provide an efficient way of transmitting the toxins while increasing the lethality of the virus. In addition, since different baculoviruses are specific to different insects, it may be possible to use a particular toxin to selectively target particularly damaging insect pests. A particularly useful vector for the toxins genes is the nuclear polyhedrosis virus. Transfer vectors using this virus have been described and are now the vectors of choice for transferring foreign genes into insects. The virus-toxin gene recombinant may be constructed in an orally transmissible form. Baculoviruses normally infect insect victims through the mid-gut intestinal mucosa. The toxin gene inserted behind a strong viral coat protein promoter would be expressed and should rapidly kill the infected insect.

In addition to an insect virus or baculovirus or transgenic plant delivery system for the protein toxins of the present invention, the proteins may be encapsulated using *Bacillus thuringiensis* encapsulation technology such as but not limited to U.S. Patent Nos. 4,695,455; 4,695,462; 4,861,595 which are all incorporated herein by reference. Another delivery system for the protein toxins of the present invention is formulation of the protein into a bait matrix, which could then be used in above and below ground insect bait stations. Examples of such technology include but are not limited to PCT Patent Application WO 93/23998, which is incorporated herein by reference.

As is described above, it might become necessary to modify the sequence encoding the protein when expressing it in a non-native host, since the codon preferences of other hosts may differ from that of *Photographus*. In such a case, translation may be quite inefficient in a new host unless compensating modifications to the coding sequence are made. Additionally, modifications to the amino acid sequence might be desirable to avoid inhibitory cross-reactivity with proteins of the new host, or to refine the insecticidal properties of the protein in the new host. A genetically modified toxin gene might encode a toxin exhibiting, for example, enhanced or reduced toxicity, altered insect

resistance development, altered stability, or modified target species specificity.

In addition to the *Photorhabdus* genes encoding the toxins, the scope of the present invention is intended to include related nucleic acid sequences which encode amino acid biopolymers homologous to the toxin proteins and which retain the toxic effect of the *Photorhabdus* proteins in insect species after oral ingestion.

For instance, the toxins used in the present invention seem to first inhibit larval feeding before death ensues. By manipulating the nucleic acid sequence of *Photorhabdus* toxins or its controlling sequences, genetic engineers placing the toxin gene into plants could modulate its potency or its mode of action to, for example, keep the eating-inhibitory activity while eliminating the absolute toxicity to the larvae. This change could permit the transformed plant to survive until harvest without having the unnecessarily dramatic effect on the ecosystem of wiping out all target insects. All such modifications of the gene encoding the toxin, or of the protein encoded by the gene, are envisioned to fall within the scope of the present invention.

Other envisioned modifications of the nucleic acid include the addition of targeting sequences to direct the toxin to particular parts of the insect larvae for improving its efficiency.

Strains W-14, ATCC 55397, 43948, 43949, 43950, 43951, 43952 have been deposited in the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD 20852 USA. Amino acid and nucleotide sequence data for the W-14 native toxin (ATCC 55397) is presented below. Isolation of the genomic DNA for the toxins from the bacterial hosts is also exemplified herein. The other strains identified herein have been deposited with the United States Department of Agriculture, 1815 North University Drive, Peoria, IL 61604.

Standard and molecular biology techniques were followed and taught in the specification herein. Additional information may be found in Sambrook, J., Fritsch, E. F., and Maniatis, T. (1989), Molecular Cloning. A Laboratory Manual, Cold Spring Harbor Press; Current Protocols in Molecular Biology, ed. F. M. Ausubel et al., (1997), which are both incorporated herein by reference.

The following abbreviations are used throughout the Examples: Tris = tris (hydroxymethyl) amino methane; SDS = sodium dodecyl sulfate; EDTA = ethylenediaminetetraacetic acid, IPTG = isopropylthio-B-galactoside, X-gal = 5-bromo-4-chloro-3-indoyl-B-D-galactoside,

CTAB = cetyltrimethylammonium bromide; kbp = kilobase pairs; dATP, dCTP, dGTP, dTTP, I = 2'-deoxynucleoside 5'-triphosphates of adenine, cytosine, guanine, thymine, and inosine, respectively; ATP = adenosine 5' triphosphate.

5

Example 1

Purification of Toxin from *Photorhabdus luminescens* and Demonstration of Toxicity after Oral Delivery of Purified Toxin

10 The insecticidal protein toxin of the present invention was purified from *Photorhabdus luminescens* strain W-14, ATCC Accession Number 55397. Stock cultures of *Photorhabdus luminescens* were maintained on petri dishes containing 2% Proteose Peptone No. 3 (i.e., PP3, Difco Laboratories, Detroit MI) in 1.5% agar, incubated
15 at 25°C and transferred weekly. Colonies of the primary form of the bacteria were inoculated into 200 ml of PP3 broth supplemented with 0.5% polyoxyethylene sorbitan mono-stearate (Tween 60, Sigma Chemical Company, St. Louis, MO) in a one liter flask. The broth cultures were grown for 72 hours at 30°C on a rotary shaker. The
20 toxin proteins can be recovered from cultures grown in the presence or absence of Tween; however, the absence of Tween can affect the form of the bacteria grown and the profile of proteins produced by the bacteria. In the absence of Tween, a variant shift occurs insofar as the molecular weight of at least one identified toxin
25 subunit shifts from about 200 kDa to about 185 kDa.

The 72 hour cultures were centrifuged at 10,000 x g for 30 minutes to remove cells and debris. The supernatant fraction that contained the insecticidal activity was decanted and brought to 50 mM K₂HPO₄ by adding an appropriate volume of 1.0 M K₂HPO₄. The pH
30 was adjusted to 8.6 by adding potassium hydroxide. This supernatant fraction was then mixed with DEAE-Sephacel (Pharmacia LKB Biotechnology) which had been equilibrated with 50 mM K₂HPO₄. The toxic activity was adsorbed to the DEAE resin. This mixture was then poured into a 2.6 x 40 cm column and washed with 50 mM
35 K₂HPO₄ at room temperature at a flow rate of 30 ml/hr until the effluent reached a steady baseline UV absorbance at 280 nm. The column was then washed with 150 mM KCl until the effluent again reached a steady 280 nm baseline. Finally the column was washed with 300 mM KCl and fractions were collected.

40 Fractions containing the toxin were pooled and filter sterilized using a 0.2 micron pore membrane filter. The toxin was then concentrated and equilibrated to 100 mM KPO₄, pH 6.9, using an ultrafiltration membrane with a molecular weight cutoff of 100 kDa

at 4°C (Centriprep 100, Amicon Division-W.R. Grace and Company). A 3 ml sample of the toxin concentrate was applied to the top of a 2.6 x 95 cm Sephacryl S-400 HR gel filtration column (Pharmacia LKB Biotechnology). The eluent buffer was 100 mM KPO₄, pH 6.9, which was run at a flow rate of 17 ml/hr, at 4°C. The effluent was monitored at 280 nm.

Fractions were collected and tested for toxic activity. Toxicity of chromatographic fractions was examined in a biological assay using *Manduca sexta* larvae. Fractions were either applied directly onto the insect diet (Gypsy moth wheat germ diet, ICN Biochemicals Division - ICN Biomedicals, Inc.) or administered by intrahemocelic injection of a 5 µl sample through the first proleg of 4th or 5th instar larva using a 30 gauge needle. The weight of each larva within a treatment group was recorded at 24 hour intervals. Toxicity was presumed if the insect ceased feeding and died within several days of consuming treated insect diet or if death occurred within 24 hours after injection of a fraction.

The toxic fractions were pooled and concentrated using the Centriprep-100 and were then analyzed by HPLC using a 7.5 mm x 60 cm TSK-GEL G-4000 SW gel permeation column with 100 mM potassium phosphate, pH 6.9 eluent buffer running at 0.4 ml/min. This analysis revealed the toxin protein to be contained within a single sharp peak that eluted from the column with a retention time of approximately 33.6 minutes. This retention time corresponded to an estimated molecular weight of 1,000 kDa. Peak fractions were collected for further purification while fractions not containing this protein were discarded. The peak eluted from the HPLC absorbs UV light at 218 and 280 nm but did not absorb at 405 nm. Absorbance at 405 nm was shown to be an attribute of xenorhabdin antibiotic compounds.

Electrophoresis of the pooled peak fractions in a non-denaturing agarose gel (Metaphor Agarose, FMC BioProducts) showed that two protein complexes are present in the peak. The peak material, buffered in 50 mM Tris-HCl, pH 7.0, was separated on a 1.5% agarose stacking gel buffered with 100 mM Tris-HCl at pH 7.0 and 1.9% agarose resolving gel buffered with 200 mM Tris-borate at pH 8.3 under standard buffer conditions (anode buffer 1M Tris-HCl, pH 8.3; cathode buffer 0.025 M Tris, 0.192 M glycine). The gels were run at 13 mA constant current at 15°C until the phenol red tracking dye reached the end of the gel. Two protein bands were visualized in the agarose gels using Coomassie brilliant blue staining.

The slower migrating band was referred to as "protein band 1" and faster migrating band was referred to as "protein band 2." The two protein bands were present in approximately equal amounts. The Coomassie stained agarose gels were used as a guide to precisely excise the two protein bands from unstained portions of the gels. The excised pieces containing the protein bands were macerated and a small amount of sterile water was added. As a control, a portion of the gel that contained no protein was also excised and treated in the same manner as the gel pieces containing the protein.

Protein was recovered from the gel pieces by electroelution into 100 mM Tris-borate pH 8.3, at 100 volts (constant voltage) for two hours. Alternatively, protein was passively eluted from the gel pieces by adding an equal volume of 50 mM Tris-HCl, pH 7.0, to the gel pieces, then incubating at 30°C for 16 hours. This allowed the protein to diffuse from the gel into the buffer, which was then collected.

Results of insect toxicity tests using HPLC-purified toxin (33.6 min. peak) and agarose gel purified toxin demonstrated toxicity of the extracts. Injection of 1.5 µg of the HPLC purified protein kills within 24 hours. Both protein bands 1 and 2, recovered from agarose gels by passive elution or electroelution, were lethal upon injection. The protein concentration estimated for these samples was less than 50 ng/larva. A comparison of the weight gain and the mortality between the groups of larvae injected with protein bands 1 or 2 indicate that protein band 1 was more toxic by injection delivery.

When HPLC-purified toxin was applied to larval diet at a concentration of 7.5 µg/larva, it caused a halt in larval weight gain (24 larvae tested). The larvae begin to feed, but after consuming only a very small portion of the toxin treated diet they began to show pathological symptoms induced by the toxin and the larvae cease feeding. The insect frass became discolored and most larva showed signs of diarrhea. Significant insect mortality resulted when several 5 µg toxin doses were applied to the diet over a 7-10 day period.

Agarose-separated protein band 1 significantly inhibited larval weight gain at a dose of 200 ng/larva. Larvae fed similar concentrations of protein band 2 were not inhibited and gained weight at the same rate as the control larvae. Twelve larvae were fed eluted protein and 45 larvae were fed protein-containing agarose pieces. These two sets of data indicate that protein band 1 was orally toxic to *Manduca sexta*. In this experiment it appeared that protein band 2 was not toxic to *Manduca sexta*.

Further analysis of protein bands 1 and 2 by SDS-PAGE under denaturing conditions showed that each band was composed of several smaller protein subunits. Proteins were visualized by Coomassie brilliant blue staining followed by silver staining to achieve maximum sensitivity.

The protein subunits in the two bands were very similar. Protein band 1 contains 8 protein subunits of 25.1, 56.2, 60.8, 65.6, 166, 171, 184 and 208 kDa. Protein band 2 had an identical profile except that the 25.1, 60.8, and 65.6 kDa proteins were not present. The 56.2, 60.8, 65.6, and 184 kDa proteins were present in the complex of protein band 1 at approximately equal concentrations and represent 80% or more of the total protein content of that complex.

The native HPLC-purified toxin was further characterized as follows. The toxin was heat labile in that after being heated to 60°C for 15 minutes it lost its ability to kill or to inhibit weight gain when injected or fed to *Manduca sexta* larvae. Assays were designed to detect lipase, type C phospholipase, nuclease or red blood cell hemolysis activities and were performed with purified toxin. None of these activities were present. Antibiotic zone inhibition assays were also done and the purified toxin failed to inhibit growth of Gram-negative or -positive bacteria, yeast or filamentous fungi, indicating that the toxin is not a xenorhabdin antibiotic.

The native HPLC-purified toxin was tested for ability to kill insects other than *Manduca sexta*. Table 3 lists insects killed by the HPLC-purified *Photorhabdus luminescens* toxin in this study.

Table 3
Insects Killed by *Photorhabdus luminescens* Toxin

<u>Common Name</u>	<u>Order</u>	<u>Genus and species</u>	<u>Route of Delivery</u>
Tobacco horn worm	Lepidoptera	<i>Manduca sexta</i>	Oral and injected
Mealworm	Coleoptera	<i>Tenebrio molitor</i>	Oral
Pharaoh ant	Hymenoptera	<i>Monomorium pharoanis</i>	Oral
German cockroach	Dictyoptera	<i>Blattella germanica</i>	Oral and injected
Mosquito	Diptera	<i>Aedes aegypti</i>	Oral

Further Characterization of the High Molecular Weight Toxin Complex

In yet further analysis, the toxin protein complex was subjected to further characterization from W-14 growth medium. The culture conditions and initial purification steps through the S-400 HR column were identical to those described above. After isolation of the high molecular weight toxin complex from the S-400 HR column fractions, the toxic fractions were equilibrated with 10 mM Tris-HCl, pH 8.6, and concentrated in the centriplus 100 (Amicon) concentrators. The protein toxin complex was then applied to a weak anion exchange (WAX) column, Vydac 301VPH575 (Hesperia, CA), at a flow rate of 0.5 ml/min. The proteins were eluted with a linear potassium chloride gradient, 0-250 mM KCl, in 10 mM Tris-HCl pH 8.6 for 50 min. Eight protein peaks were detected by absorbance at 280 nm.

Bioassays using neonate southern corn rootworm (*Diabrotica undecimpunctata howardi*, SCR) larvae and tobacco horn worm (*Manduca sexta*, THW) were performed on all fractions eluted from the HPLC column. THW were grown on Gypsy Moth wheat germ diet (ICN) at 25°C with a 16 hr light 8 hr dark cycle. SCR were grown on Southern Corn Rootworm Larval Insecta-Diet (BioServ) at 25°C with a 16 hr light / 8 hr dark cycle.

The highest mortality for SCR and THW larvae was observed for peak 6, which eluted with ca. 112 mM to 132mM KCl. SDS-PAGE analysis of peak 6 showed predominant peptides of 170 kDa, 66 kDa, 63 kDa, 59.5 kDa and 31 kDa. Western blot analysis was performed on peak 6 protein fraction with a mixture of polyclonal antibodies made against TcaA_{iii}-syn, TcaA_{iii}-syn, TcaB_{ii}-syn, TcaC-syn, and TcbA_{iii}-syn peptides (described in Example 21) and C5F2, a monoclonal antibody against the TcbA_{iii} peptide. Peak 6 contained immuno-reactive bands of 170 kDa, 90 kDa, 66 kDa, 59.5 kDa and 31 kDa. These are very close to the predicted sizes for the TcaC (166 kDa), TcaA_{ii} + TcaA_{iii} (92 kDa), TcaA_{iii} (66 kDa), TcaB_{ii} (60 kDa) and TcaA_{ii} (25 kDa), respectively. Peak 6 which was further analyzed by native agarose gel electrophoresis, as described herein, migrated as a single band with similar mobility to that of band 1.

The protein concentration of the purified peak 6 toxin protein was determined using the BCA reagents (Pierce). Dilutions of the protein were made in 10 mM Tris, pH 8.6 and applied to the diet bioassays. After 240 hours all neonate larvae on diet bioassays that received 100 ng or greater of the peak 6 protein fraction were dead. The group of larvae that received 90 ng of the same fraction

had 40% mortality. After 240 hrs the survivors that received 90 ng and 20 ng of peak 6 protein fraction were ca. 10% and 70%, respectively, of the control weight.

5

Example 2
Insecticide Utility

The *Photorhabdus luminescens* utility and toxicity were further characterized. *Photorhabdus luminescens* (strain W-14) culture
10 broth was produced as follows. The production medium was 2% Bacto Proteose Peptone[®] Number 3 (PP3, Difco Laboratories, Detroit, Michigan) in Milli-Q[®] deionized water. Seed culture flasks consisted of 175 ml medium placed in a 500 ml tribaffled flask with a Delong neck, covered with a Kaput and autoclaved for 20 minutes,
15 T=250°F. Production flasks consisted of 500 mls in a 2.8 liter 500 ml tribaffled flask with a Delong neck, covered by a Shin-etsu silicon foam closure. These were autoclaved for 45 minutes, T=250°F. The seed culture was incubated at 28°C at 150 rpm in a gyrotory shaking incubator with a 2 inch throw. After 16 hours of
20 growth, 1% of the seed culture was placed in the production flask which was allowed to grow for 24 hours before harvest. Production of the toxin appears to be during log phase growth. The microbial broth was transferred to a 1L centrifuge bottle and the cellular biomass was pelleted (30 minutes at 2500 RPM at 4°C, [R.C.F. = about
25 1600] HG-4L Rotor RC3 Sorval centrifuge, Dupont, Wilmington, DE). The primary broth was chilled at 4°C for 8 - 16 hours and recentrifuged at least 2 hours (conditions above) to further clarify the broth by removal of a putative mucopolysaccharide which precipitated upon standing. (An alternative processing method
30 combined both steps and involved the use of a 16 hour clarification centrifugation, same conditions as above.) This broth was then stored at 4°C prior to bioassay or filtration.

Photorhabdus culture broth and protein toxin(s) purified from this broth showed activity (mortality and/or growth inhibition,
35 reduced adult emergence) against a number of insects. More specifically, the activity is seen against corn rootworm (larvae and adult), Colorado potato beetle, and turf grubs, which are members of the insect order Coleoptera. Other members of the Coleoptera include wireworms, pollen beetles, flea beetles, seed
40 beetles and weevils. Activity has also been observed against aster leafhopper, which is a member of the order, Homoptera. Other members of the Homoptera include planthoppers, pear psylla, apple

sucker, scale insects, whiteflies, and spittle bugs, as well as numerous host specific aphid species. The broth and purified fractions are also active against beet armyworm, cabbage looper, black cutworm, tobacco budworm, European corn borer, corn earworm, and codling moth, which are members of the order *Lepidoptera*. Other typical members of this order are clothes moth, Indian mealmoth, leaf rollers, cabbage worm, cotton bollworm, bagworm, Eastern tent caterpillar, sod webworm, and fall armyworm. Activity is also seen against fruitfly and mosquito larvae, which are members of the order *Diptera*. Other members of the order *Diptera* are pea midge, carrot fly, cabbage root fly, turnip root fly, onion fly, crane fly, house fly, and various mosquito species. Activity is seen against carpenter ant and Argentine ant, which are members of the order that also includes fire ants, odorous house ants, and little black ants.

The broth/fraction is useful for reducing populations of insects and were used in a method of inhibiting an insect population. The method may comprise applying to a locus of the insect an effective insect inactivating amount of the active described. Results are reported in Table 4.

Activity against corn rootworm larvae was tested as follows. *Photorhabdus* culture broth (filter sterilized, cell-free) or purified HPLC fractions were applied directly to the surface (about 1.5 cm²) of 0.25 ml of artificial diet in 30 µl aliquots following dilution in control medium or 10 mM sodium phosphate buffer, pH 7.0, respectively. The diet plates were allowed to air-dry in a sterile flow-hood and the wells were infested with single, neonate *Diabrotica undecimpunctata howardi* (Southern corn rootworm, SCR) hatched from sterilized eggs, with second instar SCR grown on artificial diet or with second instar *Diabrotica virgifera virgifera* (Western corn rootworm, WCR) reared on corn seedlings grown in Metromix[®]. Second instar larvae were weighed prior to addition to the diet. The plates were sealed, placed in a humidified growth chamber and maintained at 27°C for the appropriate period (4 days for neonate and adult SCR, 2-5 days for WCR larvae, 7-14 days for second instar SCR). Mortality and weight determinations were scored as indicated. Generally, 16 insects per treatment were used in all studies. Control mortalities were as follows: neonate larvae, <5%, adult beetles, 5%.

Activity against Colorado potato beetle was tested as follows. *Photorhabdus* culture broth or control medium was applied to the surface (about 2.0 cm²) of 1.5 ml of standard artificial diet held in the wells of a 24-well tissue culture plate. Each well received

50 µl of treatment and was allowed to air dry. Individual second instar Colorado potato beetle (*Leptinotarsa decemlineata*, CPB) larvae were then placed onto the diet and mortality was scored after 4 days. Ten larvae per treatment were used in all studies.

5 Control mortality was 3.3%.

Activity against Japanese beetle grubs and beetles was tested as follows. Turf grubs (*Popillia japonica*, 2-3rd instar) were collected from infested lawns and maintained in the laboratory in soil/peat mixture with carrot slices added as additional diet.

10 Turf beetles were pheromone-trapped locally and maintained in the laboratory in plastic containers with maple leaves as food. Following application of undiluted *Photorhabdus* culture broth or control medium to corn rootworm artificial diet (30 µl/1.54 cm², beetles) or carrot slices (larvae), both stages were placed singly
15 in a diet well and observed for any mortality and feeding. In both cases there was a clear reduction in the amount of feeding (and feces production) observed.

Activity against mosquito larvae was tested as follows. The assay was conducted in a 96-well microtiter plate. Each well
20 contained 200 µl of aqueous solution (*Photorhabdus* culture broth, control medium or H₂O) and approximately 20, 1-day old larvae (*Aedes aegypti*). There were 6 wells per treatment. The results were read at 2 hours after infestation and did not change over the three day observation period. No control mortality was seen.

25 Activity against fruitflies was tested as follows. Purchased *Drosophila melanogaster* medium was prepared using 50% dry medium and a 50% liquid of either water, control medium or *Photorhabdus* culture broth. This was accomplished by placing 8.0 ml of dry medium in each of 3 rearing vials per treatment and adding 8.0 ml
30 of the appropriate liquid. Ten late instar *Drosophila melanogaster* maggots were then added to each vial. The vials were held on a laboratory bench, at room temperature, under fluorescent ceiling lights. Pupal or adult counts were made after 3, 7 and 10 days of exposure. Incorporation of *Photorhabdus* culture broth into the
35 diet media for fruitfly maggots caused a slight (17%) but significant reduction in day-10 adult emergence as compared to water and control medium (3% reduction).

Activity against aster leafhopper was tested as follows. The ingestion assay for aster leafhopper (*Macrosteles severini*) is
40 designed to allow ingestion of the active without other external contact. The reservoir for the active/"food" solution is made by making 2 holes in the center of the bottom portion of a 35 x 10 mm Petri dish. A 2 inch Parafilm M' square is placed across the top of

the dish and secured with an "O" ring. A 1 oz. plastic cup is then infested with approximately 7 leafhoppers and the reservoir is placed on top of the cup, Parafilm down. The test solution is then added to the reservoir through the holes. In tests using undiluted *Photorhabdus* culture broth, the broth and control medium were dialyzed against water to reduce control mortality. Mortality is reported at day 2 where 26.5% control mortality was seen. In the tests using purified fractions (200 mg protein/ml) a final concentration of 5% sucrose was used in all treatments to improve survivability of the aster leafhoppers. The assay was held in an incubator at 28°C, 70% RH with a 16/8 photoperiod. The assay was graded for mortality at 72 hours. Control mortality was 5.5%.

Activity against Argentine ants was tested as follows. A 1.5 ml aliquot of 100% *Photorhabdus* culture broth, control medium or water was pipetted into 2.0 ml clear glass vials. The vials were plugged with a piece of cotton dental wick that was moistened with the appropriate treatment. Each vial was placed into a separate 60x16mm Petri dish with 8 to 12 adult Argentine ants (*Linepithema humile*). There were three replicates per treatment. Bioassay plates were held on a laboratory bench, at room temperature under fluorescent ceiling lights. Mortality readings were made after 5 days of exposure. Control mortality was 24%.

Activity against carpenter ant was tested as follows. Black carpenter ant workers (*Camponotus pennsylvanicus*) were collected from trees on DowElanco property in Indianapolis, IN. Tests with *Photorhabdus* culture broth were performed as follows. Each plastic bioassay container (7 1/8" x 3") held fifteen workers, a paper harborage and 10 ml of broth or control media in a plastic shot glass. A cotton wick delivered the treatment to the ants through a hole in the shot glass lid. All treatments contained 5% sucrose. Bioassays were held in the dark at room temperature and graded at 19 days. Control mortality was 9%. Assays delivering purified fractions utilized artificial ant diet mixed with the treatment (purified fraction or control solution) at a rate of 0.2 ml treatment/2.0 g diet in a plastic test tube. The final protein concentration of the purified fraction was less than 10 µg/g diet. Ten ants per treatment, a water source, harborage and the treated diet were placed in sealed plastic containers and maintained in the dark at 27°C in a humidified incubator. Mortality was scored at day 10. No control mortality was seen.

Activity against various lepidopteran larvae was tested as follows. *Photorhabdus* culture broth or purified fractions were

applied directly to the surface (about 1.5 cm²) of 0.25 ml of standard artificial diet in 30 µl aliquots following dilution in control medium or 10 mM sodium phosphate buffer, pH 7.0, respectively. The diet plates were allowed to air-dry in a sterile flow-hood and the wells were infested with single, neonate larva. European corn borer (*Ostrinia nubilalis*) and corn earworm (*Helicoverpa zea*) eggs were supplied from commercial sources and hatched in-house, whereas beet armyworm (*Spodoptera exigua*), cabbage looper (*Trichoplusia ni*), tobacco budworm (*Heliothis virescens*), codling moth (*Laspeyresia pomonella*) and black cutworm (*Agrotis ipsilon*) larvae were supplied internally. Following infestation with larvae, the diet plates were sealed, placed in a humidified growth chamber and maintained in the dark at 27°C for the appropriate period. Mortality and weight determinations were scored at days 5-7 for *Photorhabdus* culture broth and days 4-7 for the purified fraction. Generally, 16 insects per treatment were used in all studies. Control mortality ranged from 4-12.5% for control medium and was less than 10% for phosphate buffer.

Table 4
Effect of *Photorhabdus luminescens* (Strain W-14)
Culture Broth and Purified Toxin Fraction on Mortality and Growth
Inhibition of Different Insect Orders/Species

5

Insect Order/Species	Broth		Purified Fraction	
	% Mort.	% G.I.	% Mort.	% G.I.
COLEOPTERA				
Corn Rootworm				
Southern/neonate larva	100	na	100	na
Southern/2 nd instar	na	38.5	nt	nt
Southern/adult	45	nt	nt	nt
Western/2 nd instar	na	35	nt	nt
Colorado Potato Beetle	93	nt	nt	nt
2 nd instar				
Turf Grub	na	a.f.	nt	nt
3 rd instar	na	a.f.	nt	nt
adult				
DIPTERA				
Fruit Fly (adult emergence)	17	nt	nt	nt
Mosquito larvae	100	na	nt	nt
HOMOPTERA				
Aster Leafhopper	96.5	na	100	na
HYMENOPTERA				
Argentine Ant	75	na	nt	na
Carpenter Ant	71	na	100	na
LEPIDOPTERA				
Beet Armyworm	12.5	36	18.75	41.4
Black Cutworm	nt	nt	0	71.2
Cabbage Looper	nt	nt	21.9	66.8
Codling Moth	nt	nt	6.25	45.9
Corn Earworm	56.3	94.2	97.9	na
European Corn Borer	96.7	98.4	100	na
Tobacco Budworm	13.5	52.5	19.4	85.6

Mort. = mortality, G.I. = growth inhibition,
na = not applicable, nt = not tested, a.f. = anti-feedant

Example 3

10

Insecticide Utility upon Soil Application

Photorhabdus luminescens (strain W-14) culture broth was shown to be active against corn rootworm when applied directly to soil or a soil-mix (Metromix®). Activity against neonate SCR and WCR in

Metromix[®] was tested as follows (Table 5). The test was run using corn seedlings (United Agriseeds brand CL614) that were germinated in the light on moist filter paper for 6 days. After roots were approximately 3-6 cm long, a single kernel/seedling was planted in a 591 ml clear plastic cup with 50 gm of dry Metromix[®]. Twenty neonate SCR or WCR were then placed directly on the roots of the seedling and covered with Metromix[®]. Upon infestation, the seedlings were then drenched with 50 ml total volume of a diluted broth solution. After drenching, the cups were sealed and left at room temperature in the light for 7 days. Afterwards, the seedlings were washed to remove all Metromix[®] and the roots were excised and weighed. Activity was rated as the percentage of corn root remaining relative to the control plants and as leaf damage induced by feeding. Leaf damage was scored visually and rated as either -, +, ++, or +++, with - representing no damage and +++ representing severe damage.

Activity against neonate SCR in soil was tested as follows (Table 6). The test was run using corn seedlings (United Agriseeds brand CL614) that were germinated in the light on moist filter paper for 6 days. After the roots were approximately 3-6 cm long, a single kernel/seedling was planted in a 591 ml clear plastic cup with 150 gm of soil from a field in Lebanon, IN planted the previous year with corn. This soil had not been previously treated with insecticides. Twenty neonate SCR were then placed directly on the roots of the seedling and covered with soil. After infestation, the seedlings were drenched with 50 ml total volume of a diluted broth solution. After drenching, the unsealed cups were incubated in a high relative humidity chamber (80%) at 78°F. Afterwards, the seedlings were washed to remove all soil and the roots were excised and weighed. Activity was rated as the percentage of corn root remaining relative to the control plants and as leaf damage induced by feeding. Leaf damage was scored visually and rated as either -, +, ++, or +++, with - representing no damage and +++ representing severe damage.

Table 5

Effect of *Photorhabdus luminescens* (Strain W-14) Culture Broth on Rootworm Larvae after Post-Infestation Drenching (Metromix®)

5	Treatment	Larvae	Leaf Damage	Root Weight (g)	%
	Southern Corn Rootworm				
	Water	-	-	0.4916 ± 0.023	100
	Medium (2.0% v/v)	-	-	0.4416 ± 0.029	100
10	Broth (6.25%v/v)	-	-	0.4641 ± 0.081	100
	Water	+	+++	0.1410 ± 0.006	28.7
	Media (2.0% v/v)	+	+++	0.1345 ± 0.028	30.4
15	Broth (1.56% v/v)	+	-	0.4830 ± 0.031	104
	Western Corn Rootworm				
	Water	-	-	0.4446 ± 0.019	100
	Broth (2.0% v/v)	-	-	0.4069 ± 0.026	100
20	Water	+	-	0.2202 ± 0.015	49
	Broth (2.0% v/v)	+	-	0.3879 ± 0.013	95

Table 6

Effect of *Photorhabdus luminescens* (Strain W-14) Culture Broth on Southern Corn Rootworm Larvae after Post-Infestation Drenching (Soil)

30	Treatment	Larvae	Leaf Damage	Root Weight (g)	%
	Water	-	-	0.2148 ± 0.014	100
	Broth (50% v/v)	-	-	0.2260 ± 0.016	103
35	Water	+	+++	0.0916 ± 0.009	43
	Broth (50% v/v)	+	-	0.2428 ± 0.032	113

Activity of *Photorhabdus luminescens* (strain W-14) culture broth against second instar turf grubs in Metromix® was observed in tests conducted as follows (Table 7). Approximately 50 gm of dry Metromix® was added to a 591 ml clear plastic cup. The Metromix® was then drenched with 50 ml total volume of a 50% (v/v) diluted *Photorhabdus* broth solution. The dilution of crude broth was made with water, with 50% broth being prepared by adding 25 ml of crude broth to 25 ml of water for 50 ml total volume. A 1% (w/v) solution of proteose peptone #3 (PP3), which is a 50% dilution of the normal media concentration, was used as a broth control. After drenching, five second instar turf grubs were placed on the top of the moistened Metromix®. Healthy turf grub larvae burrowed rapidly into the Metromix®. Those larvae that did not burrow within 1h were

removed and replaced with fresh larvae. The cups were sealed and placed in a 28°C incubator, in the dark. After seven days, larvae were removed from the Metromix[®] and scored for mortality. Activity was rated the percentage of mortality relative to control.

5

Table 7

Effect of *Photorhabdus luminescens* (Strain W-14) Culture Broth on Turf Grub after Pre-Infestation Drenching (Metromix[®])

10	Treatment	Mortality*	Mortality %
	Water	7/15	47
15	Control medium (1.0% w/v)	12/19	63
	Broth (50% v/v)	17/20	85
20	*expressed as a ratio of dead/living larvae		

Example 4

Insecticide Utility upon Leaf Application

25

Activity of *Photorhabdus* broth against European corn borer was seen when the broth was applied directly to the surface of maize leaves (Table 8). In these assays *Photorhabdus* broth was diluted 100-fold with culture medium and applied manually to the surface of excised maize leaves at a rate of about 6.0 µl/cm² of leaf surface. The leaves were air dried and cut into equal sized strips approximately 2 x 2 inches. The leaves were rolled, secured with paper clips and placed in 1 oz plastic shot glasses with 0.25 inch of 2% agar on the bottom surface to provide moisture. Twelve neonate European corn borers were then placed onto the rolled leaf and the cup was sealed. After incubation for 5 days at 27°C in the dark, the samples were scored for feeding damage and recovered larvae.

30

35

Table 8

Effect of *Photorhabdus luminescens* (Strain W-14) Culture Broth on European Corn Borer Larvae Following Pre-Infestation Application to Excised Maize Leaves

Treatment	Leaf Damage	Larvae Recovered	Weight (mg)
Water	Extensive	55/120	0.42 mg
Control Medium	Extensive	40/120	0.50 mg
Broth (1.0% v/v)	Trace	3/120	0.15 mg

Activity of the culture broth against neonate tobacco budworm (*Heliothis virescens*) was demonstrated using a leaf dip methodology. Fresh cotton leaves were excised from the plant and leaf disks were cut with an 18.5 mm cork-borer. The disks were individually emersed in control medium (PP3) or *Photorhabdus luminescens* (strain W-14) culture broth which had been concentrated approximately 10-fold using an Amicon (Beverly, MA), Proflux M12 tangential filtration system with a 10 kDa filter. Excess liquid was removed and a straightened paper clip was placed through the center of the disk. The paper clip was then wedged into a plastic, 1.0 oz shot glass containing approximately 2.0 ml of 1% Agar. This served to suspend the leaf disk above the agar. Following drying of the leaf disk, a single neonate tobacco budworm larva was placed on the disk and the cup was capped. The cups were then sealed in a plastic bag and placed in a darkened, 27°C incubator for 5 days. At this time the remaining larvae and leaf material were weighed to establish a measure of leaf damage (Table 9).

Table 9

Effect of *Photorhabdus luminescens* (Strain W-14) Culture Broth on Tobacco Budworm Neonates in a Cotton-Leaf Dip Assay

Treatment	Leaf Disk	Final Weights (mg) Larvae
Control leaves	55.7 ± 1.3	na*
Control Medium	34.0 ± 2.9	4.3 ± 0.91
<i>Photorhabdus</i> broth	54.3 ± 1.4	0.0**

* - not applicable, ** - no live larvae found

Example 5. Part A

Characterization of Toxin Peptide Components

In a subsequent analysis, the toxin protein subunits of the bands isolated as in Example 1 were resolved on a 7% SDS

polyacrylamide electrophoresis gel with a ratio of 38:0.8 (acrylamide:BIS-acrylamide). This gel matrix facilitates better resolution of the larger proteins. The gel system used to estimate the Band 1 and Band 2 subunit molecular weights in Example 1 was an 18% gel with a ratio of 38:0.18 (acrylamide:BIS-acrylamide), which allowed for a broader range of size separation, but less resolution of higher molecular weight components.

In this analysis, 10, rather than 8, protein bands were resolved. Table 10 reports the calculated molecular weights of the 10 resolved bands, and directly compares the molecular weights estimated under these conditions to those of the prior example. It is not surprising that additional bands were detected under the different separation conditions used in this example. Variations between the prior and new estimates of molecular weight are also to be expected given the differences in analytical conditions. In the analysis of this example, it is thought that the higher molecular weight estimates are more accurate than in Example 1, as a result of improved resolution. However, these are estimates based on SDS PAGE analysis, which are typically not analytically precise and result in estimates of peptides and which may have been further altered due to post- and co-translational modifications.

Amino acid sequences were determined for the N-terminal portions of five of the 10 resolved peptides. Table 10 + correlates the molecular weight of the proteins and the identified sequences. In SEQ ID NO:2, certain analyses suggest that the proline at residue 5 may be an asparagine (asn). In SEQ ID NO:3, certain analyses suggest that the amino acid residues at positions 13 and 14 are both arginine (arg). In SEQ ID NO:4, certain analyses suggest that the amino acid residue at position 6 may be either alanine (ala) or serine (ser). In SEQ ID NO:5, certain analyses suggest that the amino acid residue at position 3 may be aspartic acid (asp).

Table 10

	<u>ESTIMATE</u>	<u>NEW ESTIMATE*</u>	<u>SEQ. LISTING</u>
	208	200.2 kDa	SEQ ID NO:1
5	184	175.0 kDa	SEQ ID NO:2
	65.6	68.1 kDa	SEQ ID NO:3
	60.8	65.1 kDa	SEQ ID NO:4
	56.2	58.3 kDa	SEQ ID NO:5
	25.1	23.2 kDa	SEQ ID NO:15
10	*New estimates are based on SDS PAGE and are not based on gene sequences. SDS PAGE is not analytically precise.		

Example 5. Part BCharacterization of Toxin Peptide Components

15

New N-terminal sequence, SEQ ID NO:15, Ala Gln Asp Gly Asn Gln Asp Thr Phe Phe Ser Gly Asn Thr, was obtained by further N-terminal sequencing of peptides isolated from Native HPLC-purified toxin as described in Example 5, Part A, above. This peptide comes from the

20 tcaA gene. The peptide labeled TcaA_{ii}, starts at position 254 and goes to position 491, where the TcaA_{iii} peptide starts, SEQ ID NO:4. The estimated size of the peptide based on the gene sequence is 25,240 Da.

25

Example 6Characterization of Toxin Peptide Components

In yet another analysis, the toxin protein complex was re-isolated from the *Photorhabdus luminescens* growth medium (after

30 culture without Tween) by performing a 10% - 80% ammonium sulfate precipitation followed by an ion exchange chromatography step (Mono Q) and two molecular sizing chromatography steps. These conditions were like those used in Example 1. During the first molecular

sizing step, a second biologically active peak was found at about

35 100 ± 10 kDa. Based upon protein measurements, this fraction was 20 - 50 fold less active than the larger, or primary, active peak of about 860 ± 100 kDa (native). During this isolation experiment a smaller active peak of about 325 ± 50 kDa that retained a

considerable portion of the starting biological activity was also

40 resolved. It is thought that the 325 kDa peak is related to or derived from the 860 kDa peak.

A 56 kDa protein was resolved in this analysis. The N-terminal sequence of this protein is presented in SEQ ID NO:6. It

is noteworthy that this protein shares significant identity and conservation with SEQ ID NO:5 at the N-terminus, suggesting that the two may be encoded by separate members of a gene family and that the proteins produced by each gene are sufficiently similar to both be operable in the insecticidal toxin complex.

A second, prominent 185 kDa protein was consistently present in amounts comparable to that of protein 3 from Table 10, and may be the same protein or protein fragment. The N-terminal sequence of this 185 kDa protein is shown at SEQ ID NO:7.

Additional N-terminal amino acid sequence data were also obtained from isolated proteins. None of the determined N-terminal sequences appear identical to a protein identified in Table 10. Other proteins were present in isolated preparation. One such protein has an estimated molecular weight of 108 kDa and an N-terminal sequence as shown in SEQ ID NO:8. A second such protein has an estimated molecular weight of 80 kDa and an N-terminal sequence as shown in SEQ ID NO:9.

When the protein material in the approximately 325 kDa active peak was analyzed by size, bands of approximately 51, 31, 28, and 22 kDa were observed. As in all cases in which a molecular weight was determined by analysis of electrophoretic mobility, these molecular weights were subject to error effects introduced by buffer ionic strength differences, electrophoresis power differences, and the like. One of ordinary skill would understand that definitive molecular weight values cannot be determined using these standard methods and that each was subject to variation. It was hypothesized that proteins of these sizes are degradation products of the larger protein species (of approximately 200 kDa size) that were observed in the larger primary toxin complex.

Finally, several preparations included a protein having the N-terminal sequence shown in SEQ ID NO:10. This sequence was strongly homologous to known chaperonin proteins, accessory proteins known to function in the assembly of large protein complexes. Although the applicants could not ascribe such an assembly function to the protein identified in SEQ ID NO:10, it was consistent with the existence of the described toxin protein complex that such a chaperonin protein could be involved in its assembly. Moreover, although such proteins have not directly been suggested to have toxic activity, this protein may be important to determining the overall structural nature of the protein toxin, and thus, may contribute to the toxic activity or durability of the complex in vivo after oral delivery.

Subsequent analysis of the stability of the protein toxin complex to proteinase K was undertaken. It was determined that after 24 hour incubation of the complex in the presence of a 10-fold molar excess of proteinase K, activity was virtually eliminated (mortality on oral application dropped to about 5%). These data confirm the proteinaceous nature of the toxin.

The toxic activity was also retained by a dialysis membrane, again confirming the large size of the native toxin complex.

Example 7

Isolation, Characterization and Partial Amino Acid Sequencing of Photorhabdus Toxins

Isolation and N-Terminal Amino Acid Sequencing

In a set of experiments conducted in parallel to Examples 5 and 6, ammonium sulfate precipitation of *Photorhabdus* proteins was performed by adjusting *Photorhabdus* broth, typically 2-3 liters, to a final concentration of either 10% or 20% by the slow addition of ammonium sulfate crystals. After stirring for 1 hour at 4°C, the material was centrifuged at 12,000 x g for 30 minutes. The supernatant was adjusted to 80% ammonium sulfate, stirred at 4°C for 1 hour, and centrifuged at 12,000 x g for 60 minutes. The pellet was resuspended in one-tenth the volume of 10 mM Na₂PO₄, pH 7.0 and dialyzed against the same phosphate buffer overnight at 4°C. The dialyzed material was centrifuged at 12,000 x g for 1 hour prior to ion exchange chromatography.

A HR 16/50 Q Sepharose (Pharmacia) anion exchange column was equilibrated with 10 mM Na₂PO₄, pH 7.0. Centrifuged, dialyzed ammonium sulfate pellet was applied to the Q Sepharose column at a rate of 1.5 ml/min and washed extensively at 3.0 ml/min with equilibration buffer until the optical density (O.D. 280) reached less than 0.100. Next, either a 60 minute NaCl gradient ranging from 0 to 0.5 M at 3 ml/min, or a series of step elutions using 0.1 M, 0.4 M and finally 1.0 M NaCl for 60 minutes each was applied to the column. Fractions were pooled and concentrated using a Centriprep 100. Alternatively, proteins could be eluted by a single 0.4 M NaCl wash without prior elution with 0.1 M NaCl.

Two milliliter aliquots of concentrated Q Sepharose samples were loaded at 0.5 ml/min onto a HR 16/50 Superose 12 (Pharmacia) gel filtration column equilibrated with 10 mM Na₂PO₄, pH 7.0. The column was washed with the same buffer for 240 min at 0.5 ml/min and 2 min samples were collected. The void volume material was

collected and concentrated using a Centriprep 100. Two milliliter aliquots of concentrated Superose 12 samples were loaded at 0.5 ml/min onto a HR 16/50 Sepharose 4B-CL (Pharmacia) gel filtration column equilibrated with 10 mM Na_2PO_4 , pH 7.0. The column was washed with the same buffer for 240 min at 0.5 ml/min and 2 min samples were collected.

The excluded protein peak was subjected to a second fractionation by application to a gel filtration column that used a Sepharose CL-4B resin, which separates proteins ranging from about 30 kDa to 1000 kDa. This fraction was resolved into two peaks; a minor peak at the void volume (>1000 kDa) and a major peak which eluted at an apparent molecular weight of about 860 kDa. Over a one week period subsequent samples subjected to gel filtration showed the gradual appearance of a third peak (approximately 325 kDa) that seemed to arise from the major peak, perhaps by limited proteolysis. Bioassays performed on the three peaks showed that the void peak had no activity, while the 860 kDa toxin complex fraction was highly active, and the 325 kDa peak was less active, although quite potent. SDS PAGE analysis of Sepharose CL-4B toxin complex peaks from different fermentation productions revealed two distinct peptide patterns, denoted "P" and "S". The two patterns had marked differences in the molecular weights and concentrations of peptide components in their fractions. The "S" pattern, produced most frequently, had 4 high molecular weight peptides (> 150 kDa) while the "P" pattern had 3 high molecular weight peptides. In addition, the "S" peptide fraction was found to have 2-3 fold more activity against European Corn Borer. This shift may be related to variations in protein expression due to age of inoculum and/or other factors based on growth parameters of aged cultures.

Milligram quantities of peak toxin complex fractions determined to be "P" or "S" peptide patterns were subjected to preparative SDS PAGE, and transblotted with TRIS-glycine (Seprabuff™ to PVDF membranes (ProBlott™, Applied Biosystems) for 3-4 hours. Blots were sent for amino acid analysis and N-terminal amino acid sequencing at Harvard MicroChem and Cambridge ProChem, respectively. Three peptides in the "S" pattern had unique N-terminal amino acid sequences compared to the sequences identified in the previous example. A 201 kDa (TcdA_{ij}) peptide set forth as SEQ ID NO:13 below shared between 33% amino acid identity and 50% similarity (similarity and identity were calculated by hand) with SEQ ID NO:1 (TcbA_{ij}) (in Table 10 vertical lines denote amino acid

identities and colons indicate conservative amino acid substitutions). A second peptide of 197 kDa, SEQ ID NO:14 (TcdB), had 42% identity and 58% similarity with SEQ ID NO:2 (TcaC) (similarity and identity were calculated by hand). Yet a third peptide of 205 kDa was denoted TcdA_{ii}. In addition, a limited N-terminal amino acid sequence, SEQ ID NO:16 (TcbA), of a peptide of at least 235 kDa was identical with the amino acid sequence, SEQ ID NO:12, deduced from a cloned gene (*tcbA*), SEQ ID NO:11, containing a deduced amino acid sequence corresponding to SEQ ID NO:1 (TcbA_{ii}). This indicates that the larger 235+ kDa peptide was proteolytically processed to the 201 kDa peptide, (TcbA_{ii}), (SEQ ID NO:1) during fermentation, possibly resulting in activation of the molecule. In yet another sequence, the sequence originally reported as SEQ ID NO:5 (TcaB_{ii}) reported in Example 5 above, was found to contain an aspartic acid residue (Asp) at the third position rather than glycine (Gly) and two additional amino acids Gly and Asp at the eighth and ninth positions, respectively. In yet two other sequences, SEQ ID NO:2 (TcaC) and SEQ ID NO:3 (TcaB_i), additional amino acid sequence was obtained.

Densitometric quantitation was performed using a sample that was identical to the "S" preparation sent for N-terminal analysis. This analysis showed that the 201 kDa and 197 kDa peptides represent 7.0% and 7.2%, respectively, of the total Coomassie brilliant blue stained protein in the "S" pattern and are present in amounts similar to the other abundant peptides. It was speculated that these peptides may represent protein homologs, analogous to the situation found with other bacterial toxins, such as various CryI Bt toxins. These proteins vary from 40-90% similarity at their N-terminal amino acid sequence, which encompasses the toxic fragment.

Internal Amino Acid Sequencing

To facilitate cloning of toxin peptide genes, internal amino acid sequences of selected peptides were obtained as followed.

Milligram quantities of peak 2A fractions determined to be "P" or "S" peptide patterns were subjected to preparative SDS PAGE, and transblotted with TRIS-glycine (Seprabuff™ to PVDF membranes (ProBlott™, Applied Biosystems) for 3-4 hours. Blots were sent for amino acid analysis and N-terminal amino acid sequencing at Harvard MicroChem and Cambridge ProChem, respectively. Three peptides, referred to as TcbA_{ii} (containing SEQ ID NO:1), TcdA_{ii}, and TcaB_i (containing SEQ ID NO:3) were subjected to trypsin digestion by

Harvard MicroChem followed by HPLC chromatography separate individual peptides. N-terminal amino acid analysis was performed on selected tryptic peptide fragments. Two internal peptides were sequenced for the peptide TcdA_{ii} (205 kDa peptide) referred to as TcdA_{ii}-PT111 (SEQ ID NO:17) and TcdA_{ii}-PT79 (SEQ ID NO:18). Two internal peptides were sequenced for the peptide TcaB_i (68 kDa peptide) referred to as TcaB_i-PT158 (SEQ ID NO:19) and TcaB_i-PT108 (SEQ ID NO:20). Four internal peptides were sequenced for the peptide TcbA_{ii} (201 kDa peptide) referred to as TcbA_{ii}-PT103 (SEQ ID NO:21), TcbA_{ii}-PT56 (SEQ ID NO:22), TcbA_{ii}-PT81(a) (SEQ ID NO:23), and TcbA_{ii}-PT81(b) (SEQ ID NO:24).

Table 11

N-Terminal Amino Acid Sequences

(similarity and identity were calculated by hand)

201 kDa (33% identity & 50% similarity to SEQ ID NO.1)
 L I G Y N N Q F S G * A SEQ ID NO:13
 : | | : |
 20 F I Q G Y S D L F G N - A SEQ ID NO:1
 197 kDa (42% identity & 58% similarity SEQ ID NO.2)
 M Q N S Q T F S V G E L SEQ ID NO.14
 | | : | : : |
 25 M Q D S P E V S I T T L SEQ ID NO.2

Example 8

Construction of a Cosmid Library of *Phototrabdus luminescens* W-14 Genomic DNA and its Screening to Isolate Genes Encoding Peptides Comprising the Toxic Protein Preparation

As a prerequisite for the production of *Phototrabdus* insect toxic proteins in heterologous hosts, and for other uses, it is necessary to isolate and characterize the genes that encode those peptides. This objective was pursued in parallel. One approach, described later, was based on the use of monoclonal and polyclonal antibodies raised against the purified toxin which were then used to isolate clones from an expression library. The other approach, described in this example, is based on the use of the N-terminal and internal amino acid sequence data to design degenerate oligonucleotides for use in PCR amplification. Either method can be used to identify DNA clones that contain the peptide-encoding genes so as to permit the isolation of the respective genes, and the determination of their DNA base sequence.

Genomic DNA Isolation

Photorhabdus luminescens strain W-14 (ATCC accession number 55397) was grown on 2% proteose peptone #3 agar (Difco Laboratories, Detroit, MI) and insecticidal toxin competence was maintained by repeated bioassay after passage, using the method described in Example 1 above. A 50 ml shake culture was produced in a 175 ml baffled flask in 2% proteose peptone #3 medium, grown at 28°C and 150 rpm for approximately 24 hours. 15 ml of this culture was pelleted and frozen in its medium at -20°C until it was thawed for DNA isolation. The thawed culture was centrifuged, (700 x g, 30 min) and the floating orange mucopolysaccharide material was removed. The remaining cell material was centrifuged (25,000 x g, 15 min) to pellet the bacterial cells, and the medium was removed and discarded.

Genomic DNA was isolated by an adaptation of the CTAB method described in section 2.4.1 of Current Protocols in Molecular Biology (Ausubel et al. eds, John Wiley & Sons, 1994) [modified to include a salt shock and with all volumes increased 10-fold]. The pelleted bacterial cells were resuspended in TE buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8.0) to a final volume of 10 ml, then 12 ml of 5 M NaCl was added; this mixture was centrifuged 20 min at 15,000 x g. The pellet was resuspended in 5.7 ml TE and 300 µl of 10% SDS and 60 µl of 20 mg/ml proteinase K (Gibco BRL Products, Grand Island, NY; in sterile distilled water) were added to the suspension. This mixture was incubated at 37°C for 1 hr; then approximately 10 mg lysozyme (Worthington Biochemical Corp., Freehold, NJ) was added. After an additional 45 min, 1 ml of 5 M NaCl and 800 µl of CTAB/NaCl solution (10% w/v CTAB, 0.7 M NaCl) were added. This preparation was incubated 10 min at 65°C, then gently agitated and further incubated and agitated for approximately 20 min to assist clearing of the cellular material. An equal volume of chloroform/isoamyl alcohol solution (24:1, v/v) was added, mixed gently and centrifuged. After two extractions with an equal volume of PCI (phenol/chloroform/isoamyl alcohol; 50:49:1, v/v/v; equilibrated with 1 M Tris-HCl, pH 8.0; Intermountain Scientific Corporation, Kaysville, UT), the DNA was precipitated with 0.6 volume of isopropanol. The DNA precipitate was gently removed with a glass rod, washed twice with 70% ethanol, dried, and dissolved in 2 ml STE (10 mM Tris-HCl pH 8.0, 10 mM NaCl, 1 mM EDTA). This preparation contained 2.5 mg/ml DNA, as determined by optical density at 260 nm (i.e., OD₂₆₀).

The molecular size range of the isolated genomic DNA was evaluated for suitability for library construction. CHEF gel analysis was performed in 1.5% agarose (Seakem[®] LE, FMC BioProducts, Rockland, ME) gels with 0.5 X TBE buffer (44.5 mM Tris-HCl pH 8.0, 44.5 mM H₃BO₃, 1 mM EDTA) on a BioRad CHEF-DR II apparatus with a Pulsewave 760 Switcher (Bio-Rad Laboratories, Inc., Richmond, CA). The running parameters were: initial A time, 3 sec; final A time, 12 sec; 200 volts; running temperature, 4-18°C; run time, 16.5 hr. Ethidium bromide staining and examination of the gel under ultraviolet light indicated the DNA ranged from 30-250 kbp in size.

Construction of Library

A partial Sau3A I digest was made of this *Photorhabdus* genomic DNA preparation. The method was based on section 3.1.3 of Ausubel (supra.). Adaptions included running smaller scale reactions under various conditions until nearly optimal results were achieved. Several scaled-up large reactions with varied conditions were run, the results analyzed on CHEF gels, and only the best large scale preparation was carried forward. In the optimal case, 200 µg of *Photorhabdus* genomic DNA was incubated with 1.5 units of Sau3A I (New England Biolabs, "NEB", Beverly, MA) for 15 min at 37°C in 2 ml total volume of 1X NEB 4 buffer (supplied as 10X by the manufacturer). The reaction was stopped by adding 2 ml of PCI and centrifuging at 8000 x g for 10 min. To the supernatant were added 200 µl of 5 M NaCl plus 6 ml of ice-cold ethanol. This preparation was chilled for 30 min at -20°C, then centrifuged at 12,000 x g for 15 min. The supernatant was removed and the precipitate was dried in a vacuum oven at 40°C, then resuspended in 400 µl STE. Spectrophotometric assay indicated about 40% recovery of the input DNA. The digested DNA was size fractionated on a sucrose gradient according to section 5.3.2 of CPMB (op. cit.). A 10% to 40% (w/v) linear sucrose gradient was prepared with a gradient maker in Ultra-Clear[™] tubes (Beckman Instruments, Inc., Palo Alto, CA) and the DNA sample was layered on top. After centrifugation, (26,000 rpm, 17 hr, Beckman SW41 rotor, 20°C), fractions (about 750 µl) were drawn from the top of the gradient and analyzed by CHEF gel electrophoresis (as described earlier). Fractions containing Sau3A I fragments in the size range 20-40 kbp were selected and DNA was precipitated by a modification (amounts of all solutions increased approximately 6.3-fold) of the method in section 5.3.3 of Ausubel (supra.). After overnight precipitation, the DNA was collected by centrifugation (17,000 x g, 15 min), dried, redissolved in TE,

pooled into a final volume of 80 μ l, and reprecipitated with the addition of 8 μ l 3 M sodium acetate and 220 μ l ethanol. The pellet collected by centrifugation as above was resuspended in 12 μ l TE. Concentration of the DNA was determined by Hoechst 33258 dye
5 (Polysciences, Inc., Warrington, PA) fluorometry in a Hoefer TKO100 fluorimeter (Hoefer Scientific Instruments, San Francisco, CA). Approximately 2.5 μ g of the size-fractionated DNA was recovered.

Thirty μ g of cosmid pWE15 DNA (Stratagene, La Jolla, CA) was digested to completion with 100 units of restriction enzyme BamH 1
10 (NEB) in the manufacturer's buffer (final volume of 200 μ l, 37°C, 1 hr). The reaction was extracted with 100 μ l of PCI and DNA was precipitated from the aqueous phase by addition of 20 μ l 3M sodium acetate and 550 μ l -20°C absolute ethanol. After 20 min at -70°C, the DNA was collected by centrifugation (17,000 x g, 15 min), dried
15 under vacuum, and dissolved in 180 μ l of 10 mM Tris-HCl, pH 8.0. To this were added 20 μ l of 10X CIP buffer (100 mM Tris-HCl, pH 8.3; 10 mM ZnCl₂; 10 mM MgCl₂), and 1 μ l (0.25 units) of 1:4 diluted calf intestinal alkaline phosphatase (Boehringer Mannheim Corporation, Indianapolis, IN). After 30 min at 37°C, the
20 following additions were made: 2 μ l 0.5 M EDTA, pH 8.0; 10 μ l 10% SDS; 0.5 μ l of 20 mg/ml proteinase K (as above), followed by incubation at 55°C for 30 min. Following sequential extractions with 100 μ l of PCI and 100 μ l phenol (Intermountain Scientific Corporation, equilibrated with 1 M Tris-HCl, pH 8.0), the
25 dephosphorylated DNA was precipitated by addition of 72 μ l of 7.5 M ammonium acetate and 550 μ l -20°C ethanol, incubation on ice for 30 min, and centrifugation as above. The pelleted DNA was washed once with 500 μ l -20°C 70% ethanol, dried under vacuum, and dissolved in 20 μ l of TE buffer.

30 Ligation of the size-fractionated Sau3A 1 fragments to the BamH 1-digested and phosphatased pWE15 vector was accomplished using T4 ligase (NEB) by a modification (i.e., use of premixed 10X ligation buffer supplied by the manufacturer) of the protocol in section 3.33 of Ausubel. Ligation was carried out overnight in a
35 total volume of 20 μ l at 15°C, followed by storage at -20°C.

Four μ l of the cosmid DNA ligation reaction, containing about 1 μ g of DNA, was packaged into bacteriophage lambda using a commercial packaging extract (Gigapack[®] III Gold Packaging Extract, Stratagene), following the manufacturer's directions. The packaged
40 preparation was stored at 4°C until use. The packaged cosmid preparation was used to infect *Escherichia coli* XL1 Blue MR cells

(Stratagene) according to the Gigapack[®] III Gold protocols ("Titering the Cosmid Library"), as follows. XL1 Blue MR cells were grown in LB medium (g/L: Bacto-tryptone, 10; Bacto-yeast extract, 5; Bacto-agar, 15; NaCl, 5; [Difco Laboratories, Detroit, MI]) containing 0.2% (w/v) maltose plus 10 mM MgSO₄, at 37°C. After 5 hr growth, cells were pelleted at 700 x g (15 min) and resuspended in 6 ml of 10 mM MgSO₄. The culture density was adjusted with 10 mM MgSO₄ to OD₆₀₀ = 0.5. The packaged cosmid library was diluted 1:10 or 1:20 with sterile SM medium (0.1 M NaCl, 10 mM MgSO₄, 50 mM Tris-HCl pH 7.5, 0.01% w/v gelatin), and 25 µl of the diluted preparation was mixed with 25 µl of the diluted XL1 Blue MR cells. The mixture was incubated at 25°C for 30 min (without shaking), then 200 µl of LB broth was added, and incubation was continued for approximately 1 hr with occasional gentle shaking. Aliquots (20-40 µl) of this culture were spread on LB agar plates containing 100 mg/l ampicillin (i.e., LB-Amp₁₀₀) and incubated overnight at 37°C. To store the library without amplification, single colonies were picked and inoculated into individual wells of sterile 96-well microwell plates; each well containing 75 µl of Terrific Broth (TB media: 12 g/l Bacto-tryptone, 24 g/l Bacto-yeast extract, 0.4% v/v glycerol, 17 mM KH₂PO₄, 72 mM K₂HPO₄) plus 100 mg/l ampicillin (i.e., TB-Amp₁₀₀) and incubated (without shaking) overnight at 37°C. After replicating the 96-well plate into a copy plate, 75 µl/well of filter-sterilized TB:glycerol (1:1, v/v; with, or without, 100 mg/l ampicillin) was added to the plate, it was shaken briefly at 100 rpm, 37°C, and then closed with Parafilm[®] (American National Can, Greenwich, CT) and placed in a -70°C freezer for storage. Copy plates were grown and processed identically to the master plates. A total of 40 such master plates (and their copies) were prepared.

Screening of the Library with Radiolabeled DNA Probes

To prepare colony filters for probing with radioactively labeled probes, ten 96-well plates of the library were thawed at 25°C (bench top at room temperature). A replica plating tool with 96 prongs was used to inoculate a fresh 96-well copy plate containing 75 µl/well of TB-Amp₁₀₀. The copy plate was grown overnight (stationary) at 37°C, then shaken about 30 min at 100 rpm at 37°C. A total of 800 colonies was represented in these copy plates, due to nongrowth of some isolates. The replica tool was used to inoculate duplicate impressions of the 96-well arrays onto Magna NT (MSI, Westboro, MA) nylon membranes (0.45 micron, 220 x

250 mm) which had been placed on solid LB-Amp₁₀₀ (100 ml/dish) in Bio-assay plastic dishes (Nunc, 243 x 243 x 18 mm; Curtin Mathison Scientific, Inc., Wood Dale, IL). The colonies were grown on the membranes at 37°C for about 3 hr.

- 5 A positive control colony (a bacterial clone containing a GZ4 sequence insert, see below) was grown on a separate Magna NT membrane (Nunc, 0.45 micron, 82 mm circle) on LB medium supplemented with 35 mg/l chloramphenicol (i.e., LB-Cam₃₅), and processed alongside the library colony membranes. Bacterial
- 10 colonies on the membranes were lysed, and the DNA was denatured and neutralized according to a protocol taken from the Genius™ System User's Guide version 2.0 (Boehringer Mannheim, Indianapolis, IN). Membranes were placed colony side up on filter paper soaked with 0.5 N NaOH plus 1.5 M NaCl for 15 min to denature, and neutralized
- 15 on filter paper soaked with 1 M Tris-HCl pH 8.0, 1.5 M NaCl for 15 min. After UV-crosslinking using a Stratagene UV Stratalinker set on auto crosslink, the membranes were stored dry at 25°C until use. Membranes were trimmed into strips containing the duplicate impressions of a single 96-well plate, then washed extensively by
- 20 the method of section 6.4.1 in CPMB (op. cit.): 3 hr at 25°C in 3X SSC, 0.1% (w/v) SDS, followed by 1 hr at 65°C in the same solution, then rinsed in 2X SSC in preparation for the hybridization step (20X SSC = 3 M NaCl, 0.3 M sodium citrate, pH 7.0).

25 Amplification of a Specific Genomic Fragment of a TcaC Gene

- Based on the N-terminal amino acid sequence determined for the purified TcaC peptide fraction [disclosed herein as SEQ ID NO:2], a pool of degenerate oligonucleotides (pool S4Psh) was synthesized by standard β-cyanoethyl chemistry on an Applied BioSystem ABI394
- 30 DNA/RNA Synthesizer (Perkin Elmer, Foster City, CA). The oligonucleotides were deprotected 8 hours at 55°C, dissolved in water, quantitated by spectrophotometric measurement, and diluted for use. This pool corresponds to the determined N-terminal amino acid sequence of the TcaC peptide. The determined amino acid
- 35 sequence and the corresponding degenerate DNA sequence are given below, where A, C, G, and T are the standard DNA bases, and I represents inosine:

Amino	Met	Gln	Asp	Ser	Pro	Glu	Val
Acid							
S4Psh	5' ATG	CA(A/G)	GA(T/C)	(T/A) (C/G) (T/A)	CCI	GA(A/G)	GT 3'

- Another set of degenerate oligonucleotides was synthesized (pool P2.3.5R), representing the complement of the coding strand
- 45 for the determined amino acid sequence of the SEQ ID NO:17:

Amino Acid	Ala	Phe	Asn	Ile	Asp	Asp	Val
Codons	5' GCN	TT(T/C)	AA(T/C)	AT(A/T/C)	GA(T/C)	GA(T/C)	GT 3'
5 P2.3.5R	3'CG(A/C/G/T)	AA(A/G)	TT(A/G)	TA(T/A/G)	CT(A/G)	CT(A/G)	CA 5'

These oligonucleotides were used as primers in Polymerase Chain Reactions (PCR[®], Roche Molecular Systems, Branchburg, NJ) to amplify a specific DNA fragment from genomic DNA prepared from *Photorhabdus* strain W-14 (see above). A typical reaction (50 µl) contained 125 pmol of each primer pool P2Psh and P2.3.5R, 253 ng of genomic template DNA, 10 nmol each of dATP, dCTP, dGTP, and dTTP, 1X GeneAmp[®] PCR buffer, and 2.5 units of AmpliTaq[®] DNA polymerase (both from Roche Molecular Systems; 10X GeneAmp[®] buffer is 100 mM Tris-HCl pH 8.3, 500 mM KCl, 0.01% w/v gelatin). Amplifications were performed in a Perkin Elmer Cetus DNA Thermal Cycler (Perkin Elmer, Foster City, CA) using 35 cycles of 94°C (1.0 min), 55°C (2.0 min), 72°C (3.0 min), followed by an extension period of 7.0 min at 72°C. Amplification products were analyzed by electrophoresis through 2% w/v NuSieve[®] 3:1 agarose (FMC BioProducts) in TEA buffer (40 mM Tris-acetate, 2 mM EDTA, pH 8.0). A specific product of estimated size 250 bp was observed amongst numerous other amplification products by ethidium bromide (0.5 µg/ml) staining of the gel and examination under ultraviolet light.

The region of the gel containing an approximately 250 bp product was excised, and a small plug (0.5 mm dia.) was removed and used to supply template for PCR amplification (40 cycles). The reaction (50 µl) contained the same components as above, minus genomic template DNA. Following amplification, the ends of the fragments were made blunt and were phosphorylated by incubation at 25°C for 20 min with 1 unit of T4 DNA polymerase (NEB), 1 nmol ATP, and 2.15 units of T4 kinase (Pharmacia Biotech Inc., Piscataway, NJ).

DNA fragments were separated from residual primers by electrophoresis through 1% w/v GTG[®] agarose (FMC) in TEA. A gel slice containing fragments of apparent size 250 bp was excised, and the DNA was extracted using a Qiaex kit (Qiagen Inc., Chatsworth, CA).

The extracted DNA fragments were ligated to plasmid vector pBC KS(+) (Stratagene) that had been digested to completion with restriction enzyme *Sma* I and extracted in a manner similar to that described for pWE15 DNA above. A typical ligation reaction (16.3 µl) contained 100 ng of digested pBC KS(+) DNA, 70 ng of 250 bp fragment DNA, 1 nmol [Co(NH₃)₆]Cl, and 3.9 Weiss units of T4 DNA ligase (Collaborative Biomedical Products, Bedford, MA), in 1X

ligation buffer (50 mM Tris-HCl, pH 7.4; 10 mM MgCl₂; 10 mM dithiothreitol; 1 mM spermidine, 1 mM ATP, 100 mg/ml bovine serum albumin). Following overnight incubation at 14°C, the ligated products were transformed into frozen, competent *Escherichia coli* DH5α cells (Gibco BRL) according to the suppliers' recommendations, and plated on LB-Cam₁ plates, containing IPTG (119 µg/ml) and X-gal (50 µg/ml). Independent white colonies were picked, and plasmid DNA was prepared by a modified alkaline-lysis/PEG precipitation method (PRISM™ Ready Reaction DyeDeoxy™ Terminator Cycle Sequencing Kit Protocols; ABI/Perkin Elmer). The nucleotide sequence of both strands of the insert DNA was determined, using T7 primers [pBC KS(+) bases 601-623: TAAAACGACGGCCAGTGAGCGCG) and LacZ primers [pBC KS(+) bases 792-816: ATGACCATGATTACGCCAAGCGCGC) and protocols supplied with the PRISM™ sequencing kit (ABI/Perkin Elmer). Nonincorporated dye-terminator dideoxyribonucleotides were removed by passage through Centri-Sep 100 columns (Princeton Separations, Inc., Adelphia, NJ) according to the manufacturer's instructions. The DNA sequence was obtained by analysis of the samples on an ABI Model 373A DNA Sequencer (ABI/Perkin Elmer). The DNA sequences of two isolates, GZ4 and HB14, were found to be as illustrated in Fig. 1.

This sequence illustrates the following features: 1) bases 1-20 represent one of the 64 possible sequences of the S4Psh degenerate oligonucleotides, ii) the sequence of amino acids 1-3 and 6-12 correspond exactly to that determined for the N-terminus of TcaC (disclosed as SEQ ID NO:2), iii) the fourth amino acid encoded is a cysteine residue rather than serine. This difference is encoded within the degeneracy for the serine codons (see above), iv) the fifth amino acid encoded is proline, corresponding to the TcaC N-terminal sequence given as SEQ ID NO:2, v) bases 257-276 encode one of the 192 possible sequences designed into the degenerate pool, vi) the TGA termination codon introduced at bases 268-270 is the result of complementarity to the degeneracy built into the oligonucleotide pool at the corresponding position, and does not indicate a shortened reading frame for the corresponding gene.

Labeling of a TcaC Peptide Gene-specific Probe

DNA fragments corresponding to the above 276 bases were amplified (35 cycles) by PCR[®] in a 100 µl reaction volume, using 100 pmol each of P2Psh and P2.3.5R primers, 10 ng of plasmids GZ4 or HB14 as templates, 20 nmol each of dATP, dCTP, dGTP, and dTTP, 5

units of AmpliTaq[®] DNA polymerase, and 1X concentration of GeneAmp[®] buffer, under the same temperature regimes as described above. The amplification products were extracted from a 1% GTG[®] agarose gel by Qiaex kit and quantitated by fluorometry.

5 The extracted amplification products from plasmid HB14 template (approximately 400 ng) were split into five aliquots and labeled with ³²P-dCTP using the High Prime Labeling Mix (Boehringer Mannheim) according to the manufacturer's instructions. Nonincorporated radioisotope was removed by passage through NucTrap[®] Probe Purification Columns (Stratagene), according to the
10 supplier's instructions. The specific activity of the labeled DNA product was determined by scintillation counting to be 3.11 x 10⁸ dpm/μg. This labeled DNA was used to probe membranes prepared from 800 members of the genomic library.

15 Screening with a TcaC-peptide Gene Specific Probe

The radiolabeled HB14 probe was boiled approximately 10 min, then added to "minimal hyb" solution. [Note: The "minimal hyb" method is taken from a CERES protocol; "Restriction Fragment Length
20 Polymorphism Laboratory Manual version 4.0", sections 4-40 and 4-47; CERES/NPI, Salt Lake City, UT. NPI is now defunct, with its successors operating as Linkage Genetics]. "Minimal hyb" solution contains 10% w/v PEG (polyethylene glycol, M.W. approx. 8000), 7% w/v SDS; 0.6X SSC, 10 mM sodium phosphate buffer (from a 1M stock
25 containing 95 g/l NaH₂PO₄·1H₂O and 84.5 g/l Na₂HPO₄·7H₂O), 5 mM EDTA, and 100 mg/ml denatured salmon sperm DNA. Membranes were blotted dry briefly then, without prehybridization, 5 strips of membrane were placed in each of 2 plastic boxes containing 75 ml of "minimal hyb" and 2.6 ng/ml of radiolabeled HB14 probe. These were
30 incubated overnight with slow shaking (50 rpm) at 60°C. The filters were washed three times for approximately 10 min each at 25°C in "minimal hyb wash solution" (0.25X SSC, 0.2% SDS), followed by two 30-min washes with slow shaking at 60°C in the same solution. The filters were placed on paper covered with Saran Wrap[®]
35 (Dow Brands, Indianapolis, IN) in a light-tight autoradiographic cassette and exposed to X-Omat X-ray film (Kodak, Rochester, NY) with two DuPont Cronex Lightning-Plus C1 enhancers (Sigma Chemical Co., St. Louis, MO), for 4 hr at -70°C. Upon development (standard photographic procedures), significant signals were evident in both
40 replicates amongst a high background of weaker, more irregular signals. The filters were again washed for about 4 hr at 68°C in "minimal hyb wash solution" and then placed again in the cassettes

and film was exposed overnight at -70°C . Twelve possible positives were identified due to strong signals on both of the duplicate 96-well colony impressions. No signal was seen with negative control membranes (colonies of XL1 Blue MR cells containing pWE15), and a very strong signal was seen with positive control membranes (DH5 α cells containing the GZ4 isolate of the PCR product) that had been processed concurrently with the experimental samples.

The twelve putative hybridization-positive colonies were retrieved from the frozen 96-well library plates and grown overnight at 37°C on solid LB-Amp $_{100}$ medium. They were then patched (3/plate, plus three negative controls: XL1 Blue MR cells containing the pWE15 vector) onto solid LB-Amp $_{100}$. Two sets of membranes (Magna NT nylon, 0.45 micron) were prepared for hybridization. The first set was prepared by placing a filter directly onto the colonies on a patch plate, then removing it with adherent bacterial cells, and processing as below. Filters of the second set were placed on plates containing LB-Amp $_{100}$ medium, then inoculated by transferring cells from the patch plates onto the filters. After overnight growth at 37°C , the filters were removed from the plates and processed.

Bacterial cells on the filters were lysed and DNA denatured by placing each filter colony-side-up on a pool (1.0 ml) of 0.5 N NaOH in a plastic plate for 3 min. The filters were blotted dry on a paper towel, then the process was repeated with fresh 0.5 N NaOH. After blotting dry, the filters were neutralized by placing each on a 1.0 ml pool of 1 M Tris-HCl, pH 7.5 for 3 min, blotted dry, and reneutralised with fresh buffer. This was followed by two similar soakings (5 min each) on pools of 0.5 M Tris-HCl pH 7.5 plus 1.5 M NaCl. After blotting dry, the DNA was UV crosslinked to the filter (as above), and the filters were washed (25°C , 100 rpm) in about 100 ml of 3X SSC plus 0.1%(w/v) SDS (4 times, 30 min each with fresh solution for each wash). They were then placed in a minimal volume of prehybridization solution [6X SSC plus 1% w/v each of Ficoll 400 (Pharmacia), polyvinylpyrrolidone (av. M.W. 360,000; Sigma) and bovine serum albumin Fraction V; (Sigma)] for 2 hr at 65°C , 50 rpm. The prehybridization solution was removed, and replaced with the HB14 ^{32}P -labeled probe that had been saved from the previous hybridization of the library membranes and which had been denatured at 95°C for 5 min. Hybridization was performed at 60°C for 16 hr with shaking at 50 rpm.

Following removal of the labeled probe solution, the membranes were washed 3 times at 25°C (50 rpm, 15 min) in 3X SSC (about 150 ml each wash). They were then washed for 3 hr at 68°C (50 rpm) in

0.25X SSC plus 0.2% SDS (minimal hyb wash solution), and exposed to X-ray film as described above for 1.5 hr at 25°C (no enhancer screens). This exposure revealed very strong hybridization signals to cosmid isolates 22G12, 25A10, 26A5, and 26B10, and a very weak signal with cosmid isolate 8B10. No signal was seen with the negative control (pWE15) colonies, and a very strong signal was seen with positive control membranes (DH5α cells containing the GZ4 isolate of the PCR product) that had been processed concurrently with the experimental samples.

Amplification of a Specific Genomic Fragment of a TcaB Gene

Based on the N-terminal amino acid sequence determined for the purified TcaB_i peptide fraction (disclosed here as SEQ ID NO:3) a pool of degenerate oligonucleotides (pool P8F) was synthesized as described for peptide TcaC. The determined amino acid sequence and the corresponding degenerate DNA sequence are given below, where A, C, G, and T are the standard DNA bases, and I represents inosine:

Amino Acid	Leu	Phe	Thr	Gln	Thr	Leu	Lys	Glu	Ala	Arg
P8F	5'	TTT	ACI	CA(A/G)	ACI	(C/T)TI	AAA	GAA	GCI	(A/C)G 3'
		(C/T)TI								

Another set of degenerate oligonucleotides was synthesized (pool P8.108.3R), representing the complement of the coding strand for the determined amino acid sequence of the TcaB_i-PT108 internal peptide (disclosed herein as SEQ ID NO:20):

Amino Acid	Met	Tyr	Tyr	Ile	Gln	Ala	Gln	Gln
Codons	ATG	TA(T/C)	TA(T/C)	AT(T/C/A)	CA(A/G)	GC(A/C/G/T)	CA(A/G)	CA(A/G)
P8.108.3R	3'	AT(A/G)	AT(A/G)	TA(A/G/T)	GT(T/C)	CGI	GT(T/C)	GT 5'
	TAC							

These oligonucleotides were used as primers for PCR[®] using HotStart 50 Tubes[™] (Molecular Bio-Products, Inc., San Diego, CA) to amplify a specific DNA fragment from genomic DNA prepared from *Photorhabdus* strain W-14 (see above). A typical reaction (50 μl) contained (bottom layer) 25 pmol of each primer pool P8F and P8.108.3R, with 2 nmol each of dATP, dCTP, dGTP, and dTTP, in 1X GeneAmp[®] PCR buffer, and (top layer) 230 ng of genomic template DNA, 8 nmol each of dATP, dCTP, dGTP, and dTTP, and 2.5 units of AmpliTaq[®] DNA polymerase, in 1X GeneAmp[®] PCR buffer. Amplifications were performed by 35 cycles as described for the TcaC peptide. Amplification products were analyzed by electrophoresis through

0.7% w/v Seakem[®] LE agarose (FMC) in TEA buffer. A specific product of estimated size 1600 bp was observed.

Four such reactions were pooled, and the amplified DNA was extracted from a 1.0% SeaKem[®] LE gel by Qiaex kit as described for the TcaC peptide. The extracted DNA was used directly as the template for sequence determination (PRISM[™] Sequencing Kit) using the P8F and P8.108.3R primer pools. Each reaction contained about 100 ng template DNA and 25 pmol of one primer pool, and was processed according to standard protocols as described for the TcaC peptide. An analysis of the sequence derived from extension of the P8F primers revealed the short DNA sequence (and encoded amino acid sequence):

GAT GCA TTG NTT GCT

Asp Ala Leu (Val) Ala

which corresponds to a portion of the N-terminal peptide sequence disclosed as SEQ ID NO:3 (TcaB_i).

Labeling of a TcaB_i-peptide Gene-specific Probe

Approximately 50 ng of gel-purified TcaB_i DNA fragment was labeled with ³²P-dCTP as described above, and nonincorporated radioisotopes were removed by passage through a NICK Column[®] (Pharmacia). The specific activity of the labelled DNA was determined to be 6 x 10⁹ dpm/μg. This labeled DNA was used to probe colony membranes prepared from members of the genomic library that had hybridized to the TcaC-peptide specific probe.

The membranes containing the 12 colonies identified in the TcaC-probe library screen (see above) were stripped of radioactive TcaC-specific label by boiling twice for approximately 30 min each time in 1 liter of 0.1X SSC plus 0.1 % SDS. Removal of radiolabel was checked with a 6 hr film exposure. The stripped membranes were then incubated with the TcaB_i peptide-specific probe prepared above. The labeled DNA was denatured by boiling for 10 min, and then added to the filters that had been incubated for 1 hr in 100 ml of "minimal hyb" solution at 60°C. After overnight hybridization at this temperature, the probe solution was removed, and the filters were washed as follows (all in 0.3X SSC plus 0.1% SDS): once for 5 min at 25°C, once for 1 hr at 60°C in fresh solution, and once for 1 hr at 63°C in fresh solution. After 1.5 hr exposure to X-ray film by standard procedures, 4 strongly-hybridizing colonies were observed. These were, as with the TcaC-specific probe, isolates 22G12, 25A10, 26A5, and 26B10.

The same TcaB₁ probe solution was diluted with an equal volume (about 100 ml) of "minimal hyb" solution, and then used to screen the membranes containing the 800 members of the genomic library. After hybridization, washing, and exposure to X-ray film as described above, only the four cosmid clones 22G12, 25A10, 26A5, and 26B10, were found to hybridize strongly to this probe.

Isolation of Subclones Containing Genes Encoding TcaC and YcaB₁ Peptides, and Determination of DNA Base Sequence Thereof

Three hybridization-positive cosmids in strain XL1 Blue MR were grown with shaking overnight (200 rpm) at 30°C in 100 ml TB-Amp₁₀₀. After harvesting the cells by centrifugation, cosmid DNA was prepared using a commercially available kit (BIGprep™, 5 Prime 3 Prime, Inc., Boulder, CO), following the manufacturer's protocols. Only one cosmid, 26A5, was successfully isolated by this procedure. When digested with restriction enzyme *EcoR* I (NEB) and analyzed by gel electrophoresis, fragments of approximate sizes 14, 10, 8 (vector), 5, 3.3, 2.9, and 1.5 kbp were detected. A second attempt to isolate cosmid DNA from the same three strains (8 ml cultures; TB-Amp₁₀₀, 30°C) utilized a boiling miniprep method (Evans G. and G. Wahl., 1987, "Cosmid vectors for genomic walking and rapid restriction mapping." in Guide to Molecular Cloning Techniques, Meth. Enzymology, Vol. 152, S. Berger and A. Kimmel, eds., pgs. 604-610). Only one cosmid, 25A10, was successfully isolated by this method. When digested with restriction enzyme *EcoR* I (NEB) and analyzed by gel electrophoresis, this cosmid showed a fragmentation pattern identical to that previously seen with cosmid 26A5.

A 0.15 µg sample of 26A5 cosmid DNA was used to transform 50 ml of *E. coli* DH5α cells (Gibco BRL), by the supplier's protocols. A single colony isolate of that strain was inoculated into 4 ml of TB-Amp₁₀₀, and grown for 8 hr at 37°C. Chloramphenicol was added to a final concentration of 225 µg/ml, incubation was continued for another 24 hr, then cells were harvested by centrifugation and frozen at -20°C. Isolation of the 26A5 cosmid DNA was by a standard alkaline lysis miniprep (Maniatis et al., op. cit., p. 382), modified by increasing all volumes by 50% and with stirring or gentle mixing, rather than vortexing, at every step. After washing the DNA pellet in 70% ethanol, it was dissolved in TE containing 25 µg/ml ribonuclease A (Boehringer Mannheim).

Identification of EcoR I Fragments Hybridizing to GZ4-derived and TcaB_i - Probes

Approximately 0.4 µg of cosmid 25A10 (from XL1 Blue MR cells) and about 0.5 µg of cosmid 26A5 (from chloramphenicol-amplified
5 L...5α cells) were each digested with about 15 units of EcoR I (NEB) for 85 min, frozen overnight, then heated at 65°C for five min, and electrophoresed in a 0.7% agarose gel (Seakem® LE, 1X TEA, 80 volts, 90 min). The DNA was stained with ethidium bromide as described above, and photographed under ultraviolet light. The EcoR I digest
10 of cosmid 25A10 was a complete digestion, but the sample of cosmid 26A5 was only partially digested under these conditions. The agarose gel containing the DNA fragments was subjected to depurination, denaturation and neutralization, followed by Southern blotting onto a Magna NT nylon membrane, using a high salt (20X
15 SSC) protocol, all as described in section 2.9 of Ausubel et al. (CPMB, op. cit.). The transferred DNA was then UV-crosslinked to the nylon membrane as before.

An TcaC-peptide specific DNA fragment corresponding to the insert of plasmid isolate GZ4 was amplified by PCR® in a 100 ml
20 reaction volume as described previously above. The amplification products from three such reactions were pooled and were extracted from a 1% GTG® agarose gel by Qiaex kit, as described above, and quantitated by fluorometry. The gel-purified DNA (100 ng) was labeled with ³²P-dCTP using the High Prime Labeling Mix (Boehringer
25 Mannheim) as described above, to a specific activity of 6.34 x 10⁸ dpm/µg.

The ³²P-labeled GZ4 probe was boiled 10 min, then added to "minimal hyb" buffer (at 1 ng/ml), and the Southern blot membrane containing the digested cosmid DNA fragments was added, and
30 incubated for 4 hr at 60°C with gentle shaking at 50 rpm. The membrane was then washed 3 times at 25°C for about 5 min each (minimal hyb wash solution), followed by two washes for 30 min each at 60°C. The blot was exposed to film (with enhancer screens) for about 30 min at -70°C. The GZ4 probe hybridized strongly to the
35 5.0 kbp (apparent size) EcoR I fragment of both these two cosmids, 26A5 and 25A10.

The membrane was stripped of radioactivity by boiling for about 30 min in 0.1X SSC plus 0.1 % SDS, and absence of radiolabel was checked by exposure to film. It was then hybridized at 60°C
40 for 3.5 hours with the (denatured) TcaB_i probe in "minimal hyb" buffer previously used for screening the colony membranes (above), washed as described previously, and exposed to film for 40 min at -

70°C with two enhancer screens. With both cosmids, the TcaB_i probe hybridized lightly with the about 5.0 kbp *EcoR* I fragment, and strongly with a fragment of approximately 2.9 kbp.

The sample of cosmid 26A5 DNA previously described, (from DH5α cells) was used as the source of DNA from which to subclone the bands of interest. This DNA (2.5 µg) was digested with about 3 units of *EcoR* I (NEB) in a total volume of 30 µl for 1.5 hr, to give a partial digest, as confirmed by gel electrophoresis. Ten µg of pBC KS (+) DNA (Stratagene) were digested for 1.5 hr with 20 units of *EcoR* I in a total volume of 20 µl, leading to total digestion as confirmed by electrophoresis. Both *EcoR* I-cut DNA preparations were diluted to 50 µl with water, to each an equal volume of PCI was added, the suspension was gently mixed, spun in a microcentrifuge and the aqueous supernatant was collected. DNA was precipitated by 150 µl ethanol, and the mixture was placed at -20°C overnight. Following centrifugation and drying, the *EcoR* I - digested pBC KS (+) was dissolved in 100 µl TE; the partially digested 26A5 was dissolved in 20 µl TE. DNA recovery was checked by fluorometry.

In separate reactions, approximately 60 ng of *EcoR* I -digested pBC KS(+) DNA was ligated with approximately 180 ng or 270 ng of partially digested cosmid 26A5 DNA. Ligations were carried out in a volume of 20 µl at 15°C for 5 hr, using T4 ligase and buffer from New England BioLabs. The ligation mixture, diluted to 100 µl with sterile TE, was used to transform frozen, competent DH5α cells (Gibco BRL) according to the supplier's instructions. Varying amounts (25-200 µl) of the transformed cells were plated on freshly prepared solid LB-Cam₃ medium with 1 mM IPTG and 50 mg/l X-gal. Plates were incubated at 37°C about 20 hr, then chilled in the dark for approximately 3 hr to intensify color for insert selection. White colonies were picked onto patch plates of the same composition and incubated overnight at 37°C.

Two colony lifts of each of the selected patch plates were prepared as follows. After picking white colonies to fresh plates, round Magna NT nylon membranes were pressed onto the patch plates, the membrane was lifted off, and subjected to denaturation, neutralization and UV crosslinking as described above for the library colony membranes. The crosslinked colony lifts were vigorously washed, including gently wiping off the excess cell debris with a tissue. One set was hybridized with the GZ4(TcaC) probe solution described earlier, and the other set was hybridized with the TcaB_i probe solution described earlier, according to the

'minimal hyb' protocol, followed by washing and film exposure as described for the library colony membranes.

Colonies showing hybridization signals either only with the GZ4 probe, with both GZ4 and TcaB_i probes, or only with the TcaB_i probe, were selected for further work and cells were streaked for single colony isolation onto LB-Cam₃₅ media with IPTG and X-gal as before. Approximately 35 single colonies, from 16 different isolates, were picked into liquid LB-Cam₃₅ media and grown overnight at 37°C; the cells were collected by centrifugation and plasmid DNA was isolated by a standard alkaline lysis miniprep according to Maniatis et al. (op. cit. p. 368). DNA pellets were dissolved in TE + 25 µg/ml ribonuclease A and DNA concentration was determined by fluorometry. The *EcoR* I digestion pattern was analyzed by gel electrophoresis. The following isolates were picked as useful.

Isolate A17.2 contains religated pBC KS(+) only and was used for a (negative) control. Isolates D38.3 and C44.1 each contain only the 2.9 kbp, TcaB_i -hybridizing *EcoR* I fragment inserted into pBC KS(+). These plasmids, named pDAB2000 and pDAB2001, respectively, are illustrated in Fig. 2.

Isolate A35.3 contains only the approximately 5 kbp, GZ4)-hybridizing *EcoR* I fragment, inserted into pBC KS(+). This plasmid was named pDAB2002 (also Fig. 2). These isolates provided templates for DNA sequencing.

Plasmids pDAB2000 and pDAB2001 were prepared using the BIGprep™ kit as before. Cultures (30 ml) were grown overnight in TB-Cam₃₅ to an OD₆₀₀ of 2, then plasmid was isolated according to the manufacturer's directions. DNA pellets were redissolved in 100 µl TE each, and sample integrity was checked by *EcoR* I digestion and gel electrophoretic analysis.

Sequencing reactions were run in duplicate, with one replicate using as template pDAB2000 DNA, and the other replicate using as template pDAB2001 DNA. The reactions were carried out using the dideoxy dye terminator cycle sequencing method, as described above for the sequencing of the GZ4/HB14 DNAs. Initial sequencing runs utilized as primers the LacZ and T7 primers described above, plus primers based on the determined sequence of the TcaB_i PCR amplification product (TH1 = ATTGCAGACTGCCAATCGCTTCGG, TH12 = GAGAGTATCCAGACCGCGGATGATCTG).

After alignment and editing of each sequencing output, each was truncated to between 250 to 350 bases, depending on the integrity of the chromatographic data as interpreted by the Perkin Elmer Applied Biosystems Division SeqEd 675 software. Subsequent

sequencing "steps" were made by selecting appropriate sequence for new primers. With a few exceptions, primers (synthesized as described above) were 24 bases in length with a 50% G+C composition. Sequencing by this method was carried out on both
5 strands of the approximately 2.9 kbp *EcoR* I fragment.

To further serve as template for DNA sequencing, plasmid DNA from isolate pDAB2002 was prepared by BIGprep™ kit. Sequencing reactions were performed and analyzed as described above. Initially, a T3 primer (pBS SK (+) bases 774-796:
10 CGCGCAATTAACCCTCACTAAAG) and a T7 primer (pBS KS (+) bases 621-643: GCGCGTAATACGACTCACTATAG) were used to prime the sequencing reactions from the flanking vector sequences, reading into the insert DNA. Another set of primers, (GZ4F: GTATCGATTACAACGCTGTCACTTCCC; TH13: GGGAAGTGACAGCGTTGTAATCGATAC;
15 TH14: ATGTTGGGTGCGTCGGCTAATGGACATAAC; and LW1-204: GGGAAGTGACAGCGTTGTAATCGATAC) was made to prime from internal sequences, which were determined previously by degenerate oligonucleotide-mediated sequencing of subcloned TcaC-peptide PCR products. From the data generated during the initial rounds of
20 sequencing, new sets of primers were designed and used to walk the entire length of the about 5 kbp fragment. A total of 55 oligo primers was used, enabling the identification of 4832 total bp of contiguous sequence.

When the DNA sequence of the *EcoR* I fragment insert of
25 pDAB2002 is combined with part of the determined sequence of the pDAB2000/pDAB2001 isolates, a total contiguous sequence of 6005 bp was generated (disclosed herein as SEQ ID NO:25). When long open reading frames were translated into the corresponding amino acids, the sequence clearly shows the TcaB_i N-terminal peptide (disclosed
30 as SEQ ID NO:3), encoded by bases 68-124, immediately following a methionine residue (start of translation). Upstream lies a potential ribosome binding site (bases 51-58), and downstream, at bases 215-277 is encoded the TcaB_i-PT158 internal peptide (disclosed herein as SEQ ID NO:19). Further downstream, in the
35 same reading frame, at bases 1787-1822, exists a sequence encoding the TcaB_i-PT108 internal peptide (disclosed herein as SEQ ID NO:20). Also in the same reading frame, at bases 1946-1972, is encoded the TcaB_{ii} N-terminal peptide (disclosed herein as SEQ ID NO:5), and the reading frame continues uninterrupted to a
40 translation termination codon at nucleotides 3632-3634.

The lack of an in-frame stop codon between the end of the sequence encoding TcaB_i-PT108 and the start of the TcaB_{ii} encoding

region, and the lack of a discernible ribosome binding site immediately upstream of the TcaB_{ii} coding region, indicate that peptides TcaB_{ii} and TcaB_i are encoded by a single open reading frame of 3567 bp beginning at base pair 65 in SEQ ID NO:25), and are most likely derived from a single primary gene product TcaB of 1189 amino acids (131,586 Daltons; disclosed herein as SEQ ID NO:26) by post-translational cleavage. If the amino acid immediately preceding the TcaB_{ii} N-terminal peptide represents the C-terminal amino acid of peptide TcaB_i, then the predicted mass of TcaB_{ii} (627 amino acids) is 70,814 Daltons (disclosed herein as SEQ ID NO:28), somewhat higher than the size observed by SDS-PAGE (68 kDa). This peptide would be encoded by a contiguous stretch of 1881 base pairs (disclosed herein as SEQ ID NO:27). It is thought that the native C-terminus of TcaB_i lies somewhat closer to the C-terminus of TcaB_i-PT108. The molecular mass of PT108 [3.438 kDa; determined during N-terminal amino acid sequence analysis of this peptide] predicts a size of 30 amino acids. Using the size of this peptide to designate the C-terminus of the TcaB_i coding region [Glu at position 604 of SEQ ID NO:28], the derived size of TcaB_i is determined to be 604 amino acids or 68,463 Daltons, more in agreement with experimental observations.

Translation of the TcaB_{ii} peptide coding region of 1686 base pairs (disclosed herein as SEQ ID NO:29) yields a protein of 562 amino acids (disclosed herein as SEQ ID NO:30) with predicted mass of 60,789 Daltons, which corresponds well with the observed 61 kDa.

A potential ribosome binding site (bases 3682-3687) is found 48 bp downstream of the stop codon for the tcaB open reading frame. At bases 3694-3726 is found a sequence encoding the N-terminus of peptide TcaC, (disclosed as SEQ ID NO.2). The open reading frame initiated by this N-terminal peptide continues uninterrupted to base 6005 (2361 base pairs, disclosed herein as the first 2361 base pairs of SEQ ID NO.31). A gene (tcaC) encoding the entire TcaC peptide, (apparent size about 165 kDa; about 1500 amino acids), would comprise about 4500 bp.

Another isolate containing cloned *EcoR* I fragments of cosmid 26A5, E20.6, was also identified by its homology to the previously mentioned GZ4 and TcaB_i probes. Agarose gel analysis of *EcoR* I digests of the DNA of the plasmid harbored by this strain (pDAB2004, Fig. 2), revealed insert fragments of estimated sizes 2.9, 5, and 3.3 kbp. DNA sequence analysis initiated from primers designed from the sequence of plasmid pDAB2002 revealed that the

3.3 kbp *EcoR* I fragment of pDAB2004 lies adjacent to the 5 kbp *EcoR* I fragment represented in pDAB2002. The 2361 base pair open reading frame discovered in pDAB2002 continues uninterrupted for another 2094 bases in pDAB2004 [disclosed herein as base pairs 2362 to 4458 of SEQ ID NO:31]. DNA sequence analysis using the parent cosmid 26A5 DNA as template confirmed the continuity of the open reading frame. Altogether, the open reading frame (*tcaC* SEQ ID NO:31) comprises 4455 base pairs, and encodes a protein (*TcaC*) of 1485 amino acids [disclosed herein as SEQ ID NO:32]. The calculated molecular size of 166,214 Daltons is consistent with the estimated size of the *TcaC* peptide (165 kDa), and the derived amino acid sequence matches exactly that disclosed for the *TcaC* N-terminal sequence [SEQ ID NO:2].

The lack of an amino acid sequence corresponding to SEQ ID NO:17; used to design the degenerate oligonucleotide primer pool in the discovered sequence indicates that the generation of the PCR[®] products found in isolates GZ4 and HB14, which were used as probes in the initial library screen, were fortuitously generated by reverse-strand priming by one of the primers in the degenerate pool. Further, the derived protein sequence does not include the internal fragment disclosed herein as SEQ ID NO:18. These sequences reveal that plasmid pDAB2004 contains the complete coding region for the *TcaC* peptide.

Further analysis of SEQ ID NO:25 reveals the end of an open reading frame (bases 1-43), which encodes the final 13 amino acids of the *TcaA_{iii}* peptide, disclosed herein as SEQ ID NO:35. Only 24 bases separate the end of the *TcaA_{iii}* coding region and the start of the *TcaB_i* coding region. Included within the 24 bases are sequences that may serve as a ribosome binding site. Although possible, it is not likely that a *Photorhabdus* gene promoter is encoded within this short region. We propose that genomic region *tca*, which includes three long open reading frames [*tcaA* (SEQ ID NO:33), *tcaB* (SEQ ID NO:25, bases 65-36334), and *tcaC* (SEQ ID NO:31), which is separated from the end of *tcaB* by only 59 bases] is regulated as an operon, with transcription initiating upstream of the start of the *tcaA* gene (SEQ ID NO:33), and resulting in a polycistronic messenger RNA.

Example 9
Screening of the Photorhabdus Genomic Library
for Genes Encoding the TcbA_{ii} Peptide

5 This example describes a method used to identify DNA clones that contain the TcbA_{ii} peptide-encoding genes, the isolation of the gene, and the determination of its partial DNA base sequence.

Primers and PCR Reactions

10 The TcbA_{ii} polypeptide of the insect active preparation is about 206 kDa. The amino acid sequence of the N-terminus of this peptide is disclosed as SEQ ID NO:1. Four pools of degenerate oligonucleotide primers ("Forward primers": TH-4, TH-5, TH-6, and TH-7) were synthesized to encode a portion of this amino acid
 15 sequence, as described in Example 8, and are shown below.

Table 12

	Amino Acid	Phe	Ile	Gln	Gly	Tyr	Ser	Asp	Leu	Phe
20	TH-4	5'-TT(T/C)	ATI	CA(A/G)	GGI	TA(T/C)	TCI	GA(T/C)	CTI	TT-
		3'								
	TH-5	5'-TT(T/C)	ATI	CA(A/G)	GGI	TA(T/C)	AG(T/C)	GA(T/C)	CTI	TT-
		3'								
	TH-6	5'-TT(T/C)	ATI	CA(A/G)	GGI	TA(T/C)	TCI	GA(T/C)	TT(A/G)	TT-
25		3'								
	TH-7	5'-TT(T/C)	ATI	CA(A/G)	GGI	TA(T/C)	AG(T/C)	GA(T/C)	TT(A/G)	TT-
		3'								

30 In addition, a primary ("a") and a secondary ("b") sequence of an internal peptide preparation (TcbA_{ii}-PT81) have been determined and are disclosed herein as SEQ ID NO:23 and SEQ ID NO:24, respectively. Four pools of degenerate oligonucleotides ("Reverse Primers": TH-8, TH-9, TH-10 and TH-11) were similarly designed and synthesized to encode the reverse complement of sequences that
 35 encode a portion of the peptide of SEQ ID NO:23, as shown below.

Table 13

Amino Acid	Thr	Tyr	Leu	Thr	Ser	Phe	Glu	Gln	Val	Ala	Asn
TH-8	3'TGI	AT(A/G)	GAI	TGI	AGI	AA(A/G)	CT(T/C)	GT(T/C)	CAI	CGI	TT(G/A)-5'
TH-9	3'TGI	AT(A/G)	TT(A/G)	TGI	AGI	AA(A/G)	CT(T/C)	GT(T/C)	CAI	CGI	TT(G/A)-5'
TH-10	3'TGI	AT(A/G)	GAI	TGI	TC(G/A)	AA(A/G)	CT(T/C)	GT(T/C)	CAI	CGI	TT(G/A)-5'
TH-11	3'TGI	AT(A/G)	TT(A/G)	TGI	TC(G/A)	AA(A/G)	CT(T/C)	GT(T/C)	CAI	CGI	TT(G/A)-5'

Sets of these primers were used in PCR[®] reactions to amplify TcbA_{ii}- encoding gene fragments from the genomic *Photorhabdus luminescens* W-14 DNA prepared in Example 6. All PCR[®] reactions were run with the "Hot Start" technique using AmpliWax[™] gems and other Perkin Elmer reagents and protocols. Typically, a mixture (total volume 11 μ l) of MgCl₂, dNTP's, 10X GeneAmp[®] PCR Buffer II, and the primers were added to tubes containing a single wax bead. [10X GeneAmp[®] PCR Buffer II is composed of 100 mM Tris-HCl, pH 8.3; and 500 mM KCl.] The tubes were heated to 80°C for 2 minutes and allowed to cool. To the top of the wax seals, a solution containing 10X GeneAmp[®] PCR Buffer II, DNA template, and AmpliTaq[®] DNA polymerase were added. Following melting of the wax seal and mixing of components by thermal cycling, final reaction conditions (volume of 50 μ l) were: 10 mM Tris-HCl, pH 8.3; 50 mM KCl; 2.5 mM MgCl₂; 200 μ M each in dATP, dCTP, dGTP, dTTP; 1.25 mM in a single Forward primer pool; 1.25 μ M in a single Reverse primer pool, 1.25 units of AmpliTaq[®] DNA polymerase, and 170 ng of template DNA.

The reactions were placed in a thermocycler (as in Example 8) and run with the following program:

Table 14

Temperature	Time	Cycle Repetition
94°C	2 minutes	1X
94°C	15 seconds	30X
55-65°C	30 seconds	
72°C	1 minute	
72°C	7 minutes	1X
15°C	Constant	

A series of amplifications was run at three different annealing temperatures (55°, 60°, 65°C) using the degenerate primer

pools. Reactions with annealing at 65°C had no amplification products visible following agarose gel electrophoresis. Reactions having a 60°C annealing regime and containing primers TH-5+TH-10 produced an amplification product that had a mobility corresponding to 2.9 kbp. A lesser amount of the 2.9 kbp product was produced under these conditions with primers TH-7+TH-10. When reactions were annealed at 55°C, these primer pairs produced more of the 2.9 kbp product, and this product was also produced by primer pairs TH-5+TH-8 and TH-5+TH-11. Additional very faint 2.9 kbp bands were seen in lanes containing amplification products from primer pairs TH-7 plus TH-8, TH-9, TH-10, or TH-11.

To obtain sufficient PCR amplification product for cloning and DNA sequence determination, 10 separate PCR reactions were set up using the primers TH-5+TH-10, and were run using the above conditions with a 55°C annealing temperature. All reactions were pooled and the 2.9 kbp product was purified by Qiaex extraction from an agarose gel as described above.

Additional sequences determined for TcbA_{ij} internal peptides are disclosed herein as SEQ ID NO:21 and SEQ ID NO:22. As before, degenerate oligonucleotides (Reverse primers TH-17 and TH-18) were made corresponding to the reverse complement of sequences that encode a portion of the amino acid sequence of these peptides.

Table 15

From SEQ ID NO:21

Amino Acid	Met	Glu	Thr	Gln	Asn	Ile	Gln	Glu	Pro
TH-17	3'-TAC	CTT/C	TGI	GTT/C	TTA/G	TAI	GTT/C	GTT/C	GG-5'

Table 16

From SEQ ID NO:22

Amino Acid	Asn	Pro	Ile	Asn	Ile	Asn	Thr	Gly	Ile	Asp
TH-18	3'-TT(A/G)	GGI	TAI	TT(A/G)	TAI	TT(A?G)	TGI	CCI	TAI	CT(A/G)-5'

Degenerate oligonucleotides TH-18 and TH-17 were used in an amplification experiment with *Photobacterium luminescens* W-14 DNA as template and primers TH-4, TH-5, TH-6, or TH-7 as the 5' - (Forward) primers. These reactions amplified products of approximately 4 kbp and 4.5 kbp, respectively. These DNAs were transferred from agarose gels to nylon membranes and hybridized with a ³²P-labeled probe (as described above) prepared from the 2.9 kbp product

amplified by the TH-5+TH10 primer pair. Both the 4 kbp and the 4.5 kbp amplification products hybridized strongly to the 2.9 kbp probe. These results were used to construct a map ordering the TcbA_{ii} internal peptide sequences as shown in Fig. 3. Approximate distances between the primers are shown in nucleotides in Fig. 3.

DNA Sequence of the 2.9 kbp TcbA_{ii}-encoding Fragment

Approximately 200 ng of the purified 2.9 kbp fragment (prepared above) was precipitated with ethanol and dissolved in 17 ml of water. One-half of this was used as sequencing template with 25 pmol of the TH-5 pool as primers, the other half was used as template for TH-10 priming. Sequencing reactions were as given in Example 8. No reliable sequence was produced using the TH-10 primer pool; however, reactions with TH-5 primer pool produced the sequence disclosed below:.

1	AATCGTGTTG	ATCCCTATGC	CGNGCCGGGT	TCGGTGGAAT	CGATGTCCTC	ACCGGGGGTT
61	TATTNGAGGG	ANTNGTCCCG	TGAGGCCAAA	AANTGGAATG	AAAGAAGTTC	AATTTNTTAC
121	CTAGATAAAC	GTCGCCCGGN	TTTAGAAAGN	TTANTGNTCA	GCCAGAAAAT	TTTGGTTGAG
181	GAAATTCCAC	CGNTGGTTCT	CTCTATTGAT	TNGGGCCTGG	CCGGGTTCTGA	ANNAAAACNA
20	241	GGAAATNCAC	AAGTTGAGGT	GATGGNTTTG	TNGCNANCTT	NTCGTTTAGG
301	CCTTNTCANC	ACGNTTNTGA	AACTGTCCGG	GAAATCGTCC	ATGANCGTGA	NCCAGGNTTN
361	CGCCATTGG					

Based on this sequence, a sequencing primer (TH-21, 5'-CCGGGCGACGTTTATCTAGG-3') was designed to reverse complement bases 120-139, and initiate polymerization towards the 5' end (i.e., TH-5 end) of the gel-purified 2.9 kbp TcbA_{ii}-encoding PCR fragment. The determined sequence is shown below, and is compared to the biochemically determined N-terminal peptide sequence of TcbA_{ii} SEQ ID NO:1.

TcbA_{ii} 2.9 kbp PCR Fragment Sequence Confirmation

[Underlined amino acids = encoded by degenerate oligonucleotides]

35	SEQ ID NO:1	F	I	O	G	Y	S	D	L	F	G	-	-	A
	2.9 kbp seq	GC	ATG	CAG	GGG	TAT	AGT	GAC	CTG	TTT	GGT	AAT	CGT	GCT
			M	Q	G	Y	S	D	L	F	G	N	R	A >

From the homology of the derived amino acid sequence to the biochemically determined one, it is clear that the 2.9 kbp PCR fragment represents the TcbA coding region. This 2.9 kbp fragment was then used as a hybridization probe to screen the *Phototrhhabdus* W-14 genomic library prepared in Example 8 for cosmids containing the TcbA_{ii}-encoding gene.

Screening the *Photornabodus* Cosmid Library

The 2.9 kb gel-purified PCR fragment was labeled with ^{32}P using the Boehringer Mannheim High Prime labeling kit as described in Example 8. Filters containing remnants of approximately 800 colonies from the cosmid library were screened as described previously (Example 8), and positive clones were streaked for isolated colonies and rescreened. Three clones (8A11, 25G8, and 26D1) gave positive results through several screening and characterization steps. No hybridization of the *TcbA_{ii}*-specific probe was ever observed with any of the four cosmids identified in Example 8, and which contain the *tcaB* and *tcaC* genes. DNA from cosmids 8A11, 25G8, and 26D1 was digested with restriction enzymes *Bgl* II, *EcoR* I or *Hind* III (either alone or in combination with one another), and the fragments were separated on an agarose gel and transferred to a nylon membrane as described in Example 8. The membrane was hybridized with ^{32}P -labeled probe prepared from the 4.5 kbp fragment (generated by amplification of *Photornabodus* genomic DNA with primers TH-5+TH-17). The patterns generated from cosmid DNAs 8A11 and 26D1 were identical to those generated with similarly-cut genomic DNA on the same membrane. It is concluded that cosmids 8A11 and 26D1 are accurate representations of the genomic *TcbA_{ii}* encoding locus. However, cosmid 25G8 has a single *Bgl* II fragment which is slightly larger than the genomic DNA. This may result from positioning of the insert within the vector.

DNA Sequence of the *tcbA*-encoding Gene

The membrane hybridization analysis of cosmid 26D1 revealed that the 4.5 kbp probe hybridized to a single large *EcoR* I fragment (greater than 9 kbp). This fragment was gel purified and ligated into the *EcoR* I site of pBC KS (+) as described in Example 8, to generate plasmid pBC-S1/R1. The partial DNA sequence of the insert DNA of this plasmid was determined by "primer walking" from the flanking vector sequence, using procedures described in Example 8. Further sequence was generated by extension from new oligonucleotides designed from the previously determined sequence. When compared to the determined DNA sequence for the *tcbA* gene identified by other methods (disclosed herein as SEQ ID NO:11 as described in Example 12 below), complete homology was found to nucleotides 1-272, 319-826, 2578-3036, and 3068-3540 (total bases = 1712). It was concluded that both approaches can be used to identify DNA fragments encoding the *TcbA_{ii}* peptide.

Analysis of the Derived Amino Acid Sequence of the tcbA Gene

The sequence of the DNA fragment identified as SEQ ID NO:11 encodes a protein whose derived amino acid sequence is disclosed herein as SEQ ID NO:12. Several features verify the identity of the gene as that encoding the TcbA_{ii} protein. The TcbA_{ii} N-terminal peptide (SEQ ID NO:1; Phe Ile Gln Gly Tyr Ser Asp Leu Phe Gly Asn Arg Ala) is encoded as amino acids 88-100. The TcbA_{ii} internal peptide TcbA_{ii}-PT81(a) (SEQ ID NO:23) is encoded as amino acids 1065-1077, and TcbA_{ii}-PT81(b) (SEQ ID NO:24) is encoded as amino acids 1571-1592. Further, the internal peptide TcbA_{ii}-PT56 (SEQ ID NO:22) is encoded as amino acids 1474-1488, and the internal peptide TcbA_{ii}-PT103 (SEQ ID NO:21) is encoded as amino acids 1614-1639. It is obvious that this gene is an authentic clone encoding the TcbA_{ii} peptide as isolated from insecticidal protein preparations of *Photothabdus luminescens* strain W-14.

The protein isolated as peptide TcbA_{ii} is derived from cleavage of a longer peptide. Evidence for this is provided by the fact that the nucleotides encoding the TcbA_{ii} N-terminal peptide SEQ ID NO:1 are preceded by 261 bases (encoding 87 N-terminal-proximal amino acids) of a longer open reading frame (SEQ ID NO:11). This reading frame begins with nucleotides that encode the amino acid sequence Met Gln Asn Ser Leu, which corresponds to the N-terminal sequence of the large peptide TcbA, and is disclosed herein as SEQ ID NO:16. It is thought that TcbA is the precursor protein for TcbA_{ii}.

Relationship of tcbA, tcaB and tcaC Genes

The tcaB and tcaC genes are closely linked and may be transcribed as a single mRNA (Example 8). The tcbA gene is borne on cosmids that apparently do not overlap the ones harboring the tcaB and tcaC cluster, since the respective genomic library screens identified different cosmids. However, comparison of the amino sequences encoded by the tcaB and tcaC genes with the tcbA gene reveals a substantial degree of homology. The amino acid conservation (Protein Alignment Mode of MacVector™ Sequence Analysis Software, scoring matrix pam250, hash value = 2; Oxford Molecular Group, Campbell, CA) is shown in Fig. 4. On the score line of each panel in Fig. 4, up carats (^) indicate homology or conservative amino acid changes, and down carats (v) indicate nonhomology.

This analysis shows that the amino acid sequence of the TcbA peptide from residues 1739 to 1894 is highly homologous to amino acids 441 to 603 of the TcaB_i peptide (162 of the total 627 amino acids of TcaB; SEQ ID NO:28). In addition, the sequence of TcbA amino acids 1932 to 2459 is highly homologous to amino acids 12 to 531 of peptide TcaB_{ii} (520 of the total 562 amino acids; SEQ ID NO:30). Considering that the TcbA peptide (SEQ ID NO:12) comprises 2505 amino acids, a total of 684 amino acids (27%) at the C-proximal end of it is homologous to the TcaB_i or TcaB_{ii} peptides, and the homologies are arranged colinear to the arrangement of the putative TcaB preprotein (SEQ ID NO:26). A sizeable gap in the TcbA homology coincides with the junction between the TcaB_i and TcaB_{ii} portions of the TcaB preprotein. Clearly the TcbA and TcaB gene products are evolutionarily related, and it is proposed that they share some common function(s) in *Photorhabdus*.

Example 10

Characterization of Zinc-metalloproteases in *Photorhabdus* Broth: Protease Inhibition, Classification, and Purification

Protease Inhibition and Classification Assays: Protease assays were performed using FITC-casein dissolved in water as substrate (0.08% final assay concentration). Proteolysis reactions were performed at 25°C for 1 h in the appropriate buffer with 25 µl of *Photorhabdus* broth (150 µl total reaction volume). Samples were also assayed in the presence and absence of dithiothreitol. After incubation, an equal volume of 12% trichloroacetic acid was added to precipitate undigested protein. Following precipitation for 0.5 h and subsequent centrifugation, 100 µl of the supernatant was placed into a 96-well microtiter plate and the pH of the solution was adjusted by addition of an equal volume of 4N NaOH. Proteolysis was then quantitated using a Fluoroskan II fluorometric plate reader at excitation and emission wavelengths of 485 and 538 nm, respectively. Protease activity was tested over a range from pH 5.0-10.0 in 0.5 units increments. The following buffers were used at 50 mM final concentration: sodium acetate (pH 5.0 - 6.5); Tris-HCL (pH 7.0 - 8.0); and bis-Tris propane (pH 8.5-10.0). To identify the class of protease(s) observed, crude broth was treated with a variety of protease inhibitors (0.5 µg/µl final concentration) and then examined for protease activity at pH 8.0

using the substrate described above. The protease inhibitors used included E-64 (L-trans-expoxysuccinylleucylamido[4-, -guanidino]-butane), 3,4 dichloroisocoumarin, Leupeptin, pepstatin, amastatin, ethylenediaminetetraacetic acid (EDTA) and 1,10 phenanthroline.

5 Protease assays performed over a pH range revealed that indeed protease(s) were present which exhibited maximal activity at about pH 8.0 (Table 17). Addition of DTT did not have any effect on protease activity. Crude broth was then treated with a variety of protease inhibitors (Table 18). Treatment of crude broth with the
10 inhibitors described above revealed that 1,10 phenanthroline caused complete inhibition of all protease activity when added at a final concentration of 50 μ g, with the IC_{50} = 5 μ g in 100 μ l of a 2 mg/ml crude broth solution. These data indicate that the most abundant protease(s) found in the *Photorhabdus* broth are from the zinc-
15 metalloprotease class of enzymes.

Table 17

Effect of pH on the Protease Activity Found in a Day 1 Production of *Photorhabdus luminescens* (Strain W-14)

20	pH	Flu. Units ^a	Percent Activity ^b
25	5.0	3013 \pm 78	17
30	5.5	7994 \pm 448	45
35	6.0	12965 \pm 483	74
40	6.5	14390 \pm 1291	82
45	7.0	14386 \pm 1287	82
50	7.5	14135 \pm 198	80
55	8.0	17582 \pm 831	100
60	8.5	16183 \pm 953	92
65	9.0	16795 \pm 760	96
70	9.5	16279 \pm 1022	93
75	10.0	15225 \pm 210	87

a Flu. Units = Fluorescence Units (Maximum = about 28,000; background = about 2200).

b Percent activity relative to the maximum at pH 8.0

Table 18

Effect of Different Protease Inhibitors on the Protease Activity at
pH 8 Found in a Day 1 Production of *Photorhabdus luminescens*
(Strain W-14)

Inhibitor	Corrected Flu. Units ^a	Percent Inhibition ^b
Control	13053	0
E-64	14259	0
1,10 Phenanthroline ^c	15	99
3,4 Dichloroisocoumarin ^d	7956	39
Leupeptin	13074	0
Pepstatin ^c	13441	0
Amastatin	12474	4
DMSO Control	12005	8
Methanol Control	12125	7

a Corrected Flu. Units = Fluorescence Units - background(2200 flu. units).

b Percent Inhibition relative to protease activity at pH 8.0.

c Inhibitors were dissolved in methanol.

d Inhibitors were dissolved in DMSO.

The isolation of a zinc-metalloprotease was performed by applying dialyzed 10-80% ammonium sulfate pellet to a Q Sepharose column equilibrated at 50 mM Na₂PO₄, pH 7.0 as described in Example 5 for *Photorhabdus* toxin. After extensive washing, a 0 to 0.5 M NaCl gradient was used to elute toxin protein. The majority of biological activity and protein was eluted from 0.15 - 0.45 M NaCl. However, it was observed that the majority of proteolytic activity was present in the 0.25-0.35 M NaCl fraction with some activity in the 0.15-0.25 M NaCl fraction. SDS PAGE analysis of the 0.25-0.35 M NaCl fraction showed a major peptide band of approximately 60 kDa. The 0.15-0.25 M NaCl fraction contained a similar 60 kDa band but at lower relative protein concentration. Subsequent gel filtration of this fraction using a Superose 12 HR 16/50 column resulted in a major peak migrating at 57.5 kDa that contained a predominant (> 90% of total stained protein) 58.5 kDa band by SDS PAGE analysis. Additional analysis of this fraction using various protease inhibitors as described above determined that the protease was a zinc-metalloprotease. Nearly all of the protease activity present in *Photorhabdus* broth at day 1 of fermentation corresponded to the about 58 kDa zinc-metalloprotease.

In yet a second isolation of zinc-metalloprotease(s), W-14 *Photorhabdus* broth grown for three days was taken and protease activity was visualized using sodium dodecyl sulfate-polyacrylamide

gel electrophoresis (SDS-PAGE) laced with gelatin as described in Schmidt, T.M., Bleakley, B. and Neelson, K.M. 1988. SDS running gels (5.5 x 8 cm) were made with 12.5 % polyacrylamide (40% stock solution of acrylamide/bis-acrylamide; Sigma Chemical Co., St.

- 5 Louis, MO) into which 0.1% gelatin final concentration (Biorad EIA grade reagent; Richmond CA) was incorporated upon dissolving in water. SDS-stacking gels (1.0 x 8 cm) were made with 5% polyacrylamide, also laced with 0.1% gelatin. Typically, 2.5 µg of protein to be tested was diluted in 0.03 ml of SDS-PAGE loading
10 buffer without dithiothreitol (DTT) and loaded onto the gel. Proteins were electrophoresed in SDS running buffer (Laemmli, U.K. 1970. Nature 227, 680) at 0° C and at 8 mA. After electrophoresis was complete, the gel was washed for 2 h in 2.5% (v/v) Triton X-100. Gels were then incubated for 1 h at 37 °C in 0.1 M glycine
15 (pH 8.0). After incubation, gels were fixed and stained overnight with 0.1% amido black in methanol-acetic acid- water (30:10:60, vol./vol./vol.; Sigma Chemical Co.). Protease activity was visualized as light areas against a dark, amido black stained background due to proteolysis and subsequent diffusion of
20 incorporated gelatin. At least three distinct bands produced by proteolytic activity at 58-, 41-, and 38 kDa were observed.

- Activity assays of the different proteases in W-14 day three culture broth were performed using FITC-casein dissolved in water as substrate (0.02% final assay concentration). Proteolysis
25 experiments were performed at 37°C for 0-0.5 h in 0.1M Tris-HCl (pH 8.0) with different protein fractions in a total volume of 0.15 ml. Reactions were terminated by addition of an equal volume of 12% trichloroacetic acid (TCA) dissolved in water. After incubation at room temperature for 0.25 h, samples were centrifuged at 10,000 x g
30 for 0.25 h and 0.10 ml aliquots were removed and placed into 96-well microtiter plates. The solution was then neutralized by the addition of an equal volume of 2 N sodium hydroxide, followed by quantitation using a Fluoroskan II fluorometric plate reader with excitation and emission wavelengths of 485 and 538 nm,
35 respectively. Activity measurements were performed using FITC-Casein with different protease concentrations at 37°C for 0-10 min. A unit of activity was arbitrarily defined as the amount of enzyme needed to produce 1000 fluorescent units/min and specific activity was defined as units/mg of protease.

Inhibition studies were performed using two zinc-metalloprotease inhibitors; 1,10 phenanthroline and N-(a-rhamnopyranosyloxyhydroxyphosphinyl)-Leu-Trp(phosphoramidon) with stock solutions of the inhibitors dissolved in 100% ethanol and water, respectively. Stock concentrations were typically 10 mg/ml and 5 mg/ml for 1,10 phenanthroline and phosphoramidon, respectively, with final concentrations of inhibitor at 0.5-1.0 mg/ml per reaction. Treatment of three day W-14 crude broth with 1,10 phenanthroline, an inhibitor of all zinc metalloproteases, resulted in complete elimination of all protease activity while treatment with phosphoramidon, an inhibitor of thermolysin-like proteases (Weaver, L.H., Kester, W.R., and Matthews, B.W. 1977. J. Mol. Biol. 114, 119-132), resulted in about 56% reduction of protease activity. The residual proteolytic activity could not be further reduced with additional phosphoramidon.

The proteases of three day W-14 *Photobacterium* broth were purified as follows: 4.0 liters of broth were concentrated using an Amicon spiral ultra filtration cartridge Type SLY100 attached to an Amicon M-12 filtration device. The flow-through material having native proteins less than 100 kDa in size (3.8 L) was concentrated to 0.375 L using an Amicon spiral ultra filtration cartridge Type SLY10 attached to an Amicon M-12 filtration device. The retentate material contained proteins ranging in size from 10-100 kDa. This material was loaded onto a Pharmacia HR16/10 column which had been packed with PerSeptive Biosystem (Framington, MA) Poros® 50 HQ strong anion exchange packing that had been equilibrated in 10 mM sodium phosphate buffer (pH 7.0). Proteins were loaded on the column at a flow rate of 5 ml/min, followed by washing unbound protein with buffer until $A_{280} = 0.00$. Afterwards, proteins were eluted using a NaCl gradient of 0-1.0 M NaCl in 40 min at a flow rate of 7.5 ml/min. Fractions were assayed for protease activity, supra., and active fractions were pooled. Proteolytically active fractions were diluted with 50% (v/v) 10 mM sodium phosphate buffer (pH 7.0) and loaded onto a Pharmacia HR 10/10 Mono Q column equilibrated in 10 mM sodium phosphate. After washing the column with buffer until $A_{280} = 0.00$, proteins were eluted using a NaCl gradient of 0-0.5 M NaCl for 1 h at a flow rate of 2.0 ml/min. Fractions were assayed for protease activity. Those fractions having the greatest amount of phosphoramidon-sensitive protease

activity, the phosphoramidon sensitive activity being due to the 41/38 kDa protease, *infra.*, were pooled. These fractions were found to elute at a range of 0.15-0.25 M NaCl. Fractions containing a predominance of phosphoramidon-insensitive protease activity, the 58 kDa protease, were also pooled. These fractions were found to elute at a range of 0.25-0.35 M NaCl. The phosphoramidon-sensitive protease fractions were then concentrated to a final volume of 0.75 ml using a Millipore Ultrafree®-15 centrifugal filter device Biomax-5K NMWL membrane. This material was applied at a flow rate of 0.5 ml/min to a Pharmacia HR 10/30 column that had been packed with Pharmacia Sephadex G-50 equilibrated in 10 mM sodium phosphate buffer (pH 7.0)/ 0.1 M NaCl. Fractions having the maximal phosphoramidon-sensitive protease activity were then pooled and centrifuged over a Millipore Ultrafree®-15 centrifugal filter device Biomax-50K NMWL membrane. Proteolytic activity analysis, *supra.*, indicated this material to have only phosphoramidon-sensitive protease activity. Pooling of the phosphoramidon-insensitive protease, the 58 kDa protein, was followed by concentrating in a Millipore Ultrafree®-15 centrifugal filter device Biomax-50K NMWL membrane and further separation on a Pharmacia Superdex-75 column. Fractions containing the protease were pooled.

Analysis of purified 58- and 41/38 kDa purified proteases revealed that, while both types of protease were completely inhibited with 1,10 phenanthroline, only the 41/38 kDa protease was inhibited with phosphoramidon. Further analysis of crude broth indicated that protease activity of day 1 W-14 broth has 23% of the total protease activity due to the 41/38 kDa protease, increasing to 44% in day three W-14 broth.

Standard SDS-PAGE analysis for examining protein purity and obtaining amino terminal sequence was performed using 4-20% gradient MiniPlus SeptraGels purchased from Integrated Separation Systems (Natick, MA). Proteins to be amino-terminal sequenced were blotted onto PVDF membrane following purification, *infra.*, (ProBlott™ Membranes; Applied Biosystems, Foster City, CA), visualized with 0.1% amido black, excised, and sent to Cambridge Prochem; Cambridge, MA, for sequencing.

Deduced amino terminal sequence of the 58- (SEQ ID NO:45) and 41/38 kDa (SEQ ID NO:44) proteases from three day old W-14 broth

were DV-GSEKANEKLLK (SEQ ID NO: 45) and DSGDDDKVTNHR (SEQ ID NO:44), respectively.

Sequencing of the 41/38 kDa protease revealed several amino termini, each one having an additional amino acid removed by proteolysis. Examination of the primary, secondary, tertiary and quaternary sequences for the 38 and 41 kDa polypeptides allowed for deduction of the sequence shown above and revealed that these two proteases are homologous.

Example 11. Part A

Screening of *Photorhabdus* Genomic Library Via Use of Antibodies for Genes Encoding TcbA Peptide

In parallel to the sequencing described above, suitable probing and sequencing was done based on the TcbA₁₁ peptide (SEQ ID NO:1). This sequencing was performed by preparing bacterial culture broths and purifying the toxin as described in Examples 1 and 2 above.

Genomic DNA was isolated from the *Photorhabdus luminescens* strain W-14 grown in Grace's insect tissue culture medium. The bacteria were grown in 5 ml of culture medium in a 250 ml Erlenmeyer flask at 28°C and 250 rpm for approximately 24 hours. Bacterial cells from 100 ml of culture medium were pelleted at 5000 x g for 10 minutes. The supernatant was discarded, and the cell pellets then were used for the genomic DNA isolation.

The genomic DNA was isolated using a modification of the CTAB method described in Section 2.4.3 of Ausubel (*supra.*). The section entitled "Large Scale CsCl prep of bacterial genomic DNA" was followed through step 6. At this point, an additional chloroform/isoamyl alcohol (24:1) extraction was performed followed by a phenol/chloroform/isoamyl (25:24:1) extraction step and a final chloroform/isoamyl/alcohol (24:1) extraction. The DNA was precipitated by the addition of a 0.6 volume of isopropanol. The precipitated DNA was hooked and wound around the end of a bent glass rod, dipped briefly into 70% ethanol as a final wash, and dissolved in 3 ml of TE buffer.

The DNA concentration, estimated by optical density at 280/260 nm, was approximately 2 mg/ml.

Using this genomic DNA, a library was prepared. Approximately 50 µg of genomic DNA was partly digested with Sau3 A1. Then NaCl density gradient centrifugation was used to size fractionate the partially digested DNA fragments. Fractions containing DNA

fragments with an average size of 12 kb, or larger, as determined by agarose gel electrophoresis, were ligated into the plasmid BluScript, Stratagene, La Jolla, California, and transformed into an *E. coli* DH5 α or DHB10 strain.

5 Separately, purified aliquots of the protein were sent to the biotechnology hybridoma center at the University of Wisconsin, Madison for production of monoclonal antibodies to the proteins. The material that was sent was the HPLC purified fraction containing native bands 1 and 2 which had been denatured at 65°C,
10 and 20 μ g of which was injected into each of four mice. Stable monoclonal antibody-producing hybridoma cell lines were recovered after spleen cells from unimmunized mouse were fused with a stable myeloma cell line. Monoclonal antibodies were recovered from the hybridomas.

15 Separately, polyclonal antibodies were created by taking native agarose gel purified band 1 (see Example 1) protein which was then used to immunize a New Zealand white rabbit. The protein was prepared by excising the band from the native agarose gels, briefly heating the gel pieces to 65°C to melt the agarose, and
20 immediately emulsifying with adjuvant. Freund's complete adjuvant was used for the primary immunizations and Freund's incomplete was used for 3 additional injections at monthly intervals. For each injection, approximately 0.2 ml of emulsified band 1, containing 50 to 100 micrograms of protein, was delivered by multiple
25 subcutaneous injections into the back of the rabbit. Serum was obtained 10 days after the final injection and additional bleeds were performed at weekly intervals for 3 weeks. The serum complement was inactivated by heating to 56°C for 15 minutes and then stored at -20°C.

30 The monoclonal and polyclonal antibodies were then used to screen the genomic library for the expression of antigens which could be detected by the epitope. Positive clones were detected on nitrocellulose filter colony lifts. An immunoblot analysis of the positive clones was undertaken.

35 An analysis of the clones as defined by both immunoblot and Southern analysis resulted in the tentative identification of four genomic regions.

In the first region was a gene encoding the peptide designated here as TcbA₁₁. Full DNA sequence of this gene (tcbA) was
40 obtained. It is set forth as SEQ ID NO:11. Confirmation that the sequence encodes the internal sequence of SEQ ID NO:1 is demonstrated by the presence of SEQ ID NO:1 at amino acid number 88

from the deduced amino acid sequence created by the open reading frame of SEQ ID NO:11. This can be confirmed by referring to SEQ ID NO:12, which is the deduced amino acid sequence created by SEQ ID NO:11.

5 The second region of toxin peptides contains the segments referred to above as TcaB_i, TcaB_{ii} and TcaC. Following the screening of the library with the polyclonal antisera, this second region of toxin genes was identified by several clones which produced different size proteins, all of which cross-reacted with
10 the polyclonal antibody on an immunoblot and were also found to share DNA homology on a Southern Blot. Sequence comparison revealed that they belonged to the gene complex designated TcaB and TcaC above.

15 Two other regions of antibody toxin clones were also isolated in the polyclonal screen. These regions produced proteins that cross-react with a polyclonal antibody and also shared DNA homology with the regions as determined by Southern blotting. Thus, it appears that the *Photobacterium luminescens* extracellular protein genes represent a family of genes which are evolutionarily related.

20 To further pursue the concept that there might be evolutionarily related variations in the toxin peptides contained within this organism, two approaches have been undertaken to examine other strains of *Photobacterium luminescens* for the presence of related proteins. This was done both by PCR amplification of
25 genomic DNA and by immunoblot analysis using the polyclonal and monoclonal antibodies.

30 The results indicate that related proteins are produced by *Photobacterium luminescens* strains WX-2, WX-3, WX-4, WX-5, WX-6, WX-7, WX-8, WX-11, WX-12, WX-15 and W-14.

Example 11. Part B

Sequence and Analysis of tcc Toxin Clones

35 Further DNA sequencing was performed on plasmids isolated from *E. coli* clones described in Example 11, Part A. The nucleotide sequence from the third region of *E. coli* clones was shown to be three closely linked open reading frames at this genomic locus. This locus was designated tcc with the three open reading frames designated tccA SEQ ID NO:56, tccB SEQ ID NO:58 and tccC SEQ ID
40 NO:60. The close linkage between these open reading frames is revealed by examination of SEQ ID NO:56, in which 93 bp separate the stop codon of tccA from the start codon of tccB (bases 2992-2994 of SEQ ID NO:56), and by examination of SEQ ID NO:58, in which

131 bases separate the stop codon of *tccB* and the *tccC* (bases 4930-4932 of SEQ ID NO:58). The physical map is presented in Fig. 6B.

The deduced amino acid sequence from the *tccA* open reading frame indicates that the gene encodes a protein of 105,459 Da.

- 5 This protein was designated TccA (SEQ ID NO:57). The first 12 amino acids of this protein match the N-terminal sequence obtained from a 108 kDa protein, SEQ ID NO:8, previously identified as part of the toxin complex.

- 10 The deduced amino acid sequence from the *tccB* open reading frame indicates that this gene encodes a protein of 175,716 Da. This protein was designated TccB (SEQ ID NO:59). The first 11 amino acids of this protein match the N-terminal sequence obtained from a protein with estimated molecular weight of 185 kDa, SEQ ID NO:7. Similarity analysis revealed that the TccB protein is related
- 15 to the proteins identified as TcbA SEQ ID NO:12; 37% similarity and 28% identity, TcdA SEQ ID NO:47; 35% similarity and 28% identity, and TcaB SEQ ID NO:26; 32% similarity and 26% identity (using the GAP algorithm Wisconsin Package Version 9.0, Genetics Computer Group (GCG) Madison Wisconsin).

- 20 The deduced amino acid sequence of *tccC* indicated that this open reading frame encodes a protein of 111,694 Da and the protein product was designated TccC (SEQ ID NO:61).

Example 12

25 Characterization of *Photorhabdus* Strains

- In order to establish that the collection described herein was comprised of *Photorhabdus* strains, the strains herein were assessed in terms of recognized microbiological traits that are
- 30 characteristic of *Photorhabdus* and which differentiate it from other *Enterobacteriaceae* and *Xenorhabdus* spp. (Farmer, J. J. 1984. Bergey's Manual of Systemic Bacteriology, Vol 1. pp. 510-511. (ed. Kreig N. R. and Holt, J. G.). Williams & Wilkins, Baltimore; Akhurst and Boemare, 1988, Boemare et al., 1993). These
- 35 characteristic traits are as follows: Gram's stain negative rods, organism size of 0.5-2 μ m in width and 2-10 μ m in length, red/yellow colony pigmentation, presence of crystalline inclusion bodies, presence of catalase, inability to reduce nitrate, presence of bioluminescence, ability to take up dye from growth media,
- 40 positive for protease production, growth-temperature range below 37°C, survival under anaerobic conditions and positively motile.

(Table 20). Reference *Escherichia coli*, *Xenorhabdus* and *Photorhabdus* strains were included in all tests for comparison. The overall results are consistent with all strains being part of the family *Enterobacteriaceae* and the genus *Photorhabdus*.

5 A luminometer was used to establish the bioluminescence of each strain and provide a quantitative and relative measurement of light production. For measurement of relative light emitting units, the broths from each strain (cells and media) were measured at three time intervals after inoculation in liquid culture (6, 12, 10 and 24 hr) and compared to background luminosity (uninoculated media and water). Prior to measuring light emission from the various broths, cell density was established by measuring light absorbance (560 nm) in a Gilford Systems (Oberlin, OH) spectrophotometer using a sipper cell. Appropriate dilutions were 15 then made (to normalize optical density to 1.0 unit) before measuring luminosity. Aliquots of the diluted broths were then placed into cuvettes (300 μ l each) and read in a Bio-Orbit 1251 Luminometer (Bio-Orbit Oy, Twiku, Finland). The integration period for each sample was 45 seconds. The samples were continuously 20 mixed (spun in baffled cuvettes) while being read to provide oxygen availability. A positive test was determined as being \geq 5-fold background luminescence (about 5-10 units). In addition, colony luminosity was detected with photographic film overlays and visually, after adaptation in a darkroom. The Gram's staining 25 characteristics of each strain were established with a commercial Gram's stain kit (BBL, Cockeysville, MD) used in conjunction with Gram's stain control slides (Fisher Scientific, Pittsburgh, PA). Microscopic evaluation was then performed using a Zeiss microscope (Carl Zeiss, Germany) 100X oil immersion objective lens (with 10X 30 ocular and 2X body magnification). Microscopic examination of individual strains for organism size, cellular description and inclusion bodies (the latter after logarithmic growth) was performed using wet mount slides (10X ocular, 2X body and 40X objective magnification) with oil immersion and phase contrast 35 microscopy with a micrometer (Akhurst, R.J. and Boemare, N.E. 1990. Entomopathogenic Nematodes in Biological Control (ed. Gaugler, R. and Kaya, H.). pp. 75-90. CRC Press, Boca Raton, USA.; Baghdiguian S., Boyer-Giglio M.H., Thaler, J.O., Bonnot G., Boemare N. 1993. *Biol. Cell* 79, 177-185.). Colony pigmentation was observed after

inoculation on Bacto nutrient agar, (Difco Laboratories, Detroit, MI) prepared as per label instructions. Incubation occurred at 28°C and descriptions were produced after 5-7 days. To test for the presence of the enzyme catalase, a colony of the test organism was removed on a small plug from a nutrient agar plate and placed into the bottom of a glass test tube. One ml of a household hydrogen peroxide solution was gently added down the side of the tube. A positive reaction was recorded when bubbles of gas (presumptive oxygen) appeared immediately or within 5 seconds.

Controls of uninoculated nutrient agar and hydrogen peroxide solution were also examined. To test for nitrate reduction, each culture was inoculated into 10 ml of Bacto Nitrate Broth (Difco Laboratories, Detroit, MI). After 24 hours incubation at 28°C, nitrite production was tested by the addition of two drops of sulfanilic acid reagent and two drops of alpha-naphthylamine reagent (see Difco Manual, 10th edition, Difco Laboratories, Detroit, MI, 1984). The generation of a distinct pink or red color indicates the formation of nitrite from nitrate. The ability of each strain to uptake dye from growth media was tested with Bacto MacConkey agar containing the dye neutral red; Bacto Tergitol-7 agar containing the dye bromothymol blue and Bacto EMB Agar containing the dye eosin-Y (agars from Difco Laboratories, Detroit, MI, all prepared according to label instructions). After inoculation on these media, dye uptake was recorded after incubation at 28°C for 5 days. Growth on these latter media is characteristic for members of the family *Enterobacteriaceae*. Motility of each strain was tested using a solution of Bacto Motility Test Medium (Difco Laboratories, Detroit, MI) prepared as per label instructions. A butt-stab inoculation was performed with each strain and motility was judged macroscopically by a diffuse zone of growth spreading from the line of inoculum. In many cases, motility was also observed microscopically from liquid culture under wet mount slides. Biochemical nutrient evaluation for each strain was performed using BBL Enterotube II (Benton, Dickinson, Germany). Product instructions were followed with the exception that incubation was carried out at 28°C for 5 days. Results were consistent with previously cited reports for *Photorhabdus*. The production of protease was tested by observing hydrolysis of gelatin using Bacto gelatin (Difco Laboratories, Detroit, MI)

plates made as per label instructions. Cultures were inoculated and the plates were incubated at 28°C for 5 days. To assess growth at different temperatures, agar plates [2% proteose peptone #3 with two percent Bacto-Agar (Difco, Detroit, MI) in deionized water] were streaked from a common source of inoculum. Plates were sealed with Nesco[®] film and incubated at 20, 28 and 37°C for up to three weeks. Plates showing no growth at 37°C showed no cell viability after transfer to a 28°C incubator for one week. Oxygen requirements for *Photorhabdus* strains were tested in the following manner. A butt-stab inoculation into fluid thioglycolate broth medium (Difco, Detroit, MI) was made. The tubes were incubated at room temperature for one week and cultures were then examined for type and extent of growth. The indicator resazurin demonstrates the level of medium oxidation or the aerobiosis zone (Difco Manual, 10th edition, Difco Laboratories, Detroit, MI). Growth zone results obtained for the *Photorhabdus* strains tested were consistent with those of a facultative anaerobic microorganism.

Table 19
Taxonomic Traits of *Photorhabdus* Strains

Traits Assessed*																	
Strain	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
W-14	<u>-†</u>	±	±	<u>rd S</u>	±	-	±	±	±	Q	±	±	±	±	±	±	-
WX-1	-	±	±	<u>rd S</u>	±	-	±	±	±	Q	±	±	±	±	±	±	-
WX-2	-	±	±	<u>rd S</u>	±	-	±	±	±	Q	±	±	±	±	±	±	-
WX-3	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>YT</u>	±	±	±	±	±	±	-
WX-4	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>YT</u>	±	±	±	±	±	±	-
WX-5	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>LO</u>	±	±	±	±	±	±	-
WX-6	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>LY</u>	±	±	±	±	±	±	-
WX-7	-	±	±	<u>rd S</u>	±	-	±	±	±	R	±	±	±	±	±	±	-
WX-8	-	±	±	<u>rd S</u>	±	-	±	±	±	Q	±	±	±	±	±	±	-
WX-9	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>YT</u>	±	±	±	±	±	±	-
WX-10	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>RO</u>	±	±	±	±	±	±	-
WX-11	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>RO</u>	±	±	±	±	±	±	-
WX-12	-	±	±	<u>rd S</u>	±	-	±	±	±	Q	±	±	±	±	±	±	-
WX-14	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>LR</u>	±	±	±	±	±	±	-
WX-15	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>LR</u>	±	±	±	±	±	±	-
H9	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>LY</u>	±	±	±	±	±	±	-
Hb	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>YT</u>	±	±	±	±	±	±	-
Hm	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>TY</u>	±	±	±	±	±	±	-
HP88	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>LY</u>	±	±	±	±	±	±	-
NC-1	-	±	±	<u>rd S</u>	±	-	±	±	±	Q	±	±	±	±	±	±	-
W30	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>YT</u>	±	±	±	±	±	±	-
WIR	-	±	±	<u>rd S</u>	±	-	±	±	±	<u>RO</u>	±	±	±	±	±	±	-
B2	-	±	±	<u>rd S</u>	±	-	±	±	±	R	±	±	±	±	±	±	-
43948	-	±	±	<u>rd S</u>	±	-	±	±	±	Q	±	±	±	±	±	±	-
43949	-	±	±	<u>rd S</u>	±	-	±	±	±	Q	±	±	±	±	±	±	-
43950	-	±	±	<u>rd S</u>	±	-	±	±	±	Q	±	±	±	±	±	±	-
43951	-	±	±	<u>rd S</u>	±	-	±	±	±	Q	±	±	±	±	±	±	-
43952	-	±	±	<u>rd S</u>	±	-	±	±	±	Q	±	±	±	±	±	±	-

5 * - A = Gram's stain, B=Crystalline inclusion bodies,
C=Bioluminescence, D=Cell form, E=Motility, F=Nitrate reduction,
G=Presence of catalase, H=Gelatin hydrolysis, I=Dye uptake,
J=Pigmentation, K=Growth on EMB agar, L=Growth on MacConkey agar,
M=Growth on Tergitol-7 agar, N=Facultative anaerobe, O=Growth at
10 20°C, P=Growth at 28°C, Q=Growth at 37°C, † - +/- = positive or
negative for trait, rd=rod, S=sized within Genus descriptors,
RO=red-orange, LR = light red, R= red, O= orange, Y= yellow, T=
tan, LY= light yellow, YT= yellow tan, and LO= light orange.

15 Cellular fatty acid analysis is a recognized tool for
bacterial characterization at the genus and species level
(Tornabene, T. G. 1985. Lipid Analysis and the Relationship to
Chemotaxonomy in Methods in Microbiology, Vol. 18, 209-234.;
Goodfellow, M. and O'Donnell, A. G. 1993. Roots of Bacterial
20 Systematics in Handbook of New Bacterial Systematics (ed.
Goodfellow, M. & O'Donnell, A. G.) pp. 3-54. London: Academic Press
Ltd.), these references are incorporated herein by reference, and
were used to confirm that our collection was related at the genus
level. Cultures were shipped to an external, contract laboratory

for fatty acid methyl ester analysis (FAME) using a Microbial ID (MIDI, Newark, DE, USA) Microbial Identification System (MIS). The MIS system consists of a Hewlett Packard HP5890A gas chromatograph with a 25mm x 0.2mm 5% methylphenyl silicone fused silica capillary column. Hydrogen is used as the carrier gas and a flame-ionization detector functions in conjunction with an automatic sampler, integrator and computer. The computer compares the sample fatty acid methyl esters to a microbial fatty acid library and against a calibration mix of known fatty acids. As selected by the contract laboratory, strains were grown for 24 hours at 28°C on trypticase soy agar prior to analysis. Extraction of samples was performed by the contract lab as per standard FAME methodology. There was no direct identification of the strains to any luminescent bacterial group other than *Photorhabdus*. When the cluster analysis was performed, which compares the fatty acid profiles of a group of isolates, the strain fatty acid profiles were related at the genus level.

The evolutionary diversity of the *Photorhabdus* strains in our collection was measured by analysis of PCR (Polymerase Chain Reaction) mediated genomic fingerprinting using genomic DNA from each strain. This technique is based on families of repetitive DNA sequences present throughout the genome of diverse bacterial species (reviewed by Versalovic, J., Schneider, M., DE Bruijn, F. J. and Lupski, J. R. 1994. *Methods Mol. Cell. Biol.*, 5, 25-40.). Three of these, repetitive extragenic palindromic sequence (REP), enterobacterial repetitive intergenic consensus (ERIC) and the BOX element are thought to play an important role in the organization of the bacterial genome. Genomic organization is believed to be shaped by selection and the differential dispersion of these elements within the genome of closely related bacterial strains can be used to discriminate these strains (e.g., Louws, F. J., Fulbright, D. W., Stephens, C. T. and DE Bruijn, F. J. 1994. *Appl. Environ. Micro.* 60, 2286-2295). Rep-PCR utilizes oligonucleotide primers complementary to these repetitive sequences to amplify the variably sized DNA fragments lying between them. The resulting products are separated by electrophoresis to establish the DNA "fingerprint" for each strain.

To isolate genomic DNA from our strains, cell pellets were resuspended in TE buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8.0) to a

final volume of 10 ml and 12 ml of 5 M NaCl was then added. This mixture was centrifuged 20 min. at 15,000 x g. The resulting pellet was resuspended in 5.7 ml of TE and 300 μ l of 10% SDS and 60 μ l 20 mg/ml proteinase K (Gibco BRL Products, Grand Island, NY) were added. This mixture was incubated at 37 °C for 1 hr, approximately 10 mg of lysozyme was then added and the mixture was incubated for an additional 45 min. One milliliter of 5M NaCl and 800 μ l of CTAB/NaCl solution (10% w/v CTAB, 0.7 M NaCl) were then added and the mixture was incubated 10 min. at 65°C, gently agitated, then incubated and agitated for an additional 20 min. to aid in clearing of the cellular material. An equal volume of chloroform/isoamyl alcohol solution (24:1, v/v) was added, mixed gently then centrifuged. Two extractions were then performed with an equal volume of phenol/chloroform/isoamyl alcohol (50:49:1). Genomic DNA was precipitated with 0.6 volume of isopropanol. Precipitated DNA was removed with a glass rod, washed twice with 70% ethanol, dried and dissolved in 2 ml of STE (10 mM Tris-HCl pH8.0, 10 mM NaCl, 1 mM EDTA). The DNA was then quantitated by optical density at 260 nm. To perform rep-PCR analysis of *Photorhabdus* genomic DNA the following primers were used, REP1R-I; 5'-IIIICGICGICATCIGGC-3' and REP2-I; 5'-ICGICTTATCIGGCCTAC-3'. PCR was performed using the following 25 μ l reaction: 7.75 μ l H₂O, 2.5 μ l 10X LA buffer (PanVera Corp., Madison, WI), 16 μ l dNTP mix (2.5 mM each), 1 μ l of each primer at 50 pM/ μ l, 1 μ l DMSO, 1.5 μ l genomic DNA (concentrations ranged from 0.075-0.480 μ g/ μ l) and 0.25 μ l TaKaRa EX Taq (PanVera Corp., Madison, WI). The PCR amplification was performed in a Perkin Elmer DNA Thermal Cycler (Norwalk, CT) using the following conditions: 95°C/7 min. then 35 cycles of; 94°C/1 min., 44°C/1 min., 65°C/8 min., followed by 15 min. at 65°C. After cycling, the 25 μ l reaction was added to 5 μ l of 6X gel loading buffer (0.25% bromophenol blue, 40% w/v sucrose in H₂O). A 15x20cm 1%-agarose gel was then run in TBE buffer (0.09 M Tris-borate, 0.002 M EDTA) using 8 μ l of each reaction. The gel was run for approximately 16 hours at 45v. Gels were then stained in 20 μ g/ml ethidium bromide for 1 hour and destained in TBE buffer for approximately 3 hours. Polaroid® photographs of the gels were then taken under UV illumination.

The presence or absence of bands at specific sizes for each strain was scored from the photographs and entered as a similarity

matrix in the numerical taxonomy software program, NTSYS-pc (Exeter Software, Setauket, NY). Controls of *E. coli* strain HB101 and *Xanthomonas oryzae* pv. *oryzae* assayed at the same time produced PCR "fingerprints" corresponding to published reports (Versalovic, J., Koeuth, T. and Lupski, J. R. 1991. Nucleic Acids Res. 19, 6823-6831; Vera Cruz, C. M., Halda-Alija, L., Louws, F., Skinner, D. Z., George, M. L., Nelson, R. J., DE Bruijn, F. J., Rice, C. and Leach, J. E. 1995. Int. Rice Res. Notes, 20, 23-24.; Vera Cruz, C. M., Ardales, E. Y., Skinner, D. Z., Talag, J., Nelson, R. J., Louws, F. J., Leung, H., Mew, T. W. and Leach, J. E. 1996. Phytopathology (in press, respectively). The data from *Photorhabdus* strains were then analyzed with a series of programs within NTSYS-pc; SIMQUAL (Similarity for Qualitative data) to generate a matrix of similarity coefficients (using the Jaccard coefficient) and SAHN (Sequential, Agglomerative, Hierarchical and Nested) clustering [using the UPGMA (Unweighted Pair-Group Method with Arithmetic Averages) method] which groups related strains and can be expressed as a phenogram (Fig. 5). The COPH (cophenetic values) and MXCOMP (matrix comparison) programs were used to generate a cophenetic value matrix and compare the correlation between this and the original matrix upon which the clustering was based. A resulting normalized Mantel statistic (r) was generated which is a measure of the goodness of fit for a cluster analysis ($r=0.8-0.9$ represents a very good fit). In our case $r = 0.919$. Therefore, our collection is comprised of a diverse group of easily distinguishable strains representative of the *Photorhabdus* genus.

Example 13

Insecticidal Utility of Toxin(s) Produced by Various *Photorhabdus* Strains

Initial "seed" cultures of the various *Photorhabdus* strains were produced by inoculating 175 ml of 2% Proteose Peptone #3 (PP3) (Difco Laboratories, Detroit, MI) liquid media with a primary variant subclone in a 500 ml tribaffled flask with a Delong neck, covered with a Kaput. Inoculum for each seed culture was derived from oil-overlay agar slant cultures or plate cultures. After inoculation, these flasks were incubated for 16 hrs at 28°C on a rotary shaker at 150 rpm. These seed cultures were then used as

uniform inoculum sources for a given fermentation of each strain. Additionally, overlaying the post-log seed culture with sterile mineral oil, adding a sterile magnetic stir bar for future resuspension and storing the culture in the dark, at room temperature provided long-term preservation of inoculum in a toxin-competent state. The production broths were inoculated by adding 1% of the actively growing seed culture to fresh 2% PP3 media (e.g., 1.75 ml per 175 ml fresh media). Production of broths occurred in either 500 ml tribaffled flasks (see above), or 2800 ml baffled, convex bottom flasks (500 ml volume) covered by a silicon foam closure. Production flasks were incubated for 24-48 hrs under the above mentioned conditions. Following incubation, the broths were dispensed into sterile 1 L polyethylene bottles, spun at 2600 x g for 1 hr at 10°C and decanted from the cell and debris pellet. The liquid broth was then vacuum filtered through Whatman GF/D (2.7 µM retention) and GF/B (1.0 µM retention) glass filters to remove debris. Further broth clarification was achieved with a tangential flow microfiltration device (Pall Filtron, Northborough, MA) using a 0.5 µM open-channel filter. When necessary, additional clarification could be obtained by chilling the broth (to 4°C) and centrifuging for several hours at 2600 x g. Following these procedures, the broth was filter sterilized using a 0.2 µM nitrocellulose membrane filter. Sterile broths were then used directly for biological assay, biochemical analysis or concentrated (up to 15-fold) using a 10,000 MW cut-off, M12 ultra-filtration device (Amicon, Beverly MA) or centrifugal concentrators (Millipore, Bedford, MA and Pall Filtron, Northborough, MA) with a 10,000 MW pore size. In the case of centrifugal concentrators, the broth was spun at 2000 x g for approximately 2 hr. The 10,000 MW permeate was added to the corresponding retentate to achieve the desired concentration of components greater than 10,000 MW. Heat inactivation of processed broth samples was achieved by heating the samples at 100°C in a sand-filled heat block for 10 minutes.

The broth(s) and toxin complex(es) from different *Photorhabdus* strains are useful for reducing populations of insects and were used in a method of inhibiting an insect population which comprises applying to a locus of the insect an effective insect inactivating amount of the active described. A demonstration of the breadth of insecticidal activity observed from broths of a selected group of

Photorhabdus strains fermented as described above shown in Table 20. It is possible that additional insecticidal activities could be detected with these strains through increased concentration of the broth or by employing different fermentation methods.

- 5 Consistent with the activity being associated with a protein, the insecticidal activity of all strains tested was heat labile (see above).

Culture broth(s) from diverse *Photorhabdus* strains show differential insecticidal activity (mortality and/or growth
10 inhibition, reduced adult emergence) against a number of insects. More specifically, the activity is seen against corn rootworm larvae and boll weevil larvae which are members of the insect order Coleoptera. Other members of the Coleoptera include wireworms, pollen beetles, flea beetles, seed beetles and Colorado potato
15 beetle. Activity is also observed against aster leafhopper and corn plant hopper, which are members of the order Homoptera. Other members of the Homoptera include planthoppers, pear psylla, apple sucker, scale insects, whiteflies, spittle bugs as well as numerous host specific aphid species. The broths and purified toxin
20 complex(es) are also active against tobacco budworm, tobacco hornworm and European corn borer which are members of the order Lepidoptera. Other typical members of this order are beet armyworm, cabbage looper, black cutworm, corn earworm, codling moth, clothes moth, Indian mealmoth, leaf rollers, cabbage worm,
25 cotton bollworm, bagworm, Eastern tent caterpillar, sod webworm and fall armyworm. Activity is also seen against fruitfly and mosquito larvae which are members of the order Diptera. Other members of the order Diptera are, pea midge, carrot fly, cabbage root fly, turnip root fly, onion fly, crane fly and house fly and various
30 mosquito species. Activity with broth(s) and toxin complex(es) is also seen against two-spotted spider mite which is a member of the order Acarina which includes strawberry spider mites, broad mites, citrus red mite, European red mite, pear rust mite and tomato russet mite.

- 35 Activity against corn rootworm larvae was tested as follows. *Photorhabdus* culture broth(s) (0-15 fold concentrated, filter sterilized), 2% Proteose Peptone #3, purified toxin complex(es), 10 mM sodium phosphate buffer, pH 7.0 were applied directly to the surface (about 1.5 cm²) of artificial diet (Rose, R. I. and McCabe,

J. M. (1973) . Econ. Entomol. 66, (398-400) in 40 μ l aliquots. Toxin complex was diluted in 10 mM sodium phosphate buffer, pH 7.0. The diet plates were allowed to air-dry in a sterile flow-hood and the wells were infested with single, neonate *Diabrotica*
5 *undecimpunctata howardi* (Southern corn rootworm, SCR) hatched from surface sterilized eggs. The plates were sealed, placed in a humidified growth chamber and maintained at 27°C for the appropriate period (3-5 days). Mortality and larval weight determinations were then scored. Generally, 16 insects per
10 treatment were used in all studies. Control mortality was generally less than 5%.

Activity against boll weevil (*Anthonomus grandis*) was tested as follows. Concentrated (1-10 fold) *Photorhabdus* broths, control medium (2% Proteose Peptone #3), purified toxin complex(es) [0.23
15 mg/ml] or 10 mM sodium phosphate buffer, pH 7.0 were applied in 60 μ l aliquots to the surface of 0.35 g of artificial diet (Stoneville Yellow lepidopteran diet) and allowed to dry. A single, 12-24 hr boll weevil larva was placed on the diet, and the wells were sealed and held at 25°C, 50% RH for 5 days. Mortality and larval weights
20 were then assessed. Control mortality ranged between 0-13%.

Activity against mosquito larvae was tested as follows. The assay was conducted in a 96-well microtiter plate. Each well contained 200 μ l of aqueous solution (10-fold concentrated *Photorhabdus* culture broth(s), control medium (2% Proteose Peptone
25 #3), 10 mM sodium phosphate buffer, toxin complex(es) @ 0.23 mg/ml or H₂O) and approximately 20, 1-day old larvae (*Aedes aegypti*). There were 6 wells per treatment. The results were read at 3-4 days after infestation. Control mortality was between 0-20%.

Activity against fruitflies was tested as follows. Purchased
30 *Drosophila melanogaster* medium was prepared using 50% dry medium and a 50% liquid of either water, control medium (2% Proteose Peptone #3), 10-fold concentrated *Photorhabdus* culture broth(s), purified toxin complex(es) [0.23 mg/ml] or 10 mM sodium phosphate buffer, pH 7.0. This was accomplished by placing 4.0 ml of dry
35 medium in each of 3 rearing vials per treatment and adding 4.0 ml of the appropriate liquid. Ten late instar *Drosophila melanogaster* maggots were then added to each 25 ml vial. The vials were held on a laboratory bench, at room temperature, under fluorescent ceiling lights. Pupal or adult counts were made after 15 days of exposure.

Adult emergence as compared to water and control medium (0-16% reduction).

Activity against aster leafhopper adults (*Macrosteles* *severini*) and corn planthopper nymphs (*Peregrinus maidis*) was tested with an ingestion assay designed to allow ingestion of the active without other external contact. The reservoir for the active/"food" solution is made by making 2 holes in the center of the bottom portion of a 35X10 mm Petri dish. A 2 inch Parafilm M[®] square is placed across the top of the dish and secured with an "O" ring. A 1 oz. plastic cup is then infested with approximately 7 hoppers and the reservoir is placed on top of the cup, Parafilm down. The test solution is then added to the reservoir through the holes. In tests using 10-fold concentrated *Photorhabdus* culture broth(s), the broth and control medium (2% Proteose Peptone #3) were dialyzed against 10 mM sodium phosphate buffer, pH 7.0 and sucrose (to 5%) was added to the resulting solution to reduce control mortality. Purified toxin complex(es) [0.23 mg/ml] or 10 mM sodium phosphate buffer, pH 7.0 was also tested. Mortality is reported at day 3. The assay was held in an incubator at 28°C, 70% RH with a 16/8 photoperiod. The assays were graded for mortality at 72 hours. Control mortality was less than 6%.

Activity against lepidopteran larvae was tested as follows. Concentrated (10-fold) *Photorhabdus* culture broth(s), control medium (2% Proteose Peptone #3), purified toxin complex(es) [0.23 mg/ml] or 10 mM sodium phosphate buffer, pH 7.0 were applied directly to the surface (about 1.5 cm²) of standard artificial lepidopteran diet (Stoneville Yellow diet) in 40 µl aliquots. The diet plates were allowed to air-dry in a sterile flow-hood and each well was infested with a single, neonate larva. European corn borer (*Ostrinia nubilalis*) and tobacco hornworm (*Manduca sexta*) eggs were obtained from commercial sources and hatched in-house, whereas tobacco budworm (*Heliothis virescens*) larvae were supplied internally. Following infestation with larvae, the diet plates were sealed, placed in a humidified growth chamber and maintained in the dark at 27°C for the appropriate period. Mortality and weight determinations were scored at day 5. Generally, 16 insects per treatment were used in all studies. Control mortality generally ranged from about 4 to about 12.5% for control medium and was less than 10% for phosphate buffer.

Activity against two-spotted spider mite (*Tetranychus urticae*) was determined as follows. Young squash plants were trimmed to a single cotyledon and sprayed to run-off with 10-fold concentrated broth(s), control medium (2% Proteose Peptone #3), purified toxin complex(es), 10 mM sodium phosphate buffer, pH 7.0. After drying, the plants were infested with a mixed population of spider mites and held at lab temperature and humidity for 72 hr. Live mites were then counted to determine levels of control.

Table 20
Observed Insecticidal Spectrum of Broths from
Different Photorhabdus Strains

	<u>Photorhabdus Strain</u>	<u>Sensitive* Insect Species</u>
5	WX-1	3**, 4, 5, 6, 7, 8
	WX-2	2, 4
	WX-3	1, 4
	WX-4	1, 4
10	WX-5	4
	WX-6	4
	WX-7	3, 4, 5, 6, 7, 8
	WX-8	1, 2, 4
	WX-9	1, 2, 4
15	WX-10	4
	WX-11	1, 2, 4
	WX-12	2, 4, 5, 6, 7, 8
	WX-14	1, 2, 4
	WX-15	1, 2, 4
20	W30	3, 4, 5, 8
	NC-1	1, 2, 3, 4, 5, 6, 7, 8, 9
	WIR	2, 3, 5, 6, 7, 8
	HP88	1, 3, 4, 5, 7, 8
	Hb	3, 4, 5, 7, 8
25	Hm	1, 2, 3, 4, 5, 7, 8
	H9	1, 2, 3, 4, 5, 6, 7, 8
	W-14	1, 2, 3, 4, 5, 6, 7, 8, 10
	ATCC 43948	4
	ATCC 43949	4
30	ATCC 43950	4
	ATCC 43951	4
	ATCC 43952	4

* = \geq 25% mortality and/or growth inhibition vs. control

35 ** = 1; Tobacco budworm, 2; European corn borer, 3;
Tobacco hornworm, 4; Southern corn rootworm, 5;
Boll weevil, 6; Mosquito, 7; Fruit Fly, 8;
Aster Leafhopper, 9; Corn planthopper, 10;
Two-spotted spider mite.

Example 14Non W-14 Photorhabdus Strains:Purification, Characterization and Activity Spectrum5 Purification

The protocol, as follows, is similar to that developed for the purification of W-14 and was established based on purifying those fractions having the most activity against Southern corn root worm (SCR), as determined in bioassays (see Example 13). Typically, 4-
10 20 L of broth that had been filtered, as described in Example 13, were received and concentrated using an Amicon spiral ultra filtration cartridge Type S1Y100 attached to an Amicon M-12 filtration device. The retentate contained native proteins consisting of molecular sizes greater than 100 kDa, whereas the
15 flow through material contained native proteins less than 100 kDa in size. The majority of the activity against SCR was contained in the 100 kDa retentate. The retentate was then continually diafiltered with 10 mM sodium phosphate (pH = 7.0) until the filtrate reached an $A_{280} < 0.100$. Unless otherwise stated, all
20 procedures from this point were performed in buffer as defined by 10 mM sodium phosphate (pH 7.0). The retentate was then concentrated to a final volume of approximately 0.20 L and filtered using a 0.45 mm Nalgene™ Filterware sterile filtration unit. The filtered material was loaded at 7.5 ml/min onto a Pharmacia HR16/10
25 column which had been packed with PerSeptive Biosystem Poros® 50 HQ strong anion exchange matrix equilibrated in buffer using a PerSeptive Biosystem Sprint® HPLC system. After loading, the column was washed with buffer until an $A_{280} < 0.100$ was achieved. Proteins were then eluted from the column at 2.5 ml/min using
30 buffer with 0.4 M NaCl for 20 min for a total volume of 50 ml. The column was then washed using buffer with 1.0 M NaCl at the same flow rate for an additional 20 min (final volume = 50 ml). Proteins eluted with 0.4 M and 1.0 M NaCl were placed in separate dialysis bags (Spectra/Por® Membrane MWCO: 2,000) and allowed to
35 dialyze overnight at 4° C in 12 L buffer. The majority of the activity against SCR was contained in the 0.4 M fraction. The 0.4 M fraction was further purified by application of 20 ml to a Pharmacia XK 26/100 column that had been prepacked with Sepharose CL4B (Pharmacia) using a flow rate of 0.75 ml/min. Fractions were

pooled based on A₂₈₀ peak profile and concentrated to a final volume of 0.75 ml using a Millipore Ultrafree®-15 centrifugal filter device Biomax-50K NMWL membrane. Protein concentrations were determined using a Biorad Protein Assay Kit with bovine gamma globulin as a standard.

Characterization

The native molecular weight of the SCR toxin complex was determined using a Pharmacia HR 16/50 that had been prepacked with Sepharose CL4B in buffer. The column was then calibrated using proteins of known molecular size thereby allowing for calculation of the toxin approximate native molecular size. As shown in Table 21, the molecular size of the toxin complex ranged from 777 kDa with strain Hb to 1,900 kDa with strain WX-14. The yield of toxin complex also varied, from strain WX-12 producing 0.8 mg/L to strain Hb, which produced 7.0 mg/L.

Proteins found in the toxin complex were examined for individual polypeptide size using SDS-PAGE analysis. Typically, 20 mg protein of the toxin complex from each strain was loaded onto a 2-15% polyacrylamide gel (Integrated Separation Systems) and electrophoresed at 20 mA in Biorad SDS-PAGE buffer. After completion of electrophoresis, the gels were stained overnight in Biorad Coomassie blue R-250 (0.2% in methanol: acetic acid: water; 40:10:40 v/v/v). Subsequently, gels were destained in methanol:acetic acid: water; 40:10:40 (v/v/v). The gels were then rinsed with water for 15 min and scanned using a Molecular Dynamics Personal Laser Densitometer®. Lanes were quantitated and molecular sizes were calculated as compared to Biorad high molecular weight standards, which ranged from 200-45 kDa.

Sizes of the individual polypeptides comprising the SCR toxin complex from each strain are listed in Table 22. The sizes of the individual polypeptides ranged from 230 kDa with strain WX-1 to a size of 16 kDa, as seen with strain WX-7. Every strain, with the exception of strain Hb, had polypeptides comprising the toxin complex that were in the 160-230 kDa range, the 100-160 kDa range, and the 50-80 kDa range. These data indicate that the toxin complex may vary in peptide composition and components from strain to strain, however, in all cases the toxin attributes appears to consist of a large, oligomeric protein complex.

Table 21
Characterization of a Toxin Complex from
Non W-14 Photorhabdus Strains

5

Strain	Approx. Native Molecular Wt. ^a	Yield Active Fraction (mg/L) ^b
H9	972,000	1.8
Hb	777,000	7.0
Hm	1,400,000	1.1
HP88	813,000	2.5
NC1	1,092,000	3.3
WIR	979,000	1.0
WX-1	973,000	0.8
WX-2	951,000	2.2
WX-7	1,000,000	1.5
WX-12	898,000	0.4
WX-14	1,900,000	1.9
W-14	860,000	7.5

a Native molecular weight determined using a Pharmacia HR 16/50 column packed with Sepharose CL4B
b Amount of toxin complex recovered from culture broth.

Activity Spectrum

As shown in Table 23, the toxin complexes purified from strains Hm and H9 were tested for activity against a variety of insects, with the toxin complex from strain W-14 for comparison. The assays were performed as described in Example 13. The toxin complex from all three strains exhibited activity against tobacco bud worm, European corn borer, Southern corn root worm, and aster leafhopper. Furthermore, the toxin complex from strains Hm and W-14 also exhibited activity against two-spotted spider mite. In addition, the toxin complex from W-14 exhibited activity against mosquito larvae. These data indicate that the toxin complex, while having similarities in activities between certain orders of insects, can also exhibit differential activities against other orders of insects.

Table 22

The Approximate Sizes (in kDa) of Peptides in a Purified
Toxin Complex From Non W-14 *Photobacterium*

H9	Hb	Hm	HP 88	NC-1	WIR	WX-1	WX-2	WX-7	WX-12	WX-14	W-14
180	150	170	170	180	170	230	200	200	180	210	190
170	140	140	160	170	160	190	170	180	160	180	180
160	139	100	140	140	120	170	150	110	140	160	170
140	130	81	130	110	110	160	120	87	139	120	160
120	120	72	129	44	89	110	110	75	130	110	150
98	100	68	110	16	79	98	82	43	110	100	130
87	98	49	100		74	76	64	33	92	95	120
84	88	46	86		62	58	37	28	87	80	110
79	81	30	81		51	53	30	26	80	69	93
72	75	22	77		40	41		23	73	49	90
68	69	20	73		39	35		22	59	41	77
60	60	19	60		37	31		21	56	33	69
57	57		58		33	28		19	51		65
52	54		45		30	24		18	37		63
46	49		39		28	22		16	33		60
40	44		35		27				32		51
37	39				25				26		46
	37				23						40
	35										39
											29

Table 23

Observed Insecticidal Spectrum of a Purified Toxin Complex from
Photorhabdus Strains

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10

15

<u>Photorhabdus Strain</u>	<u>Sensitive* Insect Species</u>
Hm Toxin Complex	1**, 2, 3, 5, 6, 7, 8
H9 Toxin Complex	1, 2, 3, 6, 7, 8
W-14 Toxin Complex	1, 2, 3, 4, 5, 6, 7, 8
* = > 25% mortality or growth inhibition	
* = > 25% mortality or growth inhibition	
** = 1, Tobacco bud worm; 2, European corn borer; 3, Southern corn root worm; 4, Mosquito; 5, Two-spotted spider mite; 6, Aster Leafhopper; 7, Fruit Fly; 8, Boll Weevil	

Example 15

20

Sub-Fractionation of Photorhabdus Protein Toxin Complex

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The *Photorhabdus* protein toxin complex was isolated as described in Example 14. Next, about 10 mg toxin was applied to a MonoQ 5/5 column equilibrated with 20 mM Tris-HCl, pH 7.0 at a flow rate of 1ml/min. The column was washed with 20 mM Tris-HCl, pH 7.0 until the optical density at 280 nm returned to baseline absorbance. The proteins bound to the column were eluted with a linear gradient of 0 to 1.0 M NaCl in 20 mM Tris-HCl, pH 7.0 at 1 ml/min for 30 min. One ml fractions were collected and subjected to Southern corn rootworm (SCR) bioassay (see Example 13). Peaks of activity were determined by a series of dilutions of each fraction in SCR bioassays. Two activity peaks against SCR were observed and were named A (eluted at about 0.2-0.3 M NaCl) and B (eluted at 0.3-0.4 M NaCl). Activity peaks A and B were pooled separately and both peaks were further purified using a 3-step procedure described below.

40

45

Solid $(\text{NH}_4)_2\text{SO}_4$ was added to the above protein fraction to a final concentration of 1.7 M. Proteins were then applied to a phenyl-Superose 5/5 column equilibrated with 1.7 M $(\text{NH}_4)_2\text{SO}_4$ in 50 mM potassium phosphate buffer, pH 7 at 1 ml/min. Proteins bound to the column were eluted with a linear gradient of 1.7 M $(\text{NH}_4)_2\text{SO}_4$, 0% ethylene glycol, 50 mM potassium phosphate, pH 7.0 to 25% ethylene glycol, 25 mM potassium phosphate, pH 7.0 (no $(\text{NH}_4)_2\text{SO}_4$) at 0.5 ml/min. Fractions were dialyzed overnight against 10 mM sodium phosphate buffer, pH 7.0. Activities in each fraction against SCR were determined by bioassay.

The fractions with the highest activity were pooled and applied to a MonoQ 5/5 column which was equilibrated with 20 mM Tris-HCl, pH 7.0 at 1 ml/min. The proteins bound to the column were eluted at 1 ml/min by a linear gradient of 0 to 1M NaCl in 20 mM Tris-HCl, pH 7.0.

For the final step of purification, the most active fractions above (determined by SCR bioassay) were pooled and subjected to a second phenyl-Superose 5/5/ column. Solid $(\text{NH}_4)_2\text{SO}_4$ was added to a final concentration of 1.7 M. The solution was then loaded onto the column equilibrated with 1.7 M $(\text{NH}_4)_2\text{SO}_4$ in 50 mM potassium phosphate buffer, pH 7 at 1ml/min. Proteins bound to the column were eluted with a linear gradient of 1.7 M $(\text{NH}_4)_2\text{SO}_4$, 50 mM potassium phosphate, pH 7.0 to 10 mM potassium phosphate, pH 7.0 at 0.5 ml/min. Fractions were dialyzed overnight against 10 mM sodium phosphate buffer, pH 7.0. Activities in each fraction against SCR were determined by bioassay.

The final purified protein by the above 3-step procedure from peak A was named toxin A and the final purified protein from peak B was named toxin B.

Characterization and Amino Acid Sequencing of Toxin A and Toxin B

In SDS-PAGE, both toxin A and toxin B contained two major (> 90% of total Commassie stained protein) peptides: 192 kDa (named A1 and B1, respectively) and 58 kDa (named A2 and B2, respectively). Both toxin A and toxin B revealed only one major band in native PAGE, indicating A1 and A2 were subunits of one protein complex, and B1 and B2 were subunits of one protein complex. Further, the native molecular weight of both toxin A and toxin B were determined to be 860 kDa by gel filtration chromatography. The relative molar concentrations of A1 to A2 was judged to be a 1 to 1 equivalence as determined by densitometric analysis of SDS-PAGE gels. Similarly, B1 and B2 peptides were present at the same molar concentration.

Toxin A and toxin B were electrophoresed in 10% SDS-PAGE and transblotted to PVDF membranes. Blots were sent for amino acid analysis and N-terminal amino acid sequencing at Harvard MicroChem and Cambridge ProChem, respectively. The N-terminal amino sequence of B1 was determined to be identical to SEQ ID NO:1, the TcbA_{iii} region of the tcbA gene (SEQ ID NO:12, position 87 to 99). A unique N-terminal sequence was obtained for peptide B2 (SEQ ID NO:40). The N-terminal amino acid sequence of peptide B2 was identical to the TcbA_{iii} region of the derived amino acid sequence

for the *tcbA* gene (SEQ ID NO:12, position 1935 to 1945). Therefore, the B toxin contained predominantly two peptides, TcbA_{ii} and TcbA_{iii}, that were observed to be derived from the same gene product, TcbA.

5 The N-terminal sequence of A2 (SEQ ID NO:41) was unique in comparison to the TcbA_{iii} peptide and other peptides. The A2 peptide was denoted TcdA_{iii} (see Example 17). SEQ ID NO:6 was determined to be a mixture of amino acid sequences SEQ ID NO:40 and 41.

10 Peptides A1 and A2 were further subjected to internal amino acid sequencing. For internal amino acid sequencing, 10 µg of toxin A was electrophoresized in 10% SDS-PAGE and transblotted to PVDF membrane. After the blot was stained with amido black, peptides A1 and A2, denoted TcdA_{ii} and TcdA_{iii}, respectively, were
15 excised from the blot and sent to Harvard MicroChem and Cambridge ProChem. Peptides were subjected to trypsin digestion followed by HPLC chromatography to separate individual peptides. N-terminal amino acid analysis was performed on selected tryptic peptide fragments. Two internal amino acid sequences of peptide A1
20 (TcdA_{ii}-PK71, SEQ ID NO:38 and TcdA_{ii}-PK44, SEQ ID NO:39) were found to have significant homologies with deduced amino acid sequences of the TcbA_{ii} region of the *tcbA* gene (SEQ ID NO:12). Similarly, the N-terminal sequence (SEQ ID NO:41) and two internal sequences of peptides A2 (TcdA_{iii}-PK57, SEQ ID NO:42 and TcdA_{iii}-
25 PK20, SEQ ID NO:43) also showed significant homology with deduced amino acid sequences of TcbA_{iii} region of the *tcbA* gene (SEQ ID NO:12).

30 In summary of above results, the toxin complex has at least two active protein toxin complexes against SCR; toxin A and toxin B. Toxin A and toxin B are similar in their native and subunits molecular weight, however, their peptide compositions are different. Toxin A contained peptides TcdA_{ii} and TcdA_{iii} as the major peptides and the toxin B contains TcbA_{ii} and TcbA_{iii} as the major peptides.

35

Purification and Characterization of Toxin C. Tca Peptides

The *Photothabdus* protein toxin complex was isolated as described above. Next, about 50 mg toxin was applied to a MonoQ 10/10 column equilibrated with 20 mM Tris-HCl, pH 7.0 at a flow
40 rate of 2 ml/min. The column was washed with 20 mM Tris-HCl, pH7.0

until the optical density at 280 nm returned to baseline level. The proteins bound to the column were eluted with a linear gradient of 0 to 1M NaCl in 20 mM Tris-HCl, pH 7.0 at 2 ml/min for 60 min. 2 ml fractions were collected and subjected to Western analysis using pAb TcaB₁₁-syn antibody (see Example 21) as the primary antibody. Fractions reacted with pAb TcaB₁₁-syn antibody were combined and solid (NH₄)₂SO₄ was added to a final concentration of 1.7 M. Proteins were then applied to a phenyl-Superose 10/10 column equilibrated with 1.7 M (NH₄)₂SO₄ in 50 mM potassium phosphate buffer, pH 7 at 1ml/min. Proteins bound to the column were eluted with a linear gradient of 1.7 M (NH₄)₂SO₄, 50 mM potassium phosphate, pH 7.0 to 10 mM potassium phosphate, pH 7.0 at 1 ml/min for 120 min. 2ml Fractions were collected, dialyzed overnight against 10 mM sodium phosphate buffer, pH 7.0, and analyzed by Western blots using pAb TcaB₁₁-syn antibody as the primary antibody.

Fractions cross-reacted with the antibody were pooled and applied to a MonoQ 5/5 column which was equilibrated with 20 mM Tris-HCl, pH 7.0 at 1ml/min. The proteins bound to the column were eluted at 1ml/min by a linear gradient of 0 to 1M NaCl in 20 mM Tris-HCl, pH 7.0 for 30 min.

Fractions above reacted with pAb TcaB₁₁-syn antibody were pooled and subjected to a phenyl-Superose 5/5/ column. Solid (NH₄)₂SO₄ added to a final concentration of 1.7 M. The solution was then applied onto the column equilibrated with 1.7 M (NH₄)₂SO₄ in 50 mM potassium phosphate buffer, pH 7 at 1ml/min. Proteins bound to the column were then eluted with a linear gradient of 1.7 M (NH₄)₂SO₄, 50 mM potassium phosphate, pH 7.0 to 10 mM potassium phosphate, pH 7.0 at 0.5 ml/min for 60 min. Fractions were dialyzed overnight against 10 mM sodium phosphate buffer, pH 7.0.

For the final purification step, fractions reacted with pAb TcaB₁₁-syn antibody above determined by Western analysis were combined and applied to a Mono Q 5/5 column equilibrated with 20 mM Tris-HCl, pH 7.0 at 1ml/min. The proteins bound to the column were eluted at 1ml/min by a linear gradient of 0 to 1M NaCl in 20 mM Tris-HCl, pH 7.0 for 30 min.

The final purified protein fraction contained 6 major peptides examined by SDS-PAGE: 165 kDa, 90 kDa, 64 kDa, 62 kDa, 58 kDa, and 22 kDa. The LD50 of the insecticidal activities of this purified

fraction were determined to be 100 ng and 500 ng against SCR and ECB, respectively.

The above peptides were blotted to PVDF membranes and blots were sent for amino acids analysis and 5 amino acid long N-terminal sequencing at Harvard MicroChem and Cambridge ProChem, respectively. The N-terminal amino acid sequence of the 165 kDa peptide was determined to be identical to peptide TcaC (SEQ ID 2, position 1 to 5). The N-terminal amino acid sequence of the 90 kDa peptide was determined to be TcaA_{ii} region of the derived amino acid sequence for the tcaA gene (SEQ ID NO 33, position 254 to 258). The N-terminal amino acid sequence of 64 kDa peptide was determined to be identical to peptide TcaB_i (SEQ ID 3, position 1 to 5). The N-terminal amino acid sequence of the 62 kDa peptide was determined to be TcaA_{ii} region of the derived amino acid sequence for the tcaA gene (SEQ ID NO 33, position 489 to 493). The N-terminal amino acid sequence of 58 kDa peptide was determined to be identical to peptide TcaB_{ii} (SEQ ID 5, position 1 to 5). The N-terminal amino acid sequence of the 22 kDa peptide (SEQ ID NO 62) was determined to be TcaA_i region, denoted TcaA_{iv}, of the derived amino acid sequence for the tcaA gene (SEQ ID NO 34, position 98 to 102). It is noted that all tcaA, tcaB, and tcaC genes reside in the same tca operon (Fig. 6A).

Five µg of purified Tca fraction, purified toxin A, and purified toxin B were analyzed by Western blot using the following antibodies individually as primary antibody: pAb TcaB_{ii}-syn antibody, mAb CF52 antibody, pAb TcdA_{ii}-syn antibody, and pAb Tcd_{iii}-syn antibody (Example 21). With pAb TcaB_{ii}-syn antibody only the purified Tca peptides fraction reacted, but not toxin A or toxin B. With mAb CF52 antibody, only toxin B reacted but not Tca peptides fraction or toxin A. With either pAb TcdA_{ii}-syn antibody or pAb Tcd_{iii}-syn antibody only toxin A reacted, but not Tca peptides fraction or toxin B. This indicated that the insecticidal activity observed in the purified Tca peptides fraction is independent of toxin A and toxin B. The purified Tca peptide fraction is a third unique protein toxin, denoted toxin C.

Example 16Cleavage and Activation of TcbA Peptide

In the toxin B complex, peptide TcbA_{ii} and TcbA_{iii} originate
5 from the single gene product TcbA (Example 15). The processing of
TcbA peptide to TcbA_{ii} and TcbA_{iii} is presumably by the action of
Photothabdus protease(s), and most likely, the metalloproteases
described in Example 10. In some cases, it was noted that when
Photothabdus W-14 broth was processed, TcbA peptide was present in
10 toxin B complex as a major component, in addition to peptides
TcbA_{ii} and TcbA_{iii}. Identical procedures, described for the
purification of toxin B complex (Example 15), were used to enrich
peptide TcbA from toxin complex fraction of W-14 broth. The final
purified material was analyzed in a 4-20% gradient SDS-PAGE and
15 major peptides were quantified by densitometry. It was determined
that TcbA, TcbA_{ii} and TcbA_{iii} comprised 58%, 36%, and 6%,
respectively, of total protein. The identities of these peptides
were confirmed by their respective molecular sizes in SDS-PAGE and
Western blot analysis using monospecific antibodies. The native
20 molecular weight of this fraction was determined to be 860 kDa.

The cleavage of TcbA was evaluated by treating the above
purified material with purified 38 kDa and 58 kDa W-14 *Photothabdus*
metalloproteases (Example 10), and trypsin as a control enzyme
(Sigma, MO). The standard reaction consisted 17.5 µg the above
25 purified fraction, 1.5 unit protease, and 0.1 M Tris buffer, pH 8.0
in a total volume of 100 µl. For the control reaction, protease
was omitted. The reaction mixtures were incubated at 37°C for 90
min. At the end of the reaction, 20 µl was taken and boiled with
SDS-PAGE sample buffer immediately for electrophoresis analysis in
30 a 4-20% gradient SDS-PAGE. It was determined from SDS-PAGE that in
both 38 kDa and 58 kDa protease treatments, the amount of peptides
TcbA_{ii} and TcbA_{iii} increased about 3-fold while the amount of TcbA
peptide decreased proportionally (Table 24). The relative
reduction and augmentation of selected peptides was confirmed by
35 Western blot analyses. Furthermore, gel filtration of the cleaved
material revealed that the native molecular size of the complex
remained the same. Upon trypsin treatment, peptides TcbA and
TcbA_{ii} were nonspecifically digested into small peptides. This
indicated that 38 kDa and 58 kDa *Photothabdus* proteases can

specifically process peptide TcbA into peptides TcbA_{ii} and TcbA_{iii}. Protease treated and untreated control of the remaining 80 μ l reaction mixture were serially diluted with 10 mM sodium phosphate buffer, pH 7.0 and analyzed by SCR bioassay. By comparing activity in several dilutions, it was determined that the 38 kDa protease treatment increased SCR insecticidal activity approximately 3 to 4 fold. The growth inhibition of remaining insects in the protease treatment was also more severe than control (Table 24).

10

Table 24

Conversion and Activation of Peptide TcbA into Peptides TcbA_{ii} and TcbA_{iii} by Protease Treatment

	Control	38 kDa protease treatment
TcbA (% of total protein)	58	18
15 TcbA _{ii} (% of total protein)	36	64
TcbA _{iii} (% of total protein)	6	18
LD50 (μ g protein)	2.1	0.52
SCR Weight (mg/insect)*	0.2	0.1

20 *: an indication of growth inhibition by measuring the average weight of live insect after 5 days on diet in the assay.

Activation and Procession of Toxin B by SCR Gut Proteases

In yet a second demonstration of proteolytic activation, it was examined whether W-14 toxins are processed by insects. Toxin B purified from *Photorhabdus* W-14 broth (see Example 15) was comprised of predominantly intact TcbA peptides as judged by SDS-PAGE and Western blot analysis using monoclonal antibody. The LD50 of this fraction against SCR was determined to be around 700 ng.

30 SCR larva were grown on coleopteran diet until they reached the fourth instar stage (about 100-125 mg total weight each insect). SCR gut content was collected as follows: the guts were removed using dissecting scissors and forceps. After removing the excess fatty material that coats the gut lining, about 40 guts were homogenized in a microcentrifuge tube containing 100 μ l sterile water. The tube was then centrifuged at 14,000 rpm for 10 minutes and the pellet discarded. The supernatant was stored at a -70°C freezer until use.

40 The processing of toxin B by insect gut was evaluated by treating the above purified toxin B with the SCR gut content collected. The reaction consisted 40 μ g toxin B (1 mg/ml), 50 μ l

SCR gut content, and 0.1M Tris buffer, pH 8.0 in a total volume of 100 μ l. For the control reaction, SCR gut content was omitted. The reaction mixtures were incubated at 37°C for overnight. At the end of reaction, 10 μ l was withdraw and boiled with equal volume 2x SDS-PAGE sample buffer for SDS-PAGE analysis. The remaining 90 μ l reaction mixture was serial diluted with 10 mM sodium phosphate buffer, pH 7.0 and analyzed by SCR bioassay. SDS-PAGE analysis indicated in SCR gut content treatment, peptide TcbA was digested completely into smaller peptides. Analysis of the undenatured toxin fraction showed that the native size, about 860 kDa, remained the same even though larger peptides were fragmented. In SCR bioassays, it was found that the LD50 of SCR gut treated toxin B to be about 70 ng; representing a 10-fold increase. In a separate experiment, protease K treatment completely eliminated toxin activity.

Example 17

Screening of the Library for a Gene Encoding the TcdA_{ij} Peptide

The cloning and characterization of a gene encoding the TcdA_{ij} peptide, described as SEQ ID NO:17 (internal peptide TcdA_{ij}-PT111 N-terminal sequence) and SEQ ID NO:18 (internal peptide TcdA_{ij}-PT79 N-terminal sequence) was completed. Two pools of degenerate oligonucleotides, designed to encode the amino acid sequences of SEQ ID NO:17 (Table 25) and SEQ ID NO:18 (Table 26), and the reverse complements of those sequences, were synthesized as described in Example 8. The DNA sequence of the oligonucleotides is given below:

Table 25
Degenerate Oligonucleotide for SEQ ID NO:17

P2-PT111	1	2	3	4	5	6	7	8
Amino Acid	Ala	Phe	Asn	Ile	Asp	Asp	Val	Ser
Codons	5' GCN	TT(T/C)	AA(T/C)	AT(T/C/A)	GA(T/C)	GA(T/C)	GTN 3'	
P2.3.6.CB	5' GC(A/C/G/T)	TT(T/C)	AAT	ATT	GAT	GAT	GT 3'	
P2.3.5	5' GC(A/C/G/T)	TT(T/C)	AA(T/C)	AT(T/C/A)	GA(T/C)	GA(T/C)	GT 3'	
P2.3.5R	5' AC	(G/A)TC	(G/A)TC	(T/G/A)AT	(G/A)TT	(G/A)AA	(A/C/G/T)GC 3'	
P2.3.5RI	5' ACI	TCI	TCI	ATI	TTI	AAI	GC 3'	
P2.3R.CB	5' CAG	(A/G)CT	(A/C)AC	ATC	ATC	AAT	ATT	AAA 3'

Table 26
Degenerate Oligonucleotide for SEQ ID NO:18

P2-PT79	1	2	3	4	5	6	7	8	9	10	11	12	13
Amino Acid	Phe	Ile	Val	Tyr	Thr	Ser	Leu	Gly	Val	Asn	Pro	Asn	Asn
Codons*	5' TTY	ATH	GTN	TAY	ACN	6	6	GGN	GTN	AAY	CCN	AAY	AAY 3'
P2.79.2	5' TTY	ATY	GTK	TAT	ACY	TCI	YTR	GGY	GTK	AAT	CCR	AAT	AAT 3'
P2.79.3	5' TTT	ATT	GTK	TAT	ACY	AGY	YTR	GGY	GTK	AAT	CCR	AAT	AAT 3'
P2.79.R.1	5' ATT	ATT	YGG	ATT	MAC	RCC	YAR	RCT	RGT	ATA	MAC	AAT	AAA 3'
P2.79R.CB	5' ATT	ATT	YGG	ATT	MAC	ACC	CAG	RCT	GGT	ATA	MAC	AAT	AAA 3'

* According to IUPAC-IUB codes for nucleotides, Y = C or T, H = A, C or T,
 N = A, C, G or T, K = G or T, R = A or G, and M = A or C

Polymerase Chain Reactions (PCR) were performed essentially as described in Example 8, using as forward primers P2.3.6.CB or P2.3.5, and as reverse primers P2.79.R.1 or P2.79R.CB, in all forward/reverse combinations, using *Photorhabdus* W-14 genomic DNA as template. In another set of reactions, primers P2.79.2 or P2.79.3 were used as forward primers, and P2.3.5R, P2.3.5RI, and P2.3R.CB were used as reverse primers in all forward/reverse combinations. Only in the reactions containing P2.3.6.CB as the forward primers combined with P2.79.R.1 or P2.79R.CB as the reverse primers was a non-artifactual amplified product seen, of estimated size (mobility on agarose gels) of 2500 base pairs. The order of the primers used to obtain this amplification product indicates that the peptide fragment TcdA_{ii}-PT111 lies amino-proximal to the peptide fragment TcdA_{ii}-PT79.

The 2500 bp PCR products were ligated to the plasmid vector pCR™II (Invitrogen, San Diego, CA) according to the supplier's instructions, and the DNA sequences across the ends of the insert fragments of two isolates (HS24 and HS27) were determined using the supplier's recommended primers and the sequencing methods described previously. The sequence of both isolates was the same. New primers were synthesized based on the determined sequence, and used to prime additional sequencing reactions to obtain a total of 2557 bases of the insert [SEQ ID NO:36]. Translation of the partial peptide encoded by SEQ ID No: 36 yields the 845 amino acid sequence disclosed as SEQ ID NO:37. Protein homology analysis of this portion of the TcdA_{ii} peptide fragment reveals substantial amino acid homology ((68% similarity, and 53% identity using the Wisconsin Package Version 8.0, Genetics Computer Group (GCG), Madison, WI) to residues 542 to 1390 of protein TcbA [SEQ ID NO:12] or (60% similarity, and 54% identity using the Wisconsin Package Version 9.0, Genetics Computer Group (GCG), Madison, WI to residues 567 to 1389)). It is therefore apparent that the gene represented in part by SEQ ID NO:36 produces a protein of similar, but not identical, amino acid sequence as the TcbA protein, and which likely has similar, but not identical biological activity as the TcbA protein.

In yet another instance, a gene encoding the peptides TcdA_{iii}-PK44 and the TcdA_{iii} 58 kDa N-terminal peptide, described as SEQ ID NO:39 (internal peptide TcdA_{iii}-PK44 sequence), and SEQ ID NO:41 (TcdA_{iii} 58 kDa N-terminal peptide sequence) was isolated.

Two pools of degenerate oligonucleotides, designed to encode the amino acid sequences described as SEQ ID NO:39 (Table 28) and SEQ ID NO:41 (Table 27), and the reverse complements of those sequences, were synthesized as described in Example 8, and their
5 DNA sequences.

Table 27
 Degenerate Oligonucleotide for SEQ ID NO:41

Codon #	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Amino Acid	Leu	Arg	Ser	Ala	Asn	Thr	Leu	Thr	Asp	Leu	Phe	Leu	Pro	Gln
A2.1	5' YTR	CGY	AGY	GCI	AAT	ACY	YTR	ACY	GAT	YTR	TTT	YTR	CCR	CA 3'
A2.2				GCI	AAT	ACI	YTR	ACI	GAY	YTR	TTY	YTR	CCI	CA 3'
A2.3.R		5' TG	YGG	YAR	AAA	YAR	RTC	RGY	YAR	RGY	RTT	IGC	RCT	RCG 3'
A2.4.R				5' TG	IGG	CGG	AAA	CGG	RTC	IGT	CPG	IGT	ATT	IGC 3'

Table 28
 Degenerate Oligonucleotide for SEQ ID NO:39

Amino Acid #	(8)	(9)	(10)	(11)	(12)	(13)	(14)	(15)	(16)
Codon #	1	2	3	4	5	6	7	8	9
Amino Acid	Gly	Pro	Val	Glu	Ile	Asn	Thr	Ala	Ile
A1.44.1	5' GGY	CCR	GTK	GAA	ATT	AAT	ACC	GCI	AT 3'
A1.44.1R	5' ATI	GCG	GTA	TTA	ATT	TCM	ACY	GGR	CC 3'
A1.44.2	5' GGI	CCI	GTI	GAR	ATY	AAV	ACI	GCI	AT 3'
A1.44.2R	5' ATI	GCI	GTR	TTR	ATY	TCI	ACI	GGI	CC 3'

Polymerase Chain Reactions (PCR) were performed essentially as described in Example 8, using as forward primers A1.44.1 or A1.44.2, and reverse primers A2.3R or A2.4R, in all forward/reverse combinations, using *Photorhabdus* W-14 genomic DNA as template. In another set of reactions, primers A2.1 or A2.2 were used as forward primers, and A1.44.1R, and A1.44.2R were used as reverse primers in all forward/reverse combinations. Only in the reactions containing A1.44.1 or A1.44.2 as the forward primers combined with A2.3R as the reverse primer was a non-artifactual amplified product seen, of estimated size (mobility on agarose gels) of 1400 base pairs. The order of the primers used to obtain this amplification product indicates that the peptide fragment TcdA_{ii}-PK44 lies amino-proximal to the 58 kDa peptide fragment of TcdA_{iii}.

The 1400 bp PCR products were ligated to the plasmid vector pCR[™]II according to the supplier's instructions. The DNA sequences across the ends of the insert fragments of four isolates were determined using primers similar in sequence to the supplier's recommended primers and using sequencing methods described previously. The nucleic acid sequence of all isolates differed as expected in the regions corresponding to the degenerate primer sequences, but the amino acid sequences deduced from these data were the same as the actual amino acid sequences for the peptides determined previously, (SEQ ID NOS:41 and 39).

Screening of the W-14 genomic cosmid library as described in Example 8 with a radiolabeled probe comprised of the DNA prepared above (SEQ ID NO:36) identified five hybridizing cosmid isolates, namely 17D9, 20B10, 21D2, 27B10, and 26D1. These cosmids were distinct from those previously identified with probes corresponding to the genes described as SEQ ID NO:11 or SEQ ID NO:25. Restriction enzyme analysis and DNA blot hybridizations identified three *EcoR* I fragments, of approximate sizes 3.7, 3.7, and 1.1 kbp, that span the region comprising the DNA of SEQ ID NO:36. Screening of the W-14 genomic cosmid library using as probe the radiolabeled 1.4 kbp DNA fragment prepared in this example identified the same five cosmids (17D9, 20B10, 21D2, 27B10, and 26D1). DNA blot hybridization to *EcoR* I-digested cosmid DNAs also showed hybridization to the same subset of *EcoR* I fragments as seen with the 2.5 kbp TcdA_{ii} gene probe, indicating that both fragments are encoded on the genomic DNA.

DNA sequence determination of the cloned EcoRI fragments revealed an uninterrupted reading frame of 7551 base pairs (SEQ ID NO:46), encoding a 282.9 kDa protein of 2516 amino acids (SEQ ID NO:47). Analysis of the amino acid sequence of this protein revealed all expected internal fragments of peptides TcdA_{ii} (SEQ ID NOS:17, 18, 37, 38 and 39) and the TcdA_{iii} peptide N-terminus (SEQ ID NO:41) and all TcdA_{iii} internal peptides (SEQ ID NOS:42 and 43). The peptides isolated and identified as TcdA_{ii} and TcdA_{iii} are each products of the open reading frame, denoted tcdA, disclosed as SEQ ID NO:46. Further, SEQ ID NO:47 shows, starting at position 89, the sequence disclosed as SEQ ID NO:13, which is the N-terminal sequence of a peptide of size approximately 201 kDa, indicating that the initial protein produced from SEQ ID NO: 46 is processed in a manner similar to that previously disclosed for SEQ ID NO:12. In addition, the protein is further cleaved to generate a product of size 209.2 kDa, encoded by SEQ ID NO:48 and disclosed as SEQ ID NO:49 (TcdA_{ii} peptide), and a product of size 63.6 kDa, encoded by SEQ ID NO:50 and disclosed as SEQ ID NO:51 (TcdA_{iii} peptide). Thus, it is thought that the insecticidal activity identified as toxin A (Example 15) derived from the products of SEQ ID NO:46, as exemplified by the full-length protein of 282.9 kDa disclosed as SEQ ID NO:47, is processed to produce the peptides disclosed as SEQ ID NOS:49 and 51. It is thought that the insecticidal activity identified as toxin B (Example 15) derives from the products of SEQ ID NO:11, as exemplified by the 280.6 kDa protein disclosed as SEQ ID NO:12. This protein is proteolytically processed to yield the 207.6 kDa peptide disclosed as SEQ ID NO:53, which is encoded by SEQ ID NO:52, and the 62.9 kDa peptide having N-terminal sequence disclosed as SEQ ID NO:40, and further disclosed as SEQ ID NO:55, which is encoded by SEQ ID NO:54.

Amino acid sequence comparisons between the proteins disclosed as SEQ ID NO:12 and SEQ ID NO:47 reveal that they have 69% similarity and 54% identity using the Wisconsin Package Version 8.0, Genetics Computer Group (GCG), Madison, WI or 60% similarity and 54% identity using version 9.0 of the program. This high degree of evolutionary relationship is not uniform throughout the entire amino acid sequence of these peptides, but is higher towards the carboxy-terminal end of the proteins, since the peptides disclosed as SEQ ID NO:51 (derived from SEQ ID NO:47) and SEQ ID

NO:55 (derived from SEQ ID NO:12) have 76% similarity and 64% identity using the Wisconsin Package Version 8.0, Genetics Computer Group (GCG), Madison, WI or 71% similarity and 64% identity using version 9.0 of the program.

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Example 18

Control of European Cornborer-Induced Leaf Damage on Maize Plants by Spray Application of *Photorhabdus* (Strain W-14) Broth

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The ability of *Photorhabdus* toxin(s) to reduce plant damage caused by insect larvae was demonstrated by measuring leaf damage caused by European corn borer (*Ostrinia nubilalis*) infested onto maize plants treated with *Photorhabdus* broth. Fermentation broth from *Photorhabdus* strain W-14 was produced and concentrated approximately 10-fold using ultrafiltration (10,000 MW pore-size) as described in Example 13. The resulting concentrated broth was then filter sterilized using 0.2 micron nitrocellulose membrane filters. A similarly prepared sample of uninoculated 2% proteose peptone #3 was used for control purposes. Maize plants (an inbred line) were grown from seed to vegetative stage 7 or 8 in pots containing a soilless mixture in a greenhouse (27°C day; 22°C night, about 50%RH, 14 hr day-length, watered/fertilized as needed). The test plants were arranged in a randomized complete block design (3 reps/treatment, 6 plants/treatment) in a greenhouse with temperature about 22°C day; 18°C night, no artificial light and with partial shading, about 50%RH and watered/fertilized as needed. Treatments (uninoculated media and concentrated *Photorhabdus* broth) were applied with a syringe sprayer, 2.0 mls applied from directly (about 6 inches) over the whorl and 2.0 additional mls applied in a circular motion from approximately one foot above the whorl. In addition, one group of plants received no treatment. After the treatments had dried (approximately 30 minutes), twelve neonate European corn borer larvae (eggs obtained from commercial sources and hatched in-house) were applied directly to the whorl. After one week, the plants were scored for damage to the leaves using a modified Guthrie Scale (Kozziel, M. G., Beland, G. L., Bowman, C., Carozzi, N. B., Crenshaw, R., Crossland, L., Dawson, J., Desai, N., Hill, M., Kadwell, S., Launis, K., Lewis,

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K., Maddox, D., McPherson, K., Meghji, M. Z., Merriam, E., Rhodes, R., Warren, G. W., Wright, M. and Evola, S. V. 1993).

Bio/Technology, 11, 194-195.) and the scores were compared statistically [T-test (LSD) $p < 0.05$ and Tukey's Studentized Range (HSD) Test $p < 0.1$]. The results are shown in Table 29. For reference, a score of 1 represents no damage, a score of 2 represents fine "window pane" damage on the unfurled leaf with no pinhole penetration and a score of 5 represents leaf penetration with elongated lesions and/or mid rib feeding evident on more than three leaves (lesions < 1 inch). These data indicate that broth or other protein containing fractions may confer protection against specific insect pests when delivered in a sprayable formulation or when the gene or derivative thereof, encoding the protein or part thereof, is delivered via a transgenic plant or microbe.

Table 29

Effect of Photorhabdus Culture Broth on
European Corn Borer-Induced Leaf Damage on Maize

Treatment	Average Guthrie Score
No Treatment	5.02 ^a
Uninoculated medium	5.15 ^a
Photorhabdus Broth	2.24 ^b
Means with different letters are statistically different ($p < 0.05$ or $p < 0.1$).	

Example 19

Genetic Engineering of Genes for Expression in *E. coli*

Summary of Constructions

A series of plasmids were constructed to express the *tcbA* gene of *Photorhabdus* W-14 in *Escherichia coli*. A list of the plasmids is shown in Table 30. A brief description of each construction follows as well as a summary of the *E. coli* expression data obtained.

Table 30
Expression Plasmids for the *tcba* Gene

Plasmid	Gene	Vector/Selection	Compartment
pDAB2025	<i>tcba</i>	pBC/Chl	Intracellular
pDAB2026	<i>tcba</i>	pAcGP67B/Amp	Baculovirus, secreted
pDAB2027	<i>tcba</i>	pET27b/Kan	Periplasm
pDAB2028	<i>tcba</i>	pET15- <i>tcba</i>	Intracellular

Abbreviations: Kan=kanamycin, Chl=chloramphenicol, Amp=ampicillin

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Construction of pDAB2025

In Example 9, a large EcoR I fragment which hybridizes to the TcbA_{ii} probe is described. This fragment was subcloned into pBC (Stratagene, La Jolla CA) to create pDAB2025. Sequence analysis indicates that the fragment is 8816 base pairs. The fragment encodes the *tcba* gene with the initiating ATG at position 571 and the terminating TAA at position 8086. The fragment therefore carries 570 base pairs of *Photothabdus* DNA upstream of the ATG and 730 base pairs downstream of the TAA.

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Construction of Plasmid pDAB2026

The *tcba* gene was PCR amplified from plasmid pDAB2025 using the following primers; 5' primer (SlAc51) 5' TTT AAA CCA TGG GAA ACT CAT TAT CAA GCA CTA TC 3' and 3' primer (SlAc31) 5' TTT AAA GCG GCC GCT TAA CGG ATG GTA TAA CGA ATA TG 3'. PCR was performed using a TaKaRa LA PCR kit from PanVera (Madison, WI) in the following reaction: 57.5 microliters water, 10 microliters 10X LA buffer, 16 microliters dNTPs (2.5 mM each stock solution), 20 microliters each primer at 10 pmoles/ microliters, 300 ng of the plasmid pDAB2025 containing the W-14 *tcba* gene and one microliter of TaKaRa LA Taq polymerase. The cycling conditions were 98°C/20 sec, 68°C/5 min, 72°C/10 min for 30 cycles. A PCR product of the expected about 7526 bp was isolated in a 0.8% agarose gel in TBE (100 mM Tris, 90 mM boric acid, 1 mM EDTA) buffer and purified using a Qiaex II kit from Qiagen (Chatsworth, CA). The purified *tcba* gene was digested with *Nco* I and *Not* I and ligated into the baculovirus transfer vector pAcGP67B (PharMingen (San Diego, CA)) and transformed into DH5α *E. coli*. The resulting recombinant is called pDAB2026. The *tcba* gene was then cut from pDAB2026 and transferred to pET27b to

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create plasmid pDAB2027. A missense mutation in *tcbA* gene was repaired in pDAB2027.

The repaired *tcbA* gene contains two changes from the sequence shown in Sequence ID NO:11; an A>G at 212 changing an asparagine 71 to serine 71 and a G>A at 229 changing an alanine 77 to threonine 77. These changes are both upstream of the proposed TcbA_{ii} N-terminus.

Construction of pDAB2028

The *tcbA* coding region of pDAB2027 was transferred to vector pET15b. This was accomplished using shotgun ligations, the DNAs were cut with restriction enzymes *Nco* I and *Xho* I. The resulting recombinant is called pDAB2028.

Expression of TcbA in *E. coli* from Plasmid pDAB2028

Expression of *tcbA* in *E. coli* was obtained by modification of the methods previously described by Studier et al. (Studier, F.W., Rosenberg, A., Dunn, J., and Dubendorff, J., (1990) Use of T7 RNA polymerase to direct expression of cloned genes. *Methods Enzymol.*, 185: 60-89.). Competent *E. coli* cells strain BL21(DE3) were transformed with plasmid pDAB2028 and plated on LB agar containing 100 µg/mL ampicillin and 40 mM glucose. The transformed cells were plated to a density of several hundred isolated colonies/plate. Following overnight incubation at 37°C the cells were scraped from the plates and suspended in LB broth containing 100 µg/mL ampicillin. Typical culture volumes were from 200-500 mL. At time zero, culture densities (OD₆₀₀) were from 0.05-0.15 depending on the experiment. Cultures were shaken at one of three temperatures (22°C, 30°C or 37°C) until a density of 0.15-0.5 was obtained at which time they were induced with 1 mM isopropylthio-β-galactoside (IPTG). Cultures were incubated at the designated temperature for 4-5 hours and then were transferred to 4°C until processing (12-72 hours).

Purification and Characterization of TcbA Expressed in *E. coli* from Plasmid pDAB2028

E. coli cultures expressing TcbA peptides were processed as follows. Cells were harvested by centrifugation at 17,000 x G and the media was decanted and saved in a separate container.

The media was concentrated about 8x using the M12 (Amicon, Beverly MA) filtration system and a 100 kD molecular mass cut-off filter. The concentrated media was loaded onto an anion exchange column and the bound proteins were eluted with 1.0 M NaCl. The 1.0 M NaCl elution peak was found to cause mortality against Southern corn rootworm (SCR) larvae (Table 30). The 1.0 M NaCl fraction was dialyzed against 10 mM sodium phosphate buffer pH 7.0, concentrated, and subjected to gel filtration on Sepharose CL-4B (Pharmacia, Piscataway, NJ). The region of the CL-4B elution profile corresponding to calculated molecular weight (about 900 kDa) as the native W-14 toxin complex was collected, concentrated and bioassayed against larvae. The collected 900 kDa fraction was found to have insecticidal activity (see Table 31 below), with symptomology similar to that caused by native W-14 toxin complex. This fraction was subjected to Proteinase K and heat treatment, the activity in both cases was either eliminated or reduced, providing evidence that the activity is proteinaceous in nature. In addition, the active fraction tested immunologically positive for the TcbA and TcbA_{iii} peptides in immunoblot analysis when tested with an anti-TcbA_{iii} monoclonal antibody (Table 31).

Table 31

Results of Immunoblot and SCR Bioassays

Fraction	SCR Activity		Immunoblot Peptides Detected	Native Size [CL-4B Estimate d Size]
	% Mortality	% Growth Inhibit.		
TcbA Media 1.0 M Ion Exchange	+++	+++	TcbA	
TcbA Media CL-4B	+++	+++	TcbA, TcbA _{iii}	about 900 kDa
TcbA Media CL-4B + Proteinase K	++	+++	NT	
TcbA Media CL-4B + heat treatment	-	-	NT	
TcbA Cell Sup CL-4B	-	+++	NT	about 900 kD

PK = Proteinase K treatment 2 hours; Heat treatment = 100°C for 10 minutes; ND = None Detected; NT = Not Tested. Scoring system for mortality and growth inhibition as compared to control samples; 5-24%="+", 25-49%="++", 50-100%="+++".

The cell pellet was resuspended in 10 mM sodium phosphate buffer, pH=7.0, and lysed by passage through a Bio-Neb™ cell nebulizer (Glas-Col Inc., Terra Haute, IN). The pellets were

treated with DNase to remove DNA and centrifuged 17,000 x g to separate the cell pellet from the cell supernatant. The supernatant fraction was decanted and filtered through a 0.2 micron filter to remove large particles and subjected to anion exchange chromatography. Bound proteins were eluted with 1.0 M NaCl, dialyzed and concentrated using Biomax™ (Millipore Corp, Bedford, MA) concentrators with a molecular mass cut-off of 50,000 Daltons. The concentrated fraction was subjected to gel filtration chromatography using Sepharose CL-4B beaded matrix. Bioassay data for material prepared in this way is shown in Table 30 and is denoted as "TcbA Cell Sup".

In yet another method to handle large amounts of material, the cell pellets were re-suspended in 10 mM sodium phosphate buffer, pH = 7.0 and thoroughly homogenized by using a Kontes Glass Company (Vineland, NJ) 40 ml tissue grinder. The cellular debris was pelleted by centrifugation at 25,000 x g and the cell supernatant was decanted, passed through a 0.2 micron filter and subjected to anion exchange chromatography using a Pharmacia 10/10 column packed with Poros HQ 50 beads. The bound proteins were eluted by performing a NaCl gradient of 0.0 to 1.0 M. Fractions containing the TcbA protein were combined and concentrated using a 50 kDa concentrator and subjected to gel filtration chromatography using Pharmacia CL-4B beaded matrix. The fractions containing TcbA oligomer, molecular mass of approximately 900 kDa, were collected and subjected to anion exchange chromatography using a Pharmacia Mono Q 10/10 column equilibrated with 20 mM Tris buffer pH = 7.3. A gradient of 0.0 to 1.0 M NaCl was used to elute recombinant TcbA protein. Recombinant TcbA eluted from the column at a salt concentration of approximately 0.3-0.4 M NaCl, the same molarity at which native TcbA oligomer is eluted from the Mono Q 10/10 column. The recombinant TcbA fraction was found to cause SCR mortality in bioassay experiments similar to those in Table 31.

A second set of expression constructions were prepared and tested for expression of the TcbA protein toxin.

Construction of pDAB2030: An Expression Plasmid for the tcbA Coding Region

The plasmid pDAB2028 (see herein) contains the tcbA coding region in the commercial vector pET15 (Novagen, Madison, WI),

encodes an ampicillin selection marker. The plasmid pDAB2030 was created to express the *tcbA* coding region from a plasmid which encodes a kanamycin selection marker. This was done by cutting pET27 (Novagen, Madison, WI) a kanamycin selection plasmid, and pDAB2028 with *Xba* I and *Xho* I. This releases the entire multiple cloning site, including the *tcbA* coding region from plasmid pDAB2028. The two cut plasmids, were mixed and ligated. Recombinant plasmids were selected on kanamycin and those containing the pDAB2028 fragment were identified by restriction analysis. The new recombinant plasmid is called pDAB2030.

Construction of Plasmid pDAB2031: Correction of Mutations in *tcbA*;

The two mutations in the N-terminus of the *tcbA* coding region as described in Example 19 (Sequence ID NO:11; A>G at 212 changing an asparagine 71 to serine 71; G>A at 229 changing an alanine 77 to threonine 77) were corrected as follows: A PCR product was generated using the primers TH50 (5' ACC GTC TTC TTT ACG ATC AGT G 3') and SlAc51 (5' TTT AAA CCA TGG GAA ACT CAT TAT CAA GCA CTA TC 3') and pDAB2025 as template to generate a 1778 bp product. This PCR product was cloned into plasmid pCR2.1 (Invitrogen, San Diego, CA) and a clone was isolated and sequenced. The clone was digested with *Nco* I and *Pin* AI and a 1670 bp fragment was purified from a 1% agarose gel. A plasmid containing the mutated *tcbA* coding region (pDAB2030) was digested with *Nco* I and *Not* I and purified away from the 1670 bp fragment in a 0.8% agarose with Qiaex II (Qiagen, Chatsworth, CA). The corrected *Nco* I/*Pin* AI fragment was then ligated into pDAB2030. The ligated DNA was transformed into DH5 α *E. coli*. A clone was isolated, sequenced and found to be correct. This plasmid, containing the corrected *tcbA* coding region, is called pDAB2031.

Construction of pDAB2033 and pDAB2034: Expression Plasmids for *tcbA*

The expression plasmids pDAB2025 and pDAB2027-2031 all rely on the Bacteriophage T7 expression system. An additional vector system was used for bacterial expression of the *tcbA* gene and its derivatives. The expression vector Trc99a (Pharmacia Biotech, Piscataway, NJ) contains a strong *trc* promoter upstream of a multiple cloning site with a 5' *Nco* I site which is compatible with the *tcbA* coding region from pDAB2030 and 2031. However, the plasmid does not have a compatible 3' site. Therefore, the *Hind* III site of Trc99a was cut and made blunt by treatment with T4 DNA

polymerase (Boehringer Mannheim, Indianapolis, IN). The vector plasmid was then cut by *Nco I* followed by treatment with alkaline phosphatase. The plasmids pDAB2030 and pDAB2031 were each cut with *Xho I* (cuts at the 3' end of the *tcbA* coding region) followed by treatment with T4 DNA polymerase to blunt the ends. The plasmids were then cut with *Nco I*, the DNAs were extracted with phenol, ethanol precipitated and resuspended in buffer. The Trc99a and pDAB2030 and pDAB2031 plasmids were mixed separately, ligated and transformed into DH5 α cells and plated on LB media containing ampicillin and 50 mM glucose. Recombinant plasmids were identified by restriction digestion. The new plasmids are called pDAB2033 (contains the *tcbA* coding sequence with the two mutations in *tcbA_{ii}*) and pDAB2034 (contains the corrected version of *tcbA* from pDAB2031).

Construction of Plasmid pDAB2032: An Expression Plasmid for *tcbA_{ii}A_{iii}*

A plasmid encoding the *TcbA_{ii}A_{iii}* portion of *TcbA* was created in a similar way as plasmid pDAB2031. A PCR product was generated using TH42 (5' TAG GTC TCC ATG GCT TTT ATA CAA GGT TAT AGT GAT CTG 3') and TH50 (5' ACC GTC TTC TTT ACG ATC AGT G 3') primers and plasmid pDAB2025 as template. This yielded a product of 1521 bp having an initiation codon at the beginning of the coding sequence of *tcbA_{ii}*. This PCR product was isolated in a 1% agarose gel and purified. The purified product was cloned into pCR2.1 as above and a correct clone was identified by DNA sequence analysis. This clone was digested with *Nco I* and *Pin AI*, a 1414 bp fragment was isolated in a 1% agarose gel and ligated into the *Nco I* and *Pin AI* sites of plasmid pDAB2030 and transformed into DH5 α *E. coli*. This new plasmid, designed to express *TcbA_{ii}A_{iii}* in *E. coli*, is called pDAB2032.

Expression of *tcbA* and *tcbA_{ii}A_{iii}* from Plasmids pDAB2030, pDAB2031 and pDAB2032

Expression of *tcbA* in *E. coli* from plasmids pDAB2030, pDAB2031 and pDAB2032 was as described herein, except expression of *tcbA_{ii}A_{iii}* was done in *E. coli* strain HMS174 (DE3) (Novagen, Madison, WI).

Expression of TcbA from Plasmid pDAB2033

The plasmid pDAB2033 was transformed into BL21 cells (Novagen, Madison, WI) and plated on LB containing 100 micrograms/mL ampicillin and 50 mM glucose. The plates were spread such that several hundred well separated colonies were present on each plate following incubation at either 30°C or 37°C overnight. The colonies were scraped from the plates and suspended in LB containing 100 micrograms/mL ampicillin, but no glucose. Typical culture volume was 250 mL in a single 1 L baffled bottom flask. The cultures were induced when the culture reached a density of 0.3-0.6 OD_{600 nm}. Most often this density was achieved immediately after suspension of the cells from the plates and did not require a growth period in liquid media. Two induction methods were used. Method 1: cells were induced with 1 mM IPTG at 37°C. The cultures were shaken at 200 rpm on a platform shaker for 5 hours and harvested. Method 2: The cultures were induced with 25 micromolar IPTG at 30°C and shaken at 200 rpm for 15 hours at either 20°C or 30°C. The cultures were stored at 4°C until used for purification.

20 Purification of TcbA from E. coli

Purification, bioassay and immunoblot analysis of TcbA and TcbA_{III}A_{III} was as described herein. Results of several representative E. coli expression experiments are shown in Table 32. All materials shown in Table 32 were purified from the media fraction of the cultures. The predicted native molecular weight is approximately 900 kD as described herein. The purity of the samples, the amount of TcbA relative to contaminating proteins, varied with each preparation.

Table 32

Bioassay Activity and Immunoblot Analysis of TcbA and Derivatives
Produced in E. coli and Purified from the Culture Media

Plasmid	Coding Region	E. coli Strain	Southern Corn Rootworm Bioassay Activity		Peptides Detected by Immunoblot	Micrograms Protein Applied to Diet
			% Growth Inhibit.	% Mortal.		
pDAB2030	<i>tcba</i>	BL21 (DE3)	-	+++	TcBA + TcbA _{iii}	1-8
pDAB2031	<i>tcba</i>	BL21 (DE3)	-	+++	TcBA + TcbA _{iii}	1-10
pDAB2033	<i>tcba</i>	BL21	-	+++	TcBA + TcbA _{iii}	1-2
pDAB2032	<i>tcba_{ii}A_{iii}</i>	HMS174 (DE3)	+++	+	TcBA _{ii} A _{iii} + TcbA _{iii}	13-27

5 Scoring system for mortality and growth inhibition on Southern Corn Rootworm as compared to control samples; 5-24%="+", 25-49%="++", 50-100%="+++".

Example 20

10 Characterization of Toxin Peptides with Matrix-Assisted Laser Desorption Ionization Time-of-Flight Mass Spectroscopy

Toxins isolated from W-14 broth were purified as described in Example 15. In some cases, the TcaB protein toxin was pretreated with proteases (Example 16) that had been isolated from W-14 broth as previously described (Example 15). Protein molecular mass was determined using matrix-assisted laser desorption ionization time-of-flight mass spectroscopy, hereinafter MALDI-TOF, on a VOYAGER BIOSPECTROMETRY workstation with DELAYED EXTRACTION technology (PerSeptive Biosystems, Framingham, MA). Typically, the protein of interest (100-500 pmoles in 5 μ l) was mixed with 1 μ l of acetonitrile and dialyzed for 0.5 to 1 h on a Millipore VS filter having a pore size of 0.025 μ M (Millipore Corp. Bedford, MA). Dialysis was performed by floating the filter on water (shiny side up) followed by adding protein-acetonitrile mixture as a droplet to the surface of the filter. After dialysis, the dialyzed protein removed using a pipette and was then mixed with a matrix consisting of sinapinic acid and trifluoroacetic acid according to manufacturers instructions. The protein and matrix were allowed to co-crystallize on a about 3 cm² gold-plated sample plate (PerSeptive Corp.). Excitation of the crystals and subsequent mass analysis was performed using the following conditions: laser setting of 3050; pressure of 4.55e-07; low mass gate of 1500.0; negative ions off; accelerating voltage of 25,000; grid voltage of

90.0%; guide wire voltage of 0.010%; linear mode; and a pulse delay time of 350 ns.

Protein mass analysis data are shown in Table 33. The data obtained from MALDI-TOF was compared to that hypothesized from gene sequence information and as previously determined by SDS-PAGE.

Table 33

Molecular Analysis of Peptides by MALDI-TOF, SDS-PAGE and Predicted Determination Based on Gene Sequence

Peptide	Predicted (Gene)	SDS PAGE	MALDI-TOF
TcbA	280,634 Da	240,000 Da	281,040 Da
TcbAi/ii	217,710 Da	not resolved	216,812 Da
TcbAii	207,698 Da	201,000 Da	206,473 Da
TcbAiii	62,943 Da	58,000 Da	63,520 Da

TcdAii	209,218 Da	188,000 Da	208,186 Da
TcdAiii	63,520 Da	56,000 Da	63,544 Da

TcbAii Protease Generated		201,000 Da	216,614 Da [^]
			215,123 Da [^]
			210,391 Da [^]
			208,680 Da [^]
TcbAiii Protease Generated		56,000 Da	64,111 Da

[^]Data normalized TcbA, multiple fragments observed at TcbAi/ii

Example 21

Production of Peptide Specific Polyclonal Antibodies

Nine peptide components of the W-14 toxin complex, namely, TcaA, TcaAiii, TcaBi, TcaBii, TcaC, TcbAii, TcbAiii, TcdAii, and TcdAiii were selected as targets against which antibodies were produced. Comprehensive DNA and deduced amino acid sequence data for these peptides indicated that the sequence homology between some of these peptides was substantial. If a whole peptide was used as the immunogen to induce antibody production, the resulting antibodies might bind to multiple peptides in the toxin preparation. To avoid this problem antibodies were generated that would bind specifically to a unique region of each peptide of interest. The unique region (subpeptide) of each target peptide was selected based on the analyses described below.

Each entire peptide sequence was analyzed using MacVector™ Protein Analysis Tool (IBI Sequence Analysis Software, International Biotechnologies, Inc., P. O. Box 9558, New Haven, CT 06535) to determine its antigenicity index. This program was designed to locate possible externally-located amino acid

sequences, i.e., regions that might be antigenic. This method combined information from hydrophilicity, surface probability, and backbone flexibility predictions along with the secondary structure predictions in order to produce a composite prediction of the surface contour of a protein. The scores for each of the analyses were normalized to a value between -1.0 and +1.0 (MacVector™ Manual). The antigenicity index value was obtained for the entire sequence of the target peptide. From each peptide, an area covering 19 or more amino acids that showed a high antigenicity index from the original sequence was re-analyzed to determine the antigenicity index of the subpeptide without the flanking residues. This re-analysis was necessary because the antigenicity index of a peptide could be influenced by the flanking amino acid residues. If the isolated subpeptide sequence did not maintain a high antigenicity index, a new region was chosen and the analysis was repeated.

Each selected subpeptide sequence was aligned and compared to all seven target peptide sequences using MacVector™ alignment program. If a selected subpeptide sequence showed identity (greater than 20%) to another target peptide, a new 19 or more amino acid region was isolated and re-analyzed. Unique subpeptide sequences covering 19 or more amino acid showing high antigenicity index were selected from all target peptides.

The sequences of seven subpeptides were sent to Genemed Biotechnology Inc. The last amino acid residue on each subpeptide was deleted because it showed no apparent effect on the antigenicity index. A cysteine residue was added to the N-terminal of each subpeptide sequence, except TcaB₁-syn which contains an internal cysteine residue. The presence of a cysteine residue facilitates conjugation of a carrier protein (KLH). The final peptide products corresponding to the appropriate toxin peptides and SEQ ID NO.s are shown in Table 34.

Table 34
Amino Acid Sequences for Synthetic Peptides

	SEQ ID No.	Peptide	Amino Acid Sequence
5	63	TcaAii-syn	NH2-(C)LRGNSPTNPDKDGI FAQVA
	64	TcaAiii-syn	NH2-(C)YTPDQTPSFYETA FR SADG
	65	TcaBi-syn	NH2-HGQSYNDNNYCNFTLSINT
	66	TcaBiii-syn	NH2-(C)VDPKTLQRQQAGGDGTGSS
10	67	TcaC-syn	NH2-(C)YKAPQRQEDGDSNAVTYDK
	68	TcbAii-syn	NH2-(C)YNENPSSSEDKKWYFSSKDD
	69	TcbAiii-syn	NH2-(C)FDSYSQLYEENINAGEQRA
	70	TcdAii-syn	NH2-(C)NPNNSSNKL MFYPVYQYSGNT
	71	TcdAiii-syn	NH2-(C)VSQGS G SAGSGNNNLA FGAG

15

Each conjugated synthetic peptide was injected into two rabbits according to Genemed accelerated program. The pre- and post-immune sera were available for testing after one month.

20 The preliminary test of both pre- and post-immune sera from each rabbit was performed by Genemed Biotechnologies Inc. Genemed reported that by using both ELISA and Western blot techniques, they detected the reaction of post-immune sera to the respective synthetic peptides. Subsequently, the sera were tested with the whole target peptides, by Western blot analysis. Two batches of

25 partially purified *Photorhabdus* strain W-14 toxin complex was used as the antigen. The two samples had shown activity against the Southern corn rootworm. Their peptide patterns on an SDS-PAGE gel were slightly different.

Pre-cast SDS-polyacrylamide gels with 4-20% gradient

30 (Integrated Separation Systems, Natick, MA 01760) were used. Between 1 to 8 μ g of protein was applied to each gel well. Electrophoresis was performed and the protein was electroblotted onto Hybond-ECL[™] nitrocellulose membrane (Amersham International). The membrane was blocked with 10% milk in TBST (25 mM Tris HCl pH

35 7.4, 136 mM NaCl, 2.7 mM KCl, 0.1% Tween 20) for one hour at room temperature. Each rabbit serum was diluted in 10% milk/TBST to 1:500. Other dilutions between 1:50 to 1:1000 were also used. The serum was added to the membrane and placed on a platform rocker for at least one hour. The membrane was washed thoroughly with the

40 blocking solution or TBST. A 1:2000 dilution of secondary antibodies (goat anti-mouse IgG conjugated to horse radish peroxidase; BioRad Laboratories) in 10% milk/TBST was applied to the membrane placed on a platform rocker for one hour. The membrane was subsequently washed with excess amount of TBST. The

detection of the protein was performed by using a CL (Enhanced Chemiluminescence) detection kit (Amersham International).

Western blot analyses were performed to identify binding specificity of each anti-synthetic peptide antibodies. All synthetic polyclonal antibodies showed specificity toward to processed and, when applicable, unprocessed target peptides from protein fractions derived from *Photothabdus* culture broth. Various antibodies were shown to recognize either unprocessed or processed recombinant proteins derived from heterologous expression systems such as bacteria or insect cells, using baculovirus expression constructs. In one case, the anti-TcbA_{iii}-syn antibody showed some cross-reactivity to anti-TcdA_{iii} peptide. In a second case, the anti-TcaC-syn antibody, recognized an unidentified 190 kDa peptide in W-14 toxin complex fractions.

Example 22

Characterization of *Photothabdus* Strains

In order to establish that the collection described herein was comprised of *Photothabdus* strains, the strains herein were assessed in terms of recognized microbiological traits that are characteristic of the bacterial genus *Photothabdus* and which differentiate it from other *Enterobacteriaceae* and *Xenorhabdus* spp. (Farmer, J. J. 1984. *Bergey's Manual of Systemic Bacteriology*, Vol 1. pp. 510-511. (ed. Kreig N. R. and Holt, J. G.). Williams & Wilkins, Baltimore.; Akhurst and Boemare, 1988, *J. Gen. Microbiol.* 134, 1835-1845; Forst and Nealson, 1996. *Microbiol. Rev.* 60, 21-43). These characteristic traits are as follows: Gram stain negative rods, organism size of 0.3-2 μm in width and 2-10 μm in length [with occasional filaments (15-50 μm) and spheroplasts], yellow to orange/red colony pigmentation on nutrient agar, presence of crystalline inclusion bodies, presence of catalase, inability to reduce nitrate, presence of bioluminescence, ability to take up dye from growth media, positive for protease production, growth at temperatures below 37°C, survival under anaerobic conditions and positively motile. (Table 33). Test methods were checked using reference *Escherichia coli*, *Xenorhabdus* and *Photothabdus* strains. The overall results are consistent with all strains being part of the family *Enterobacteriaceae* and the genus *Photothabdus*. Note that DEP1, DEP2, and DEP3 refer to *Photothabdus* strains obtained

from the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD 20852 USA (#29304, 29999 and 51583, respectively).

A luminometer was used to establish the bioluminescence associated with these *Photorhabdus* strains. To measure the presence or absence of relative light emitting units, the broths from each strain (cells and media) were measured at three time intervals after inoculation in liquid culture (24, 48, 72 hr) and compared to background luminosity (uninoculated media). Several *Xenorhabdus* strains were tested as negative controls for luminosity. Prior to measuring light emission from the various broths, cell density was established by measuring light absorbance (560 nm) in a Gilford Systems (Oberlin, OH) spectrophotometer using a sipper cell. The resulting light emitting units could then be normalized to density of cells. Aliquots of the broths were placed into 96-well microtiter plates (100 μ l each) and read in a Packard Lumicount™ luminometer (Packard Instrument Co., Meriden, CT). The measurement period for each sample was 0.1 to 1.0 second. The samples were agitated in the luminometer for 10 sec prior to taking readings. A positive test was determined as being about 5-fold background luminescence (about 1-15 relative light units). In addition, degree of colony luminosity was confirmed with photographic film overlays and by eye, after visual adaptation in a darkroom. The Gram's staining characteristics of each strain were established with a commercial Gram's stain kit (BBL, Cockeysville, MD) used in conjunction with Gram's stain control slides (Fisher Scientific, Pittsburgh, PA). Microscopic evaluation was then performed using a Zeiss microscope (Carl Zeiss, Germany) 100X oil immersion objective lens (with 10X ocular and 2X body magnification). Microscopic examination of individual strains for organism size, cellular description and inclusion bodies (the latter two observations after logarithmic growth) was performed using wet mount slides (10X ocular, 2X body and 40X objective magnification) and phase contrast microscopy with a micrometer (Akhurst, R. J. and Boemare, N. E. 1990. Entomopathogenic Nematodes in Biological Control (ed. Gaugler, R. and Kaya, H.). pp. 75-90. CRC Press, Boca Raton, USA.; Baghdiguan S., Boyer-Giglio M. H., Thaler, J. O., Bonnot G., Boemare N. 1993. Biol. Cell 79, 177-185.). Colony pigmentation was observed after inoculation on Bacto nutrient agar, (Difco Laboratories, Detroit, MI) prepared as per

label instructions. Incubation occurred at 28°C and descriptions were produced after 5 days. To test for the presence of the enzyme catalase, a colony of the test organism was removed on a small plug from a nutrient agar plate and placed into the bottom of a glass test tube. One ml of a household hydrogen peroxide solution was gently added down the side of the tube. A positive reaction was recorded when bubbles of gas (presumptive oxygen) appeared immediately or within 5 seconds. Controls of uninoculated nutrient agar and hydrogen peroxide solution were also examined. To test for nitrate reduction, each culture was inoculated into 10 ml of Bacto Nitrate Broth (Difco Laboratories, Detroit, MI). After 24 hours incubation with gentle agitation at 28°C, nitrite production was tested by the addition of two drops of sulfanilic acid reagent and two drops of alpha-naphthylamine reagent (see Difco Manual, 10th edition, Difco Laboratories, Detroit, MI, 1984). The generation of a distinct pink or red color indicates the formation of nitrite from nitrate whereas the lack of color formation indicates that the strain is nitrate reduction negative. In the latter case, finely powdered zinc was added to further confirm the presence of unreduced nitrate; established by the formation of nitrite and the resultant red color. The ability of each strain to uptake dye from growth media was tested with Bacto MacConkey agar containing the dye neutral red; Bacto Tergitol-7 agar containing the dye bromothymol blue and Bacto EMB Agar containing the dye eosin-Y (formulated agars from Difco Laboratories, Detroit, MI, all prepared according to label instructions). After inoculation on these media, dye uptake was recorded after incubation at 28°C for 5 days. Growth on these latter media is characteristic for members of the family *Enterobacteriaceae*. Motility of each strain was tested using a solution of Bacto Motility Test Medium (Difco Laboratories, Detroit, MI) prepared as per label instructions. A butt-stab inoculation was performed with each strain and motility was judged macroscopically by a diffuse zone of growth spreading from the line of inoculum. The production of protease was tested by observing hydrolysis of gelatin using Bacto gelatin (Difco Laboratories, Detroit, MI) made as per label instructions. Cultures were inoculated and the tubes or plates were incubated at 28°C for 5 days. Gelatin hydrolysis was then checked at room temperature, i.e. less than 22°C. To assess growth at different

temperatures, agar plates [2% proteose peptone #3 with two percent Bacto-Agar (Difco, Detroit, MI) in deionized water] were streaked from a common source of inoculum. Plates were incubated at 20, 28 and 37°C for up to three weeks. The incubator temperature levels were checked with an electronic thermocouple and meter to insure valid temperature settings. Oxygen requirements for *Photorhabdus* strains were tested in the following manner. A butt-stab inoculation into fluid thioglycolate broth medium (Difco, Detroit, MI) was made. The tubes were incubated at room temperature for one week and cultures were then examined for type and extent of growth. The indicator resazurin demonstrates the presence of medium oxygenation or the aerobiosis zone (Difco Manual, 10th edition, Difco Laboratories, Detroit, MI). Growth zone results obtained for the *Photorhabdus* strains tested were consistent with those of a facultative anaerobic microorganism. In the case of unclear results, the final agar concentration of fluid thioglycolate broth medium was raised to 0.75% and the growth characteristics rechecked.

Table 35
Taxonomic Traits of *Photorhabdus* Strains

Strain	A*	B	C	D	E	F	G	H	I	J [†]	K	L	M	N	O	P	Q
P. zealandica	- [†]	+	+	rd S	+	-	+	+	+	PO	+	+	+	+	+	+	-
P. heplialis	-	+	+	rd S	+	-	+	+	+	Y	+	+	+	+	+	+	-
HB-Arg	-	+	+	rd S	+	-	+	+	+	W	+	+	+	+	+	+	-
HB Oswego	-	+	+	rd S	+	-	+	+	+	W	+	+	+	+	+	+	-
HB Lewiston	-	+	+	rd S	+	-	+	+	+	T	+	+	+	+	+	+	-
K-122	-	+	+	rd S	+	-	+	+	+	Y	+	+	+	+	+	+	-
HMGD	-	+	+	rd S	+	-	+	+	+	Rd	+	+	+	+	+	+	-
Indicus	-	+	+	rd S	+	-	+	+	+	W	+	+	+	+	+	+	-
GD	-	+	+	rd S	+	-	+	+	+	YT	+	+	+	+	+	+	-
PWH-5	-	+	+	rd S	+	-	+	+	+	Y	+	+	+	+	+	+	-
Megidis	-	+	+	rd S	+	-	+	+	+	R	+	+	+	+	+	+	-
HF-85	-	+	+	rd S	+	-	+	+	+	R	+	+	+	+	+	+	-
A. Cows	-	+	+	rd S	+	-	+	+	+	PR	+	+	+	+	+	+	-
MP1	-	+	+	rd S	+	-	+	+	+	T	+	+	+	+	+	+	-
MP2	-	+	+	rd S	+	-	+	+	+	T	+	+	+	+	+	+	-
MP3	-	+	+	rd S	+	-	+	+	+	R	+	+	+	+	+	+	-
MP4	-	+	+	rd S	+	-	+	+	+	Y	+	+	+	+	+	+	-
MP5	-	+	+	rd S	+	-	+	+	+	PR	+	+	+	+	+	+	-
GL98	-	+	+	rd S	+	-	+	+	+	W	+	+	+	+	+	+	-
GL101	-	+	+	rd S	+	-	+	+	+	W	+	+	+	+	+	+	-
GL138	-	+	+	rd S	+	-	+	+	+	W	+	+	+	+	+	+	-
GL155	-	+	+	rd S	+	-	+	+	+	W	+	+	+	+	+	+	-
GL217	-	+	+	rd S	+	-	+	+	+	Y	+	+	+	+	+	+	-
GL257	-	+	+	rd S	+	-	+	+	+	O	+	+	+	+	+	+	-
DEP1	-	+	+	rd S	+	-	+	+	+	W	+	+	+	+	+	+	-
DEP2	-	+	+	rd S	+	-	+	+	+	PR	+	+	+	+	+	+	-
DEP3	-	+	+	rd S	+	-	+	+	+	CR	+	+	+	+	+	+	-

- 5 *: A=Gram's stain, B=Crystalline inclusion bodies,
C=Bioluminescence, D=Cell form, E=Motility, F=Nitrate reduction,
G=Presence of catalase, H=Gelatin hydrolysis, I=Dye uptake,
J=Pigmentation on Nutrient Agar (some color shifts after Day 5),
10 K=Growth on EMB agar, L=Growth on MacConkey agar, M=Growth on
Tergitol-7 agar, N =Facultative anaerobe, O=Growth at 20°C,
P=Growth at 28°C, Q=Growth at 37°C.
†: +=positive for trait, - =negative for trait; rd=rod, S=sized
within Genus descriptors.
§: W = white, CR = cream, Y =yellow, YT=yellow tan, T=tan PO=pale
15 orange, O=orange, PR=pale red, R=red.

The evolutionary diversity of the *Photorhabdus* strains in our collection was measured by analysis of PCR (Polymerase Chain Reaction) mediated genomic fingerprinting using genomic DNA from
20 each strain. This technique is based on families of repetitive DNA sequences present throughout the genome of diverse bacterial species (reviewed by Versalovic, J., Schneider, M., DE Bruijn, F. J. and Lupski, J. R. 1994. Methods Mol. Cell. Biol., 5, 25-40). Three of these, repetitive extragenic palindromic sequence (REP),
25 enterobacterial repetitive intergenic consensus (ERIC) and the BOX

element are thought to play an important role in the organization of the bacterial genome. Genomic organization is believed to be shaped by selection and the differential dispersion of these elements within the genome of closely related bacterial strains can be used to discriminate these strains (e.g., Louws, F. J., Fulbright, D. W., Stephens, C. T. and DE Bruijn, F. J. 1994. Appl. Environ. Micro. 60, 2286-2295). Rep-PCR utilizes oligonucleotide primers complementary to these repetitive sequences to amplify the variably sized DNA fragments lying between them. The resulting products are separated by electrophoresis to establish the DNA "fingerprint" for each strain.

To isolate genomic DNA from our strains, cell pellets were resuspended in TE buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8.0) to a final volume of 10 ml and 12 ml of 5 M NaCl was then added. This mixture was centrifuged 20 min. at 15,000 x g. The resulting pellet was resuspended in 5.7 ml of TE and 300 μ l of 10% SDS and 60 μ l 20 mg/ml proteinase K (Gibco BRL Products, Grand Island, NY) were added. This mixture was incubated at 37°C for 1 hr, approximately 10 mg of lysozyme was then added and the mixture was incubated for an additional 45 min. One milliliter of 5M NaCl and 800 μ l of CTAB/NaCl solution (10% w/v CTAB, 0.7 M NaCl) were then added and the mixture was incubated 10 min. at 65°C, gently agitated, then incubated and agitated for an additional 20 min. to aid in clearing of the cellular material. An equal volume of chloroform/isoamyl alcohol solution (24:1, v/v) was added, mixed gently then centrifuged. Two extractions were then performed with an equal volume of phenol/chloroform/isoamyl alcohol (50:49:1). Genomic DNA was precipitated with 0.6 volume of isopropanol. Precipitated DNA was removed with a glass rod, washed twice with 70% ethanol, dried and dissolved in 2 ml of STE (10 mM Tris-HCl pH8.0, 10 mM NaCl, 1 mM EDTA). The DNA was then quantitated by optical density at 260 nm. To perform rep-PCR analysis of *Photothabdus* genomic DNA the following primers were used, REP1R-I; 5'-IIIIICGICGICATCIGGC-3' and REP2-I; 5'-ICGICTTATCIGGCCTAC-3'. PCR was performed using the following 25 μ l reaction: 7.75 μ l H₂O, 2.5 μ l 10X LA buffer (PanVera Corp., Madison, WI), 16 μ l dNTP mix (2.5 mM each), 1 μ l of each primer at 50 pM/ μ l, 1 μ l DMSO, 1.5 μ l genomic DNA (concentrations ranged from 0.075-0.480 μ g/ μ l) and 0.25 μ l TaKaRa EX Taq (PanVera Corp., Madison, WI). The PCR

amplification was performed in a Perkin Elmer DNA Thermal Cycler (Norwalk, CT) using the following conditions: 95°C/7 min. then 35 cycles of; 94°C/1 min., 44°C/1 min., 65°C/8 min., followed by 15 min. at 65°C. After cycling, the 25 µl reaction was added to 5 µl of 6X gel loading buffer (0.25% bromophenol blue, 40% w/v sucrose in H₂O). A 15x20cm 1%-agarose gel was then run in TBE buffer (0.09 M Tris-borate, 0.002 M EDTA) using 8 µl of each reaction. The gel was run for approximately 16 hours at 45v. Gels were then stained in 20 µg/ml ethidium bromide for 1 hour and destained in TBE buffer for approximately 3 hours. Polaroid[®] photographs of the gels were then taken under UV illumination.

The presence or absence of bands at specific sizes for each strain was scored from the photographs and entered as a similarity matrix in the numerical taxonomy software program, NTSYS-pc (Exeter Software, Setauket, NY). Controls of *E. coli* strain HB101 and *Xanthomonas oryzae* pv. *oryzae* assayed under the same conditions produced PCR fingerprints corresponding to published reports (Versalovic, J., Koeuth, T. and Lupski, J. R. 1991. Nucleic Acids Res. 19, 6823-6831; Vera Cruz, C. M., Halda-Alija, L., Louws, F., Skinner, D. Z., George, M. L., Nelson, R. J., DE Bruijn, F. J., Rice, C. and Leach, J. E. 1995. Int. Rice Res. Notes, 20, 23-24.; Vera Cruz, C. M., Ardales, E. Y., Skinner, D. Z., Talag, J., Nelson, R. J., Louws, F. J., Leung, H., Mew, T. W. and Leach, J. E. 1996. Phytopathology 86, 1352-1359). The data from *Photorhabdus* strains were then analyzed with a series of programs within NTSYS-pc; SIMQUAL (Similarity for Qualitative data) to generate a matrix of similarity coefficients (using the Jaccard coefficient) and SAHN (Sequential, Agglomerative, Heirarchical and Nested) clustering [using the UPGMA (Unweighted Pair-Group Method with Arithmetic Averages) method] which groups related strains and can be expressed as a phenogram (Fig. 7). The COPH (cophenetic values) and MXCOMP (matrix comparison) programs were used to generate a cophenetic value matrix and compare the correlation between this and the original matrix upon which the clustering was based. A resulting normalized Mantel statistic (r) was generated which is a measure of the goodness of fit for a cluster analysis (r=0.8-0.9 represents a very good fit). In our case r=0.924. Therefore, the collection is comprised of a diverse group of easily distinguishable strains representative of the *Photorhabdus* genus.

Example 23Insecticidal Utility of Toxin(s) Produced
by Various *Photorhabdus* Strains

5

Initial "storage" cultures of the various *Photorhabdus* strains were produced by inoculating 175 ml of 2% Proteose Peptone #3 (PP3) (Difco Laboratories, Detroit, MI) liquid medium with a primary variant colony in a 500 ml tribaffled flask with a Delong neck, covered with a Kaput closure. After inoculation, the flask was incubated for between 24-72 hrs at 28°C on a rotary shaker at 150 rpm, until stationary phase was reached. The culture was transferred to a sterile bottle containing a sterile magnetic stir bar and the culture was overlayered with sterile mineral oil, to limit exposure to air. The storage culture was kept in the dark, at room temperature. These cultures were then used as inoculum sources for the fermentation of each strain.

"Seed" flasks or cultures were produced by either inoculating 2 mls of an oil overlayered storage culture or by transferring a primary variant colony into 175 ml sterile medium in a 500 ml tribaffled flask covered with a Kaput closure. (The use of other inoculum sources is also possible.) Typically, following 16 hours incubation at 28°C on a rotary shaker at 150 rpm, the seed culture was transferred into production flasks. Production flasks were usually inoculated by adding about 1% of the actively growing seed culture to sterile 2% PP3 medium (e.g. 2.0 ml per 175 ml sterile medium). Production of broths occurred in 500 ml tribaffled flasks covered with a Kaput. Production flasks were agitated at 28°C on a rotary shaker at 150 rpm. Production fermentations were terminated after 24-72 hrs although successful fermentation is not confined to this time duration. Following appropriate incubation, the broths were dispensed into sterile 1.0 L polyethylene bottles, spun at 2600xg for 1 hr at 10°C and decanted from the cell and debris pellet. Further broth clarification was achieved with a tangential flow microfiltration device (Pall Filtron, Northborough, MA) using a 0.5 µm open-channel poly-ether sulfone (PES) membrane filter. The resulting broths were then concentrated (up to 10-fold) using a 10,000 or 100,000 MW cut-off membrane, M12 ultra-filtration device (Amicon, Beverly MA) or centrifugal concentrators (Millipore, Bedford, MA and Pall Filtron, Northborough, MA) with a 10,000 or

100,000 MW pore size. In the case of centrifugal concentrators, the broth was spun at 2000xg for approximately 2 hr. The membrane permeate was added to the corresponding retentate to achieve the desired concentration of components greater than the pore size used. Following these procedures, the broth was used for biochemical analysis or filter sterilized using a 0.2 μ M cellulose nitrate membrane filter for biological assessment. Heat inactivation of processed broth samples was achieved by heating the samples at 100°C in a sand-filled heat block for 10 minutes.

The broth(s) and toxin complex(es) from different *Photorhabdus* strains are useful for reducing populations of insects and were used in a method of inhibiting an insect population which comprises applying to a locus of the insect an effective insect inactivating amount of the active described. A demonstration of the breadth of insecticidal activity observed from broths of a selected group of *Photorhabdus* strains fermented as described above is shown in Table 36. It is possible that improved or additional insecticidal activities could be detected with these strains through increased concentration of the broth or by employing different fermentation methods. Consistent with the activity being associated with a protein, the insecticidal activity of all strains tested was heat labile.

Culture broth(s) from diverse *Photorhabdus* strains show differential insecticidal activity (mortality and/or growth inhibition) against a number of insects. More specifically, the activity is seen against corn rootworm which is a member of the insect order Coleoptera. Other members of the Coleoptera include boll weevils, wireworms, pollen beetles, flea beetles, seed beetles and Colorado potato beetle. The broths and purified toxin complex(es) are also active against tobacco budworm, tobacco hornworm and European corn borer which are members of the order Lepidoptera. Other typical members of this order are beet armyworm, cabbage looper, black cutworm, corn earworm, codling moth, clothes moth, Indian mealmoth, leaf rollers, cabbage worm, cotton bollworm, bagworm, Eastern tent caterpillar, sod webworm and fall armyworm. Activity is also observed against German cockroach which is a member of the order Dictyoptera (or Blattodea). Other members of this order are oriental cockroach and American cockroach.

Activity against corn rootworm larvae was tested as follows. *Photorhabdus* culture broth(s) (10 fold concentrated, filter sterilized), 2% Proteose Peptone #3 (10 fold concentrated), purified toxin complex(es), 10 mM sodium phosphate buffer, pH 7.0 were applied directly to the surface (about 1.5 cm²) of artificial diet (Rose, R. I. and McCabe, J. M. 1973. J. Econ. Entomol. 66, 398-400) in 40 µl aliquots. Toxin complex was diluted in 10 mM sodium phosphate buffer, pH 7.0. The diet plates were allowed to air-dry in a sterile flow-hood and the wells were infested with single, neonate *Diabrotica undecimpunctata howardi* (Southern corn rootworm, SCR) hatched from surface sterilized eggs. The plates were sealed, placed in a humidified growth chamber and maintained at 27°C for the appropriate period (3-5 days). Mortality and larval weight determinations were then scored. Generally, 16 insects per treatment were used in all studies. Control mortality was generally less than 5%.

Activity against lepidopteran larvae was tested as follows. Concentrated (10-fold) *Photorhabdus* culture broth(s), control medium (2% Proteose Peptone #3), purified toxin complex(es), 10 mM sodium phosphate buffer, pH 7.0 were applied directly to the surface (about 1.5 cm²) of standard artificial lepidopteran diet (Stoneville Yellow diet) in 40 µl aliquots. The diet plates were allowed to air-dry in a sterile flow-hood and each well was infested with a single, neonate larva. European corn borer (*Ostrinia nubilalis*) and tobacco hornworm (*Manduca sexta*) eggs were obtained from commercial sources and hatched in-house, whereas tobacco budworm (*Heliothis virescens*) larvae were supplied internally. Following infestation with larvae, the diet plates were sealed, placed in a humidified growth chamber and maintained in the dark at 27°C for the appropriate period. Mortality and weight determinations were scored at day 5. Generally, 16 insects per treatment were used in all studies. Control mortality generally ranged from about 0 to about 12.5% for control medium and was less than 10% for phosphate buffer.

Activity against cockroach was tested as follows. Concentrated (10-fold) *Photorhabdus* culture broth(s) and control medium (2% Proteose Peptone #3) were applied directly to the surface (about 1.5 cm²) of standard artificial lepidopteran diet (Stoneville Yellow diet) in 40 µl aliquots. The diet plates were allowed to

air-dry in a sterile flow-hood and each well was infected with a single, CO₂ anesthetized first instar German cockroach (*Blatella germanica*). Following infestation, the diet plates were sealed, placed in a humidified growth chamber and maintained in the dark at 27°C for the appropriate period. Mortality and weight determinations were scored at day 5. Control mortality less than 10%.

Table 36
Observed Insecticidal Spectrum of Broths
from Different Photorhabdus Strains

	Photorhabdus Strain	Sensitive* Insect Species
5	P. zealandica	1**, 2, 4
	P. hepialus	1, 2, 4
	HB-Arg	1, 2, 4
	HB Oswego	1, 2, 4
10	HB Lewiston	1, 2, 4
	K-122	1, 4
	HMGD	1, 4
	Indicus	1, 2, 4
	GD	2, 4
15	PWH-5	1, 2, 4
	Megidis	1, 2, 4
	HF-85	1, 2, 4
	A. Cows	1, 4
	MP1	1, 2, 4
20	MP2	1, 2, 4
	MP3	4
	MP4	1, 4
	MP5	4
	GL98	1, 4
25	GL101	1, 4, 5
	GL138	1, 2, 4
	GL155	1, 4
	GL217	1, 2, 4
	GL257	1, 4
30	DEP1	1, 4
	DEP2	1, 2, 3, 4
	DEP3	4
* = 25% mortality and/or growth inhibition vs. control ** = 1; Tobacco budworm, 2; European corn borer, 3; Tobacco hornworm, 4; Southern corn rootworm, 5; German cockroach.		

Example 24
Southern Analysis of Non-W-14 Photorhabdus Strains
Using W-14 Gene Probes

5 *Photorhabdus* strains were grown on 2% proteose peptone #3 agar
(Difco Laboratories, Detroit, MI) and insecticidal toxin competence
was maintained by repeated bioassay after passage. A 50 ml shake
culture was produced in 175 ml baffled flasks in 2% proteose
10 peptone #3 medium, grown at 28° and 150 rpm for approximately 24
hours. Fifteen ml of this culture were centrifuged (700 x g, 30
min) and frozen in its medium at -20° until it was thawed (slowly
in ice water) for DNA isolation. The thawed W-14 culture was
centrifuged (900 x g, 15 min 4°), and the floating orange
15 mucopolysaccharide material was removed. The remaining cell
material was centrifuged (25,000 x g, 4°) to pellet the bacterial
cells, and the medium was removed and discarded.

Total DNA was isolated by an adaptation of the CTAB method
described in section 2.4.1 of Ausubel et al. (1994). The
modifications included a high salt shock, and all volumes were
20 increased ten-fold over the "miniprep" recommended volumes. All
centrifugations were at 4°C unless otherwise specified. The
pelleted bacterial cells were resuspended in TE buffer (10 mM Tris-
HCl, 1 mM EDTA, pH 8) to a final volume of 10 ml, then 12 ml 5 M
NaCl were added; this mixture was centrifuged 20 min at 15,000 x g.
25 The pellet was resuspended in 5.7 ml TE, and 300 µl of 10% SDS and
60 µl of 20 mg/ml proteinase K (in sterile distilled water, Gibco
BRL Products, Grand Island, NY) were added to the suspension. The
mixture was incubated at 37°C for 1 hr; then approximately 10 mg
lysozyme (Worthington Biochemical Corp., Freehold, NJ) were added.
30 After an additional 45 min incubation, 1 ml of 5 M NaCl and 800 µl
of CTAB/NaCl solution (10% w/v CTAB, 0.7 M NaCl) were added. This
preparation was incubated 10 min at 65°C, then gently agitated and
further incubated and agitated for approximately 20 min to assist
clearing of the cellular material. An equal volume of
35 chloroform/isoamyl alcohol solution (24:1, v:v) was added, mixed
very gently, and the phases separated by centrifugation at 12,000 x
g for 15 min. The upper (aqueous) phase was gently removed with a
wide-bore pipette and extracted twice as above with an equal volume
of PCI (phenol/choloroform/ isoamyl alcohol; 50:49:1, v:v:v;
40 equilibrated with 1M Tris-HCl, pH 8.0; Intermountain Scientific
Corporation, Kaysville, UT). The DNA precipitated with 0.6 volume
of isopropanol was gently removed on a glass rod, washed twice with
70% ethanol, dried, and dissolved in 2 ml STE (10 mM Tris-HCl, 10

mM NaCl, 1 mM EDTA, pH 8). This preparation contained 2.5 mg/ml DNA, as determined by optical density at 260nm.

Identification of Bgl II/Hind III Fragments Hybridizing to tc-gene Specific Probes

5 Approximately 10 µg of genomic DNA was digested to completion with about 30 units each of Bgl II and Hind III (NEB) for 180 min, frozen overnight, then heated at 65°C for five min, and electrophoresed in a 0.8% agarose gel (Seakem® LE, 1X TEA, 80
10 volts, 90 min). The DNA was stained with ethidium bromide (50 µg/ml) as described earlier, and photographed under ultraviolet light. The DNA fragments in the agarose gel were subjected to depurination (5 min in 0.2 M HCl), denaturation (15 min in 0.5 M NaOH, 1.5 M NaCl), and neutralization (15 min in 0.5 M Tris HCl pH
15 8.0, 1.5 M NaCl), with 3 rinses of distilled water between each step. The DNA was transferred by Southern blotting from the gel onto a NYTRAN nylon membrane (Amersham, Arlington Heights, IL) using a high salt (20X SSC) protocol, as described in section 2.9 of Ausubel et al. (CPMB, op. cit.). The transferred DNA was then
20 UV-crosslinked to the nylon membrane using a Stratagene UV Stratalinker set on auto crosslink. The membranes were stored dry at 25°C until use.

Hybridization was performed using the ECL™direct (Amersham, Arlington Heights, IL) labeling and detection system following
25 protocols provided by the manufacturer. In brief, probes were prepared by covalently linking the denatured DNA to the enzyme horseradish peroxidase. Once labeled the probe was used under hybridization conditions which maintain the enzymatic activity. Unhybridized probe was removed by two gentle washes 20 minutes each
30 at 42°C in 0.5xSSC, 0.4% SDS, and 6M Urea. This was followed by two washes 5 minutes each at room temperature in 2xSSC. As directed by the manufacturer, ECL™ reagents were used to detect the hybridizing DNA bands. There are several factors which influence the ability to detect gene relatedness between various *Photorhabdus* strains and
35 strain W-14. First, high stringency conditions have not been employed in these hybridizations. It is known in the art that varying the stringency of hybridization and wash conditions will influence the pattern and intensity of hybridizing bands. Second, Southern blots' blot to blot variation will influence the mobility
40 of hybridizing bands and molecular weight estimates. Therefore, W-14 was included as a standard on all Southern blots.

Gene specific probes derived from the W-14 n genes were used in these hybridizations. The following lists the specific coordinates within each gene sequence to which the probe corresponds. A probe specific for *tcaB_i/B_{ii}*: 1174 to 3642 of Sequence ID #25, a probe specific for *tcaC*: 3637 to 6005 of Sequence ID #25, a probe specific for *tcbA*: 2097 to 4964 of Sequence ID #11, and a probe specific for *tcdA*: 1660 to 4191 of sequence ID #46. The following tables summarize Southern Blot analyses of *Photorhabdus* strains. In the event that hybridization of probes occurred, the hybridized fragment(s) were noted as either identical or different from the pattern observed for the W-14 strain.

Table 37
Southern Analysis of Photorhabdus Strains

Strains	tcdA	tcbA	tcaC	tcaB _{i/ii}
WX-1	D	D	D	D
WX-2	D	D	-	D
WX-3	D	D	D	D
WX-4	D	D	ND	D
WX-5	D	D	D	D
WX-6	D	D	D	D
WX-7	D	D	ND	D
WX-8	D	D	D	D
WX-9	ND	D	D	D
WX-10	ND	D	D	D
WX-11	ND	D	D	D
WX-12	D	D	D	D
WX-14	D	D	D	D
WX-15	D	D	D	D
HP88	D	-	D	D
Hm	D	-	D	D
H6	D	-	D	-
H9	D	-	I	D
B2	D	-	D	-
NC-1	D	-	D	D
W1R	D	-	D	D
W30	D	D	D	D
W-14	I	I	I	I

ND = Not determined; - = no detectable hybridization product;

5 I = Identical fragment pattern; D = Different fragment pattern.

Table 38
Southern Analysis of Photorhabdus Strains

Strains	<i>tcdA</i>	<i>tcdB</i>	<i>tcdC</i>	<i>tcdB_{i/ii}</i>
K-122	3.3, 2.8	D	-	ND
PWH-5	+	D	D	-
Indicus	D	D	3.0	I
Megidis	D	D	D	-
GD	D	D	D	-
HF-85	D	D	D	-
MP 3	D	-	D	-
MP 1	D	+	D	-
A. Cows	D	+	D	-
HB-Arg	D	ND	D	-
HMGD	D	D	D	-
HB Lewiston	D	D	D	-
HB Oswego	D	D	D	-
W-14	I	I	I	I

ND = Not determined; - = no detectable hybridization product;

5 I = Identical fragment pattern; D = Different fragment pattern.

+ = Hybridization fragment pattern not determined.

Table 39
Southern Analysis of *Photorhabdus* Strains

Strains	<i>tcdA</i>	<i>tcdB</i>	<i>tcdC</i>	<i>tcdB_i/B_{ii}</i>
GL98	+	+	D	
GL101	-	+	D	
GL138	-	+	D	
GL155	-	-	-	
GL217	+	-	D	
GL257	+	+	D	
MP4	-	+	-	
MP5	-	-	-	
<i>P. hepialus</i>	+	-	D	
<i>P. zealandia</i>	+	-	11.0	
DEP1				
DEP2				
DEP3				
W-14	3.8, 2.8	2.8	2.8	

ND = Not determined; - = no detectable hybridization product;

5 I = Identical fragment pattern; D = Different fragment pattern.

+ = Hybridization fragment pattern not determined.

10 From these analyses it is apparent that homologs of W-14 genes are dispersed throughout these diverse *Photorhabdus* strains, as evidenced by differences in gene fragment sizes between W-14 and the other strains.

Example 25

N-Terminal Amino Acid Sequences of Toxin Complex Peptides from 15 Different *Photorhabdus* Strains

The relationship of peptides isolated from different *Photorhabdus* strains, as described in Example 14, were subjected to

N-terminal amino acid sequencing. The N-terminal amino acid sequences of toxin peptides in several strains were compared to W-14 toxin peptides. In Table 40, a comparison of toxin peptides compared to date showed that identical or homologous (at least 40% similarity to W14 gene/peptides) toxin peptides were present in all of the strains. For example, the N-terminal amino acid sequence of TcaC, SEQ ID NO: 2, was found to be identical to that for 160 kDa peptide in HP88 but also homologs were present in strains WIR, H9, Hb, WX-1, and Hm. Some W-14 peptides or homologs have not been observed in other strains; however, not all peptides have been sequenced for toxin complexes from other strains due to N-terminal blockage or low abundance. In addition, many other N-terminal amino acid sequences (SEQ ID NOS: 82 to 88) have been obtained for toxin complex peptides from other strains that have no similarity to peptides from W-14 and in some case were identical to each other. For example, an identical amino acid sequence, SEQ ID NO: 82, was obtained for 64 kDa peptide present in both HP88 and Hb strains and a homologous sequence for a 70 kDa peptide in NC-1 strain (SEQ ID NO: 83).

Table 40

A Comparison of Amino Terminal Sequence Homology Between Proteins
Isolated From Non-W-14 Strains

W-14 Peptide	W-14 Gene	W-14 SEQ ID	SEQ ID NO:	Strain	Identical	Homology
TcaAii	tcaA	15				
TcaAiii	tcaA	4				
TcaBi	tcaB	3	76	H9	-	74 kDa
			76	Hm	-	71 kDa
TcaBii	tcaB	5		H9	61 kDa	-
				Hm	61 kDa	-
TcaC	tcaA	2	72	Hb	-	160 kDa
				HP88	160 kDa	-
			73	WIR	-	170 kDa
			74	H9	-	180 kDa
			75	Hm	-	170 kDa
			80	WX-1	-	170 kDa
TcbAii	tcbA	1				
TcbAiii	tcbA	40				
TccA	tccA	8	77	Hb	-	81 kDa
TccB	tccB	7		WX-1	170 kDa	-
				WX-2	180 kDa	-
				WX-14	180 kDa	-
				WIR	170 kDa	-
			78	H9	-	170 kDa
				NC-1	140 kDa	-
			79	Hm	-	190 kDa
TcdAii	tcdA					
TcdAiii	tcdA	41		Hb	57 kDa	-
			81	H9	-	69 kDa
		9		Hb	86 kDa	-
				HP88	86 kDa	-

Homology refers to amino acid sequences that were at least 40% similarity to W14 gene / peptides. Similar residues were identified as being a member in one of the following five groups: (P, A, G, S, T); (Q, N, E, B, D, Z); (H, K, R); (L, I, V, M); and (F, Y, W).

Example 26Immunological Analysis of Photorhabdus Strains

Culture broths of *Photorhabdus* strains were concentrated 10 to 15 times using Centriprep-10 ultrafiltration device (Amicon, Inc. Beverly, MA 01915). The concentration of the protein ranges from 0.3 to 3.0 mg per ml. Ten to 20 µg of total protein was loaded in each well of a precast 4-20% polyacrylamide gel (Integrated Separation Systems, Natick, MA 01760). Gel electrophoresis was performed for 1.25 hours using a constant current set at 25 ma per gel. The gel was electro-blotted on to Hybond-ECLTM nitrocellulose membrane (Amersham Corporation, Arlington Hts, IL 60005) using a semi-dry electro-blotter (Pharmacia Biotech Inc., Piscataway, NJ

08854). A constant current was applied at 0.75 mA per cm for 2.5 hours. The membrane was blocked with 10% milk in TBST (25 mM Tris HCl pH 7.4, 136 mM NaCl, 2.7 mM KCl, 0.1% Tween 20) for one hour at room temperature. Each primary antibody was diluted in 10% milk/TBST to 1:500. Other dilution between 1:50 to 1:1000 was also used. The membrane was incubated in primary antibody for at least one hour. Then it was washed thoroughly with the blocking solution or TBST. A 1:2000 dilution of secondary antibodies (goat anti-mouse IgG or goat anti rabbit TgG conjugated to horseradish peroxidase; BioRad Laboratories, Hercules, CA 94547) in 10% milk/TBST was applied to the membrane which was placed on a platform rocker for one hour. The membrane was subsequently washed with excess amount of TBST. The detection of the protein was performed by using an ECL (Enhanced Chemiluminescence) detection kit (Amersham International).

A panel of peptide specific-antibodies generated against W-14 peptides were used to characterize the protein composition of broths from nine non-W-14 *Photothabdus* strains using Western blot analysis. In addition, one monoclonal antibody (MAb-C5F2) which recognizes TcbA_{III} protein in W-14-derived toxin complex was used. The results (Table 39) showed cross recognition of the antibodies to some of the proteins in these broths. In some cases, the proteins that were recognized by the antibodies were the same size as the W-14 target peptides. In other cases, the proteins that were recognized by the antibodies were smaller than the W-14 target peptides. This data indicate that some of the non-W-14 *Photothabdus* strains may produce similar proteins to the W-14 strain. The difference could be due to deletion or protein processing or degradation process. Some of the strains did not contain protein(s) that could be recognized by some antibodies, however, it is possible that the concentration is significantly lower than those observed for W-14 peptides. When compared for various toxin peptide homologs these results showed peptide diversity among the *Photothabdus* strains.

Table 41

Cross Recognition by Monoclonal Antibodies or Polyclonal Antibodies
Generated Against W-14 Peptides to Protein(s) in Broths of Selected
Non-W-14 Photorhabdus

Photo- rhabdus Strain	MAB C5F2	PAB TcdA ii- syn	PAB TcdA iii- syn	PAB TcaC -syn	PAB- TcaB ii- syn	PAB TcbA iii- syn	PAB TcaB i- syn	PAB TcaA ii- syn	PAB TcaA iii- syn
MP1	-	+	+	+	-	+	+	+	+
MP2	+	+	+	+	-	+	+	+	+
MP3	-	+	+	+	-	NT	+	+	-
A. Cows	-	+	+	+	-	NT	+	+	+
Hb-osw	-	-	NT	+	+	NT	+	+	+
H-Arg	-	+	+	+	-	NT	+	+	+
Hb-leu	-	+	+	+	-	NT	+	+	+
Indicus	+	+	+	+	+	NT	+	+	+
HF85	-	+	+	+	-	+	+	+	+
W-14	+	+	+	+	+	+	+	+	+

5 +: Positive reaction; -: Negative reaction; NT: Not Tested

Additional non-W-14 Photorhabdus strains were characterized by Western blot analysis using the culture broth and/or partial purified protein fractions as antigen. The panel of antibodies include MAb-C5F2, MAb-DE1 (recognizing TcdA_{ii}), PAb-DE2 (recognizing TcaB), PAb-TcbA_{ii}-syn, PAb-TcaC-syn, PAb TcaB_{ii}-syn, PAb-TcbA_{iii}-syn, PAb-TcaB_i-syn. These antibodies showed cross-reactivity with proteins in the broth and in the partial purified fractions of non-W-14 strains.

The data indicate that antibodies could be used to identify proteins in the broth as well as in the partially purified protein fractions.

Table 42

Cross Recognition by Monoclonal Antibodies or Polyclonal Antibodies
Generated Against W-14 Peptides to Protein(s) in Broths and/or
Partial Purified Protein Fractions of Selected Non-W14 Photorhabdus

5

Photo-rhabdus Strain	Monoclonal Antibodies		Polyclonal Antibodies					
	Mab C5F2	Mab-DE1	PAb-DE2	PAb TcbA _{ii} -syn	PAb TcaC-syn	PAb TcaB _{ii} -syn	PAb TcbA _{iii} -syn	PAb TcaB _i -syn
WX-1	+	+	+	+	+	+	+	+
WX-2	+	+	+	+	+	+	NT	+
WX-3	+	NT	+	NT	NT	NT	NT	NT
WX-5	+	NT	+	NT	NT	NT	NT	NT
WX-6	+	NT	NT	NT	NT	NT	NT	NT
WX-7	+	+	+	+	+	+	NT	+
WX-8	+	NT	NT	NT	NT	NT	NT	NT
WX-9	+	NT	NT	NT	NT	NT	NT	NT
WX-10	-	NT	NT	NT	NT	NT	NT	NT
WX-12	+	+	+	+	+	+	+	+
WX-14	+	+	+	+	NT	+	NT	+
WX-15	+	NT	NT	NT	NT	NT	NT	NT
W30	+	+	+	NT	NT	NT	NT	NT
Hb	-	NT	+	NT	+	NT	-	+
H9	-	-	+	NT	+	+	NT	NT
Hm	-	NT	+	+	+	+	NT	++
HP88	-	NT	+	-	+	-	-	+
NC-1	+	-	+	+	+	+	NT	+
WIR	-	NT	+	+	+	+	+	+
W-14	+	+	+	+	+	+	+	+

-: Negative reaction; +: Positive reaction; NT: Not tested

Example 27

10 Bacterial Expression of the *tcdA* Coding Region

Engineering of the *tcdA* Gene for Bacterial Expression

The 5' and 3' ends of the *tcdA* coding region (SEQ ID NO:46) were modified to add useful cloning sites for inserting the segment into heterologous expression vectors. The ends were modified using unique primers in Polymerase Chain Reactions (PCR), performed essentially as described in Example 8. Primer sets, as described below, were used in conjunction with cosmid 21D2.4 as template, to created products with the appropriately modified ends.

20 The first primer set was used to modify the 5' end of the gene, to insert a unique *Nco* I site at the initiator codon using the forward primer A0F1 (5' GAT CGA TCG ATC CAT GGC CAA CGA GTC TGT AAA AGA GAT ACC TGA TG TAT TAA AAA GCC AGT GTG 3') and to add unique *Bgl* II, *Sal* I and *Not* I sites to facilitate insertion of the remainder
 25 of the gene using the reverse primer A0R1 (5' GAT CGA TCG TAC GCG

GCC GCT CGA TCG ATC GTC GAC CCA TTG ATT TGA GAT CTG GGC GGC GGG TAT
CCA GAT AAT AAA CGG AGT CAC 3').

Another PCR reaction was designed to modify the 3' end of the gene by adding an additional stop codon and convenient restriction sites for cloning. The forward primer A0F2 (5' ACT GGC TGC GTG GTC GAC TGG CGG CGA TTT ACT 3') was used to amplify across a unique Sal I site in the gene, later used to clone the modified 3' end. The reverse primer A0R2 (5' CGA TGC ATG CTG CGG CCG CAG GCC TTC CTC GAG TCA TTA TTT AAT GGT GTA GCG AAT ATG CAA AAT 3') was used to insert a second stop codon (TGA) and cloning sites *Xho I*, *Stu I* and *Not I*. Bacterial expression vector pET27b (Novagen, Madison, WI), was modified to delete the *Bgl II* site at position 446, according to standard molecular biology techniques.

The 497 bp PCR product from the first amplification reaction (A0F1+A0R1), to modify the 5' end of the gene, was ligated to the modified pET27b vector according to the supplier's instructions. The DNA sequences of the amplified portion of three isolates were determined using the supplier's recommended primers and the sequencing methods described previously. The sequence of all isolates was the same.

One isolate was then used as a cloning vector to insert the middle portion of the *tcdA* gene on a 6341 bp *Bgl II* to *Sal I* fragment. The resulting clone was called MC4 and contained all but the 3' most portion of the *tcdA* coding sequence. Finally, to complete the full-length coding region, the 832 bp PCR product from the second PCR amplification (A0F2+A0R2), to modify the 3' end of the gene, was ligated to isolate MC4 on a *Sal I* to *Not I* fragment, according to standard molecular biology techniques. The *tcdA* coding region was sequenced and found to be complete, the resulting plasmid is called pDAB2035.

Construction of Plasmids pDAB2036, pDAB2037 and pDAB2038 for Bacterial Expression of *tcdA*

The *tcdA* coding region was cut from plasmid pDAB2035 with restriction enzymes *Nco I* and *Xho I* and gel purified. The fragment was ligated into the *Nco I* and *Xho I* sites of the expression vector pET15 to create plasmid pDAB2036. Additionally, pDAB2035 was cut with *Nco I* and *Not I* to release the *tcdA* coding region which was ligated into the *Nco I* and *Not I* sites of the expression vector pET28b to create plasmid pDAB2037. Finally, plasmid pDAB2035 was cut with *Nco I* and *Stu I* to release the *tcdA* coding region. This fragment was ligated into the expression vector Trc99a which was cut with *Hind III* followed by treatment with T4 DNA polymerase to blunt

the ends. The vector was then cut with Nco I and ligated with the Nco I/Stu I cut *tcdA* fragment. The resulting plasmid is called pDAB2038.

5 Expression of *tcdA* from Plasmid pDAB2038

Plasmid pDAB2038 was transformed into *BL21* cells and expressed as described above for plasmid pDAB2033 in Example 19.

Purification of *tcdA* from *E. coli*

- 10 The expression culture was centrifuged at 10,300 g for 30 min and the supernatant was collected. It was diluted with two volumes of H₂O and applied at a flow rate of 7.5 ml/min to a poros 50 HQ (Perspective Systems, MA) column (1.6 cm x 10 cm) which was pre-equilibrated with 10 mM sodium phosphate buffer, pH 7.0 (Buffer A).
- 15 The column was washed with Buffer A until the optical density at 280 nm returned to baseline level. The proteins bound to the column were then eluted with 1M NaCl in Buffer A.

- The fraction was loaded in 20 ml aliquots onto a gel filtration column, Sepharose CL-4B (2.6 x 100 cm), which was equilibrated with Buffer A. The protein was eluted in Buffer A at a flow rate of 0.75 mL/min. Fractions with a retention time between 260 minutes and 460 minutes were pooled and applied at 1 mL/min to a Mono Q 5/5 column which was equilibrated with 20 mM Tris-HCl, pH 7.0 (Buffer B). The column was washed with Buffer B until the optical density at 280 nm
- 25 returned to baseline level. The proteins bound to the column were eluted with a linear gradient of 0 to 1 M NaCl in Buffer B at 1mL/min for 30 min. One milliliter fractions were collected, serially diluted, and subjected to SCR bioassay. Fractions eluted out between 0.1 and 0.3 M NaCl were found to have the highest
- 30 insecticidal activity. Western analysis of the active fractions using pAb TcdA₁₁-syn antibody and pAb Tcd₁₁₁-syn antibody indicated the presence of peptides TcdA₁₁ and TcdA₁₁₁.

SEQUENCE LISTING

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(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
35 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
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(B) FILING DATE: 28-FEB-1995
- (vii) PRIOR APPLICATION DATA:
50 (A) APPLICATION NUMBER: US 60/007,255
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS :

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1 (TcbA_{ii} N-terminus):

Phe Ile Gln Gly Tyr Ser Asp Leu Phe Gly Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2 (TcaC N-terminus):

Met Gln Asp Ser Pro Glu Val Ser Ile Thr Thr Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3 (TcaB_i N-terminus):

Ser Glu Ser Leu Phe Thr Gln Thr Leu Lys Glu Ala Arg Arg Asp Ala
1 5 10 15

Leu Val Ala

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4 (TcaA_{iii} N-terminus):

Ala Ser Pro Leu Ser Thr Ser Glu Leu Thr Ser Lys Leu Asn
 1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5 (TcaB_{ii} N-terminus):

Ala Gly Asp Thr Ala Asn Ile Gly Asp
 1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu Gly Gly Ala Ala Thr Leu Leu Asp Leu Leu Leu Pro Gln Ile
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7 (TccB N-terminus):

Met Leu Ser Thr Met Glu Lys Gln Leu Asn Glu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8 (TccA N-terminus):

Met Asn Leu Ala Ser Pro Leu Ile Ser
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ile Asn Leu Asp Ile Asn Glu Gln Asn Lys Ile Met Val Val Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Ala Lys Asp Val Lys Phe Gly Ser Asp Ala Arg Val Lys Met Leu
1 5 10 15

Arg Gly Val Asn
20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7515 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..7515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11 (tcbA gene):

5	ATG CAA AAC TCA TTA TCA AGC ACT ATC GAT ACT ATT TGT CAG AAA CTG Met Gln Asn Ser Leu Ser Ser Thr Ile Asp Thr Ile Cys Gln Lys Leu	48
10	CAA TTA ACT TGT CCG GCG GAA ATT GCT TTG TAT CCC TTT GAT ACT TTC Gln Leu Thr Cys Pro Ala Glu Ile Ala Leu Tyr Pro Phe Asp Thr Phe	96
15	CGG GAA AAA ACT CCG GGA ATG GTT AAT TGG GGG GAA GCA AAA CGG ATT Arg Glu Lys Thr Arg Gly Met Val Asn Trp Gly Glu Ala Lys Arg Ile	144
20	TAT GAA ATT GCA CAA GCG GAA CAG GAT AGA AAC CTA CTT CAT GAA AAA Tyr Glu Ile Ala Gln Ala Glu Gln Asp Arg Asn Leu Leu His Glu Lys	192
25	CGT ATT TTT GCC TAT GCT AAT CCG CTG CTG AAA AAC GCT GTT CGG TTG Arg Ile Phe Ala Tyr Ala Asn Pro Leu Leu Lys Asn Ala Val Arg Leu	240
30	GGT ACC CGG CAA ATG TTG GGT TTT ATA CAA GGT TAT AGT GAT CTG TTT Gly Thr Arg Gln Met Leu Gly Phe Ile Gln Gly Tyr Ser Asp Leu Phe	288
35	GGT AAT CGT GCT GAT AAC TAT GCC GCG CCG GGC TCG GTT GCA TCG ATG Gly Asn Arg Ala Asp Asn Tyr Ala Ala Pro Gly Ser Val Ala Ser Met	336
40	TTC TCA CCG GCG GCT TAT TTG ACG GAA TTG TAC CGT GAA GCC AAA AAC Phe Ser Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Lys Asn	384
45	TTG CAT GAC AGC AGC TCA ATT TAT TAC CTA GAT AAA CGT CGC CCG GAT Leu His Asp Ser Ser Ser Ile Tyr Tyr Leu Asp Lys Arg Arg Pro Asp	432
50	TTA GCA AGC TTA ATG CTC AGC CAG AAA AAT ATG GAT GAG GAA ATT TCA Leu Ala Ser Leu Met Leu Ser Gln Lys Asn Met Asp Glu Glu Ile Ser	480
55	ACG CTG GCT CTC TCT AAT GAA TTG TGC CTT GCC GGG ATC GAA ACA AAA Thr Leu Ala Leu Ser Asn Glu Leu Cys Leu Ala Gly Ile Glu Thr Lys	528
60	ACA GGA AAA TCA CAA GAT GAA GTG ATG GAT ATG TTG TCA ACT TAT CGT Thr Gly Lys Ser Gln Asp Glu Val Met Asp Met Leu Ser Thr Tyr Arg	576
65	TTA AGT GGA GAG ACA CCT TAT CAT CAC GCT TAT GAA ACT GTT CGT GAA Leu Ser Gly Glu Thr Pro Tyr His His Ala Tyr Glu Thr Val Arg Glu	624
70	ATC GTT CAT GAA CGT GAT CCA GGA TTT CGT CAT TTG TCA CAG GCA CCC Ile Val His Glu Arg Asp Pro Gly Phe Arg His Leu Ser Gln Ala Pro	672
	ATT GTT GCT GCT AAG CTC GAT CCT GTG ACT TTG TTG GGT ATT AGC TCC Ile Val Ala Ala Lys Leu Asp Pro Val Thr Leu Leu Gly Ile Ser Ser	720
	CAT ATT TCG CCA GAA CTG TAT AAC TTG CTG ATT GAG GAG ATC CCG GAA His Ile Ser Pro Glu Leu Tyr Asn Leu Leu Ile Glu Glu Ile Pro Glu	768
	AAA GAT GAA GCC GCG CTT GAT ACG CTT TAT AAA ACA AAC TTT GGC GAT Lys Asp Glu Ala Ala Leu Asp Thr Leu Tyr Lys Thr Asn Phe Gly Asp	816
	ATT ACT ACT GCT CAG TTA ATG TCC CCA AGT TAT CTG GCC CGG TAT TAT	864

	Ile	Thr	Thr	Ala	Gln	Leu	Met	Ser	Pro	Ser	Tyr	Leu	Ala	Arg	Tyr	
			275					280					285			
5	GGC	GTC	TCA	CCG	GAA	GAT	ATT	GCC	TAC	GTG	ACG	ACT	TCA	TTA	TCA	912
	Gly	Val	Ser	Pro	Glu	Asp	Ile	Ala	Tyr	Val	Thr	Thr	Ser	Leu	Ser	
		290					295					300				
10	GTT	GGA	TAT	AGC	AGT	GAT	ATT	CTG	GTT	ATT	CCG	TTG	GTC	GAT	GGT	960
	Val	Gly	Tyr	Ser	Ser	Asp	Ile	Leu	Val	Ile	Pro	Leu	Val	Asp	Gly	
	305					310					315				320	
15	GGT	AAG	ATG	GAA	GTA	GTT	CGT	GTT	ACC	CGA	ACA	CCA	TCG	GAT	AAT	1008
	Gly	Lys	Met	Glu	Val	Val	Arg	Val	Thr	Arg	Thr	Pro	Ser	Asp	Asn	
					325					330					335	
20	ACC	AGT	CAG	ACG	AAT	TAT	ATT	GAG	CTG	TAT	CCA	CAG	GGT	GGC	GAC	1056
	Thr	Ser	Gln	Thr	Asn	Tyr	Ile	Glu	Leu	Tyr	Pro	Gln	Gly	Gly	Asp	
				340					345					350		
25	TAT	TTG	ATC	AAA	TAC	AAT	CTA	AGC	AAT	AGT	TTT	GGT	TTG	GAT	GAT	1104
	Tyr	Leu	Ile	Lys	Tyr	Asn	Leu	Ser	Asn	Ser	Phe	Gly	Leu	Asp	Asp	
			355				360						365			
30	TAT	CTG	CAA	TAT	AAA	GAT	GGT	TCC	GCT	GAT	TGG	ACT	GAG	ATT	GCC	1152
	Tyr	Leu	Gln	Tyr	Lys	Asp	Gly	Ser	Ala	Asp	Trp	Thr	Glu	Ile	Ala	
		370				375						380				
35	AAT	CCC	TAT	CCT	GAT	ATG	GTC	ATA	AAT	CAA	AAG	TAT	GAA	TCA	CAG	1200
	Asn	Pro	Tyr	Pro	Asp	Met	Val	Ile	Asn	Gln	Lys	Tyr	Glu	Ser	Gln	
		385				390					395					400
40	ACA	ATC	AAA	CGT	AGT	GAC	TCT	GAC	AAT	ATA	CTC	AGT	ATA	GGG	TTA	1248
	Thr	Ile	Lys	Arg	Ser	Asp	Ser	Asp	Asn	Ile	Leu	Ser	Ile	Gly	Leu	
				405						410					415	
45	AGA	TGG	CAT	AGC	GGT	AGT	TAT	AAT	TTT	GCC	GCC	GCC	AAT	TTT	AAA	1296
	Arg	Trp	His	Ser	Gly	Ser	Tyr	Asn	Phe	Ala	Ala	Ala	Asn	Phe	Lys	
				420					425					430		
50	GAC	CAA	TAC	TCC	CCG	AAA	GCT	TTC	CTG	CTT	AAA	ATG	AAT	AAG	GCT	1344
	Asp	Gln	Tyr	Ser	Pro	Lys	Ala	Phe	Leu	Leu	Lys	Met	Asn	Lys	Ala	
			435				440						445			
55	CGG	TTG	CTC	AAA	GCT	ACC	GGC	CTC	TCT	TTT	GCT	ACG	TTG	GAG	CGT	1392
	Arg	Leu	Leu	Lys	Ala	Thr	Gly	Leu	Ser	Phe	Ala	Thr	Leu	Glu	Arg	
		450				455						460				
60	GTT	GAT	AGT	GTT	AAT	AGC	ACC	AAA	TCC	ATC	ACG	GTT	GAG	GTA	TTA	1440
	Val	Asp	Ser	Val	Asn	Ser	Thr	Lys	Ser	Ile	Thr	Val	Glu	Val	Leu	
		465			470						475				480	
65	AAG	GTT	TAT	CGG	GTA	AAA	TTC	TAT	ATT	GAT	CGT	TAT	GGC	ATC	AGT	1488
	Lys	Val	Tyr	Arg	Val	Lys	Phe	Tyr	Ile	Asp	Arg	Tyr	Gly	Ile	Ser	
				485					490					495		
70	GAG	ACA	GCC	GCT	ATT	TTG	GCT	AAT	ATT	AAT	ATC	TCT	CAG	CAA	GCT	1536
	Glu	Thr	Ala	Ala	Ile	Leu	Ala	Asn	Ile	Asn	Ile	Ser	Gln	Gln	Ala	
				500					505					510		
75	GGC	AAT	CAG	CTT	AGC	CAG	TTT	GAG	CAA	CTA	TTT	AAT	CAC	CCG	CCG	1584
	Gly	Asn	Gln	Leu	Ser	Gln	Phe	Glu	Gln	Leu	Phe	Asn	His	Pro	Pro	
			515				520						525			
80	AAT	GGT	ATT	CGC	TAT	GAA	ATC	AGT	GAG	GAC	AAC	TCC	AAA	CAT	CTT	1632
	Asn	Gly	Ile	Arg	Tyr	Glu	Ile	Ser	Glu	Asp	Asn	Ser	Lys	His	Leu	
		530				535						540				
85	AAT	CCT	GAT	CTG	AAC	CTT	AAA	CCA	GAC	AGT	ACC	GGT	GAT	GAT	CAA	1680
	Asn	Pro	Asp	Leu	Asn	Leu	Lys	Pro	Asp	Ser	Thr	Gly	Asp	Asp	Gln	
		545				550					555				560	

	AAG	GCG	GTT	TTT	AAA	CGC	GCG	TTT	CAG	GTT	AAC	GCC	AGT	GAG	TTG	TAT	1728
	Lys	Ala	Val	Leu	Lys	Arg	Ala	Phe	Gln	Val	Asn	Ala	Ser	Glu	Leu	Tyr	
					565					570						575	
5	CAG	ATG	TTA	TTG	ATC	ACT	GAT	CGT	AAA	GAA	GAC	GGT	GTT	ATC	AAA	AAT	1776
	Gln	Met	Leu	Leu	Ile	Thr	Asp	Arg	Lys	Glu	Asp	Gly	Val	Ile	Lys	Asn	
				580					585					590			
10	AAC	TTA	GAG	AAT	TTG	TCT	GAT	CTG	TAT	TTG	GTT	AGT	TTG	CTG	GCC	CAG	1824
	Asn	Leu	Glu	Asn	Leu	Ser	Asp	Leu	Tyr	Leu	Val	Ser	Leu	Leu	Ala	Gln	
			595					600					605				
15	ATT	CAT	AAC	CTG	ACT	ATT	GCT	GAA	TTG	AAC	ATT	TTG	TTG	GTG	ATT	TGT	1872
	Ile	His	Asn	Leu	Thr	Ile	Ala	Glu	Leu	Asn	Ile	Leu	Leu	Val	Ile	Cys	
		610					615					620					
20	GGC	TAT	GGC	GAC	ACC	AAC	ATT	TAT	CAG	ATT	ACC	GAC	GAT	AAT	TTA	GCC	1920
	Gly	Tyr	Gly	Asp	Thr	Asn	Ile	Tyr	Gln	Ile	Thr	Asp	Asp	Asn	Leu	Ala	
	625					630					635					640	
25	AAA	ATA	GTG	GAA	ACA	TTG	TTG	TGG	ATC	ACT	CAA	TGG	TTG	AAG	ACC	CAA	1968
	Lys	Ile	Val	Glu	Thr	Leu	Leu	Trp	Ile	Thr	Gln	Trp	Leu	Lys	Thr	Gln	
					645					650					655		
30	AAA	TGG	ACA	GTT	ACC	GAC	CTG	TTT	CTG	ATG	ACC	ACG	GCC	ACT	TAC	AGC	2016
	Lys	Trp	Thr	Val	Thr	Asp	Leu	Phe	Leu	Met	Thr	Thr	Ala	Thr	Tyr	Ser	
				660					665					670			
35	ACC	ACT	TTA	ACG	CCA	GAA	ATT	AGC	AAT	CTG	ACG	GCT	ACG	TTG	TCT	TCA	2064
	Thr	Thr	Leu	Thr	Pro	Glu	Ile	Ser	Asn	Leu	Thr	Ala	Thr	Leu	Ser	Ser	
			675					680					685				
40	ACT	TTG	CAT	GGC	AAA	GAG	AGT	CTG	ATT	GGG	GAA	GAT	CTG	AAA	AGA	GCA	2112
	Thr	Leu	His	Gly	Lys	Glu	Ser	Leu	Ile	Gly	Glu	Asp	Leu	Lys	Arg	Ala	
		690					695					700					
45	ATG	GCG	CCT	TGC	TTC	ACT	TCG	GCT	TTG	CAT	TTG	ACT	TCT	CAA	GAA	GTT	2160
	Met	Ala	Pro	Cys	Phe	Thr	Ser	Ala	Leu	His	Leu	Thr	Ser	Gln	Glu	Val	
	705					710					715					720	
50	GCG	TAT	GAC	CTG	CTG	TTG	TGG	ATA	GAC	CAG	ATT	CAA	CCG	GCA	CAA	ATA	2208
	Ala	Tyr	Asp	Leu	Leu	Leu	Trp	Ile	Asp	Gln	Ile	Gln	Pro	Ala	Gln	Ile	
					725					730					735		
55	ACT	GTT	GAT	GGG	TTT	TGG	GAA	GAA	GTG	CAA	ACA	ACA	CCA	ACC	AGC	TTG	2256
	Thr	Val	Asp	Gly	Phe	Trp	Glu	Glu	Val	Gln	Thr	Thr	Pro	Thr	Ser	Leu	
				740					745					750			
60	AAG	GTG	ATT	ACC	TTT	GCT	CAG	GTG	CTG	GCA	CAA	TTG	AGC	CTG	ATC	TAT	2304
	Lys	Val	Ile	Thr	Phe	Ala	Gln	Val	Leu	Ala	Gln	Leu	Ser	Leu	Ile	Tyr	
			755					760					765				
65	CGT	CGT	ATT	GGG	TTA	AGT	GAA	ACG	GAA	CTG	TCA	CTG	ATC	GTG	ACT	CAA	2352
	Arg	Arg	Ile	Gly	Leu	Ser	Glu	Thr	Glu	Leu	Ser	Leu	Ile	Val	Thr	Gln	
			770				775					780					
70	TCT	TCT	CTG	CTA	GTG	GCA	GGC	AAA	AGC	ATA	CTG	GAT	CAC	GGT	CTG	TTA	2400
	Ser	Ser	Leu	Leu	Val	Ala	Gly	Lys	Ser	Ile	Leu	Asp	His	Gly	Leu	Leu	
	785					790					795					800	
75	ACC	CTG	ATG	GCC	TTG	GAA	GGT	TTT	CAT	ACC	TGG	GTT	AAT	GGC	TTG	GGG	2448
	Thr	Leu	Met	Ala	Leu	Glu	Gly	Phe	His	Thr	Trp	Val	Asn	Gly	Leu	Gly	
					805					810					815		
80	CAA	CAT	GCC	TCC	TTG	ATA	TTG	GCG	GCG	TTG	AAA	GAC	GGA	GCC	TTG	ACA	2496
	Gln	His	Ala	Ser	Leu	Ile	Leu	Ala	Ala	Leu	Lys	Asp	Gly	Ala	Leu	Thr	
				820					825					830			
85	GTT	ACC	GAT	GTA	GCA	CAA	GCT	ATG	AAT	AAG	GAG	GAA	TCT	CTC	CTA	CAA	2544
	Val	Thr	Asp	Val	Ala	Gln	Ala	Met	Asn	Lys	Glu	Glu	Ser	Leu	Leu	Gln	
			835					840						845			

5 ATG GCA GCT AAT CAG GTG GAG AAG GAT CTA ACA AAA CTG ACC AGT TGG 2592
 Met Ala Ala Asn Gln Val Glu Lys Asp Leu Thr Lys Leu Thr Ser Trp
 850 855 860

10 ACA CAG ATT GAC GCT ATT CTG CAA TGG TTA CAG ATG TCT TCG GCC TTG 2640
 Thr Gln Ile Asp Ala Ile Leu Gln Trp Leu Gln Met Ser Ser Ala Leu
 865 870 875 880

15 GCG GTT TCT CCA CTG GAT CTG GCA GGG ATG ATG GCC CTG AAA TAT GGG 2688
 Ala Val Ser Pro Leu Asp Leu Ala Gly Met Met Ala Leu Lys Tyr Gly
 885 890 895

20 ATA GAT CAT AAC TAT GCT GCC TGG CAA GCT GCG GCG GCT GCG CTG ATG 2736
 Ile Asp His Asn Tyr Ala Ala Trp Gln Ala Ala Ala Ala Ala Leu Met
 900 905 910

25 GCT GAT CAT GCT AAT CAG GCA CAG AAA AAA CTG GAT GAG ACG TTC AGT 2784
 Ala Asp His Ala Asn Gln Ala Gln Lys Lys Leu Asp Glu Thr Phe Ser
 915 920 925

30 AAG GCA TTA TGT AAC TAT TAT ATT AAT GCT GTT GTC GAT AGT GCT GCT 2832
 Lys Ala Leu Cys Asn Tyr Tyr Ile Asn Ala Val Val Asp Ser Ala Ala
 930 935 940

35 GGA GTA CGT GAT CGT AAC GGT TTA TAT ACC TAT TTG CTG ATT GAT AAT 2880
 Gly Val Arg Asp Arg Asn Gly Leu Tyr Thr Tyr Leu Leu Ile Asp Asn
 945 950 955 960

40 CAG GTT TCT GCC GAT GTG ATC ACT TCA CGT ATT GCA GAA GCT ATC GCC 2928
 Gln Val Ser Ala Asp Val Ile Thr Ser Arg Ile Ala Glu Ala Ile Ala
 965 970 975

45 GGT ATT CAA CTG TAC GTT AAC CGG GCT TTA AAC CGA GAT GAA GGT CAG 2976
 Gly Ile Gln Leu Tyr Val Asn Arg Ala Leu Asn Arg Asp Glu Gly Gln
 980 985 990

50 CTT GCA TCG GAC GTT AGT ACC CGT CAG TTC TTC ACT GAC TGG GAA CGT 3024
 Leu Ala Ser Asp Val Ser Thr Arg Gln Phe Phe Thr Asp Trp Glu Arg
 995 1000 1005

55 TAC AAT AAA CGT TAC AGT ACT TGG GCT GGT GTC TCT GAA CTG GTC TAT 3072
 Tyr Asn Lys Arg Tyr Ser Thr Trp Ala Gly Val Ser Glu Leu Val Tyr
 1010 1015 1020

60 TAT CCA GAA AAC TAT GTT GAT CCC ACT CAG CGC ATT GGG CAA ACC AAA 3120
 Tyr Pro Glu Asn Tyr Val Asp Pro Thr Gln Arg Ile Gly Gln Thr Lys
 1025 1030 1035 1040

65 ATG ATG GAT GCG CTG TTG CAA TCC ATC AAC CAG AGC CAG CTA AAT GCG 3168
 Met Met Asp Ala Leu Leu Gln Ser Ile Asn Gln Ser Gln Leu Asn Ala
 1045 1050 1055

70 GAT ACG GTG GAA GAT GCT TTC AAA ACT TAT TTG ACC AGC TTT GAG CAG 3216
 Asp Thr Val Glu Asp Ala Phe Lys Thr Tyr Leu Thr Ser Phe Glu Gln
 1060 1065 1070

75 GTA GCA AAT CTG AAA GTA ATT AGT GCT TAC CAC GAT AAT GTG AAT GTG 3264
 Val Ala Asn Leu Lys Val Ile Ser Ala Tyr His Asp Asn Val Asn Val
 1075 1080 1085

80 GAT CAA GGA TTA ACT TAT TTT ATC GGT ATC GAC CAA GCA GCT CCG GGT 3312
 Asp Gln Gly Leu Thr Tyr Phe Ile Gly Ile Asp Gln Ala Ala Pro Gly
 1090 1095 1100

85 ACG TAT TAC TGG CGT AGT GTT GAT CAC AGC AAA TGT GAA AAT GGC AAG 3360
 Thr Tyr Tyr Trp Arg Ser Val Asp His Ser Lys Cys Glu Asn Gly Lys
 1105 1110 1115 1120

90 TTT GCC GCT AAT GCT TGG GGT GAG TGG AAT AAA ATT ACC TGT GCT GTC 3408
 Phe Ala Ala Asn Ala Trp Gly Glu Trp Asn Lys Ile Thr Cys Ala Val

	1125										1130										1135									
5	AAT	CCT	TGG	AAA	AAT	ATC	ATC	CGT	CCG	GTT	GTT	TAT	ATG	TCC	CGC	TTA	3456													
	Asn	Pro	Trp	Lys	Asn	Ile	Ile	Arg	Pro	Val	Val	Tyr	Met	Ser	Arg	Leu														
				1140					1145					1150																
10	TAT	CTG	CTA	TGG	CTG	GAG	CAG	CAA	TCA	AAG	AAA	AGT	GAT	GAT	GGT	AAA	3504													
	Tyr	Leu	Leu	Trp	Leu	Glu	Gln	Gln	Ser	Lys	Lys	Ser	Asp	Asp	Gly	Lys														
				1155				1160					1165																	
15	ACC	ACG	ATT	TAT	CAA	TAT	AAC	TTA	AAA	CTG	GCT	CAT	ATT	CGT	TAC	GAC	3552													
	Thr	Thr	Ile	Tyr	Gln	Tyr	Asn	Leu	Lys	Leu	Ala	His	Ile	Arg	Tyr	Asp														
				1170			1175					1180																		
20	GGT	AGT	TGG	AAT	ACA	CCA	TTT	ACT	TTT	GAT	GTG	ACA	GAA	AAG	GTA	AAA	3600													
	Gly	Ser	Trp	Asn	Thr	Pro	Phe	Thr	Phe	Asp	Val	Thr	Glu	Lys	Val	Lys	1200													
				1185		1190					1195																			
25	AAT	TAC	ACG	TCG	AGT	ACT	GAT	GCT	GCT	GAA	TCT	TTA	GGG	TTG	TAT	TGT	3648													
	Asn	Tyr	Thr	Ser	Ser	Thr	Asp	Ala	Ala	Glu	Ser	Leu	Gly	Leu	Tyr	Cys														
				1205						1210					1215															
30	ACT	GGT	TAT	CAA	GGG	GAA	GAC	ACT	CTA	TTA	GTT	ATG	TTC	TAT	TCG	ATG	3696													
	Thr	Gly	Tyr	Gln	Gly	Glu	Asp	Thr	Leu	Leu	Val	Met	Phe	Tyr	Ser	Met														
				1220					1225					1230																
35	CAG	AGT	AGT	TAT	AGC	TCC	TAT	ACC	GAT	AAT	AAT	GCG	CCG	GTC	ACT	GGG	3744													
	Gln	Ser	Ser	Tyr	Ser	Ser	Tyr	Thr	Asp	Asn	Asn	Ala	Pro	Val	Thr	Gly														
				1235				1240					1245																	
40	CTA	TAT	ATT	TTC	GCT	GAT	ATG	TCA	TCA	GAC	AAT	ATG	ACG	AAT	GCA	CAA	3792													
	Leu	Tyr	Ile	Phe	Ala	Asp	Met	Ser	Ser	Asp	Asn	Met	Thr	Asn	Ala	Gln														
				1250			1255					1260																		
45	GCA	ACT	AAC	TAT	TGG	AAT	AAC	AGT	TAT	CCG	CAA	TTT	GAT	ACT	GTG	ATG	3840													
	Ala	Thr	Asn	Tyr	Trp	Asn	Asn	Ser	Tyr	Pro	Gln	Phe	Asp	Thr	Val	Met	1280													
				1265		1270					1275																			
50	GCA	GAT	CCG	GAT	AGC	GAC	AAT	AAA	AAA	GTC	ATA	ACC	AGA	AGA	GTT	AAT	3888													
	Ala	Asp	Pro	Asp	Ser	Asp	Asn	Lys	Lys	Val	Ile	Thr	Arg	Arg	Val	Asn														
				1285						1290					1295															
55	AAC	CGT	TAT	GCG	GAG	GAT	TAT	GAA	ATT	CCT	TCC	TCT	GTG	ACA	AGT	AAC	3936													
	Asn	Arg	Tyr	Ala	Glu	Asp	Tyr	Glu	Ile	Pro	Ser	Ser	Val	Thr	Ser	Asn														
				1300				1305						1310																
60	AGT	AAT	TAT	TCT	TGG	GGT	GAT	CAC	AGT	TTA	ACC	ATG	CTT	TAT	GGT	GGT	3984													
	Ser	Asn	Tyr	Ser	Trp	Gly	Asp	His	Ser	Leu	Thr	Met	Leu	Tyr	Gly	Gly														
				1315			1320						1325																	
65	AGT	GTT	CCT	AAT	ATT	ACT	TTT	GAA	TCG	GCG	GCA	GAA	GAT	TTA	AGG	CTA	4032													
	Ser	Val	Pro	Asn	Ile	Thr	Phe	Glu	Ser	Ala	Ala	Glu	Asp	Leu	Arg	Leu														
				1330			1335					1340																		
70	TCT	ACC	AAT	ATG	GCA	TTG	AGT	ATT	ATT	CAT	AAT	GGA	TAT	GCG	GGA	ACC	4080													
	Ser	Thr	Asn	Met	Ala	Leu	Ser	Ile	Ile	His	Asn	Gly	Tyr	Ala	Gly	Thr	1360													
				1345		1350					1355																			
75	CGC	CGT	ATA	CAA	TGT	AAT	CTT	ATG	AAA	CAA	TAC	GCT	TCA	TTA	GGT	GAT	4128													
	Arg	Arg	Ile	Gln	Cys	Asn	Leu	Met	Lys	Gln	Tyr	Ala	Ser	Leu	Gly	Asp														
				1365						1370					1375															
80	AAA	TTT	ATA	ATT	TAT	GAT	TCA	TCA	TTT	GAT	GAT	GCA	AAC	CGT	TTT	AAT	4176													
	Lys	Phe	Ile	Ile	Tyr	Asp	Ser	Ser	Phe	Asp	Asp	Ala	Asn	Arg	Phe	Asn														
				1380					1385				1390																	
85	CTG	GTG	CCA	TTG	TTT	AAA	TTC	GGA	AAA	GAC	GAG	AAC	TCA	GAT	GAT	AGT	4224													
	Leu	Val	Pro	Leu	Phe	Lys	Phe	Gly	Lys	Asp	Glu	Asn	Ser	Asp	Asp	Ser														
				1395			1400					1405																		
90	ATT	TGT	ATA	TAT	AAT	GAA	AAC	CCT	TCC	TCT	GAA	GAT	AAG	AAG	TGG	TAT	4272													

	Ile	Cys	Ile	Tyr	Asn	Gln	Asn	Pro	Ser	Ser	Glu	Asp	Lys	Lys	Pro	Tyr	
	1410						1415					1420					
5	TTT	TCT	TCG	AAA	GAT	GAC	AAT	AAA	ACA	GCG	GAT	TAT	AAT	GGT	GGA	ACT	4320
	Phe	Ser	Ser	Lys	Asp	Asp	Asn	Lys	Thr	Ala	Asp	Tyr	Asn	Gly	Gly	Thr	
	1425					1430					1435					1440	
10	CAA	TGT	ATA	GAT	GCT	GGA	ACC	AGT	AAC	AAA	GAT	TTT	TAT	TAT	AAT	CTC	4368
	Gln	Cys	Ile	Asp	Ala	Gly	Thr	Ser	Asn	Lys	Asp	Phe	Tyr	Tyr	Asn	Leu	
					1445					1450					1455		
15	CAG	GAG	ATT	GAA	GTA	ATT	AGT	GTT	ACT	GGT	GGG	TAT	TGG	TCG	AGT	TAT	4416
	Gln	Glu	Ile	Glu	Val	Ile	Ser	Val	Thr	Gly	Gly	Tyr	Trp	Ser	Ser	Tyr	
				1460					1465				1470				
20	AAA	ATA	TCC	AAC	CCG	ATT	AAT	ATC	AAT	ACG	GGC	ATT	GAT	AGT	GCT	AAA	4464
	Lys	Ile	Ser	Asn	Pro	Ile	Asn	Ile	Asn	Thr	Gly	Ile	Asp	Ser	Ala	Lys	
			1475				1480					1485					
25	GTA	AAA	GTC	ACC	GTA	AAA	GCG	GGT	GGT	GAC	GAT	CAA	ATC	TTT	ACT	GCT	4512
	Val	Lys	Val	Thr	Val	Lys	Ala	Gly	Gly	Asp	Asp	Gln	Ile	Phe	Thr	Ala	
		1490				1495					1500						
30	GAT	AAT	AGT	ACC	TAT	GTT	CCT	CAG	CAA	CCG	GCA	CCC	AGT	TTT	GAG	GAG	4560
	Asp	Asn	Ser	Thr	Tyr	Val	Pro	Gln	Gln	Pro	Ala	Pro	Ser	Phe	Glu	Glu	
	1505					1510				1515					1520		
35	ATG	ATT	TAT	CAG	TTC	AAT	AAC	CTG	ACA	ATA	GAT	TGT	AAG	AAT	TTA	AAT	4608
	Met	Ile	Tyr	Gln	Phe	Asn	Asn	Leu	Thr	Ile	Asp	Cys	Lys	Asn	Leu	Asn	
				1525				1530						1535			
40	TTC	ATC	GAC	AAT	CAG	GCA	CAT	ATT	GAG	ATT	GAT	TTC	ACC	GCT	ACG	GCA	4656
	Phe	Ile	Asp	Asn	Gln	Ala	His	Ile	Glu	Ile	Asp	Phe	Thr	Ala	Thr	Ala	
			1540				1545					1550					
45	CAA	GAT	GGC	CGA	TTC	TTG	GGT	GCA	GAA	ACT	TTT	ATT	ATC	CCG	GTA	ACT	4704
	Gln	Asp	Gly	Arg	Phe	Leu	Gly	Ala	Glu	Thr	Phe	Ile	Ile	Pro	Val	Thr	
		1555				1560					1565						
50	AAA	AAA	GTT	CTC	GGT	ACT	GAG	AAC	GTG	ATT	GCG	TTA	TAT	AGC	GAA	AAT	4752
	Lys	Lys	Val	Leu	Gly	Thr	Glu	Asn	Val	Ile	Ala	Leu	Tyr	Ser	Glu	Asn	
		1570				1575				1580							
55	AAC	GGT	GTT	CAA	TAT	ATG	CAA	ATT	GGC	GCA	TAT	CGT	ACC	CGT	TTG	AAT	4800
	Asn	Gly	Val	Gln	Tyr	Met	Gln	Ile	Gly	Ala	Tyr	Arg	Thr	Arg	Leu	Asn	
	1585				1590				1595					1600			
60	ACG	TTA	TTC	GCT	CAA	CAG	TTG	GTT	AGC	CGT	GCT	AAT	CGT	GGC	ATT	GAT	4848
	Thr	Leu	Phe	Ala	Gln	Gln	Leu	Val	Ser	Arg	Ala	Asn	Arg	Gly	Ile	Asp	
			1605				1610					1615					
65	GCA	GTG	CTC	AGT	ATG	GAA	ACT	CAG	AAT	ATT	CAG	GAA	CCG	CAA	TTA	GGA	4896
	Ala	Val	Leu	Ser	Met	Glu	Thr	Gln	Asn	Ile	Gln	Glu	Pro	Gln	Leu	Gly	
			1620				1625					1630					
70	GCG	GGC	ACA	TAT	GTG	CAG	CTT	GTG	TTG	GAT	AAA	TAT	GAT	GAG	TCT	ATT	4944
	Ala	Gly	Thr	Tyr	Val	Gln	Leu	Val	Leu	Asp	Lys	Tyr	Asp	Glu	Ser	Ile	
		1635				1640					1645						
75	CAT	GGC	ACT	AAT	AAA	AGC	TTT	GCT	ATT	GAA	TAT	GTT	GAT	ATA	TTT	AAA	4992
	His	Gly	Thr	Asn	Lys	Ser	Phe	Ala	Ile	Glu	Tyr	Val	Asp	Ile	Phe	Lys	
		1650				1655					1660						
80	GAG	AAC	GAT	AGT	TTT	GTG	ATT	TAT	CAA	GGA	GAA	CTT	AGC	GAA	ACA	AGT	5040
	Glu	Asn	Asp	Ser	Phe	Val	Ile	Tyr	Gln	Gly	Glu	Leu	Ser	Glu	Thr	Ser	
	1665				1670					1675				1680			
85	CAA	ACT	GTT	GTG	AAA	GTT	TTC	TTA	TCC	TAT	TTT	ATA	GAG	GCG	ACT	GGA	5088
	Gln	Thr	Val	Val	Lys	Val	Phe	Leu	Ser	Tyr	Phe	Ile	Glu	Ala	Thr	Gly	
			1685				1690						1695				

AAT AAG AAC CAC TTA TGG GTA CGT GCT AAA TAC CAA AAG GAA ACG ACT 5136
 Asn Lys Asn His Leu Trp Val Arg Ala Lys Tyr Gln Lys Glu Thr Thr
 1700 1705 1710

5 GAT AAG ATC TTG TTC GAC CGT ACT GAT GAG AAA GAT CCG CAC GGT TGG 5184
 Asp Lys Ile Leu Phe Asp Arg Thr Asp Glu Lys Asp Pro His Gly Trp
 1715 1720 1725

10 TTT CTC AGC GAC GAT CAC AAG ACC TTT AGT GGT CTC TCT TCC GCA CAG 5232
 Phe Leu Ser Asp Asp His Lys Thr Phe Ser Gly Leu Ser Ser Ala Gln
 1730 1735 1740

15 GCA TTA AAG AAC GAC AGT GAA CCG ATG GAT TTC TCT GGC GCC AAT GCT 5280
 Ala Leu Lys Asn Asp Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ala
 1745 1750 1755 1760

20 CTC TAT TTC TGG GAA CTG TTC TAT TAC ACG CCG ATG ATG ATG GCT CAT 5328
 Leu Tyr Phe Trp Glu Leu Phe Tyr Tyr Thr Pro Met Met Met Ala His
 1765 1770 1775

CGT TTG TTG CAG GAA CAG AAT TTT GAT GCG GCG AAC CAT TGG TTC CGT 5376
 Arg Leu Leu Gln Glu Gln Asn Phe Asp Ala Ala Asn His Trp Phe Arg
 1780 1785 1790

25 TAT GTC TGG AGT CCA TCC GGT TAT ATC GTT GAT GGT AAA ATT GCT ATC 5424
 Tyr Val Trp Ser Pro Ser Gly Tyr Ile Val Asp Gly Lys Ile Ala Ile
 1795 1800 1805

30 TAC CAC TGG AAC GTG CGA CCG CTG GAA GAA GAC ACC AGT TGG AAT GCA 5472
 Tyr His Trp Asn Val Arg Pro Leu Glu Glu Asp Thr Ser Trp Asn Ala
 1810 1815 1820

35 CAA CAA CTG GAC TCC ACC GAT CCA GAT GCT GTA GCC CAA GAT GAT CCG 5520
 Gln Gln Leu Asp Ser Thr Asp Pro Asp Ala Val Ala Gln Asp Asp Pro
 1825 1830 1835 1840

40 ATG CAC TAC AAG GTG GCT ACC TTT ATG GCG ACG TTG GAT CTG CTA ATG 5568
 Met His Tyr Lys Val Ala Thr Phe Met Ala Thr Leu Asp Leu Met
 1845 1850 1855

GCC CGT GGT GAT GCT GCT TAC CGC CAG TTA GAG CGT GAT ACG TTG GCT 5616
 Ala Arg Gly Asp Ala Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Ala
 1860 1865 1870

45 GAA GCT AAA ATG TGG TAT ACA CAG GCG CTT AAT CTG TTG GGT GAT GAG 5664
 Glu Ala Lys Met Trp Tyr Thr Gln Ala Leu Asn Leu Leu Gly Asp Glu
 1875 1880 1885

50 CCA CAA GTG ATG CTG AGT ACG ACT TGG GCT AAT CCA ACA TTG GGT AAT 5712
 Pro Gln Val Met Leu Ser Thr Thr Trp Ala Asn Pro Thr Leu Gly Asn
 1890 1895 1900

55 GCT GCT TCA AAA ACC ACA CAG CAG GTT CGT CAG CAA GTG CTT ACC CAG 5760
 Ala Ala Ser Lys Thr Thr Gln Gln Val Arg Gln Gln Val Leu Thr Gln
 1905 1910 1915 1920

60 TTG CGT CTC AAT AGC AGG GTA AAA ACC CCG TTG CTA GGA ACA GCC AAT 5808
 Leu Arg Leu Asn Ser Arg Val Lys Thr Pro Leu Leu Gly Thr Ala Asn
 1925 1930 1935

TCC CTG ACC GCT TTA TTC CTG CCG CAG GAA AAT AGC AAG CTC AAA GGC 5856
 Ser Leu Thr Ala Leu Phe Leu Pro Gln Glu Asn Ser Lys Leu Lys Gly
 1940 1945 1950

65 TAC TGG CGG ACA CTG GCG CAG CGT ATG TTT AAT TTA CGT CAT AAT CTG 5904
 Tyr Trp Arg Thr Leu Ala Gln Arg Met Phe Asn Leu Arg His Asn Leu
 1955 1960 1965

70 TCG ATT GAC GGC CAG CCG CTC TCC TTG CCG CTG TAT GCT AAA CCG GCT 5952
 Ser Ile Asp Gly Gln Pro Leu Ser Leu Pro Leu Tyr Ala Lys Pro Ala
 1970 1975 1980

5 GAT CCA AAA GCT TTA CTG AGT GCG GCG GTT TCA GCT TCT CAA GGG GGA 6000
 Asp Pro Lys Ala Leu Leu Ser Ala Ala Val Ser Ala Ser Gln Gly Gly 2000
 1985 1990 1995

10 GCC GAC TTG CCG AAG GCG CCG CTG ACT ATT CAC CGC TTC CCT CAA ATG 6048
 Ala Asp Leu Pro Lys Ala Pro Leu Thr Ile His Arg Phe Pro Gln Met 2015
 2005 2010

15 CTA GAA GGG GCA CGG GGC TTG GTT AAC CAG CTT ATA CAG TTC GGT AGT 6096
 Leu Glu Gly Ala Arg Gly Leu Val Asn Gln Leu Ile Gln Phe Gly Ser 2030
 2020 2025

20 TCA CTA TTG GGG TAC AGT GAG CGT CAG GAT GCG GAA GCT ATG AGT CAA 6144
 Ser Leu Leu Gly Tyr Ser Glu Arg Gln Asp Ala Glu Ala Met Ser Gln 2045
 2035 2040

25 CTA CTG CAA ACC CAA GCC AGC GAG TTA ATA CTG ACC AGT ATT CGT ATG 6192
 Leu Leu Gln Thr Gln Ala Ser Glu Leu Ile Leu Thr Ser Ile Arg Met 2060
 2050 2055

30 CAG GAT AAC CAA TTG GCA GAG CTG GAT TCG GAA AAA ACC GCC TTG CAA 6240
 Gln Asp Asn Gln Leu Ala Glu Leu Asp Ser Glu Lys Thr Ala Leu Gln 2080
 2065 2070 2075

35 GTC TCT TTA GCT GGA GTG CAA CAA CGG TTT GAC AGC TAT AGC CAA CTG 6288
 Val Ser Leu Ala Gly Val Gln Gln Arg Phe Asp Ser Tyr Ser Gln Leu 2095
 2085 2090

40 TAT GAG GAG AAC ATC AAC GCA GGT GAG CAG CGA GCG CTG GCG TTA CGC 6336
 Tyr Glu Glu Asn Ile Asn Ala Gly Glu Gln Arg Ala Leu Ala Leu Arg 2110
 2100 2105

45 TCA GAA TCT GCT ATT GAG TCT CAG GGA GCG CAG ATT TCC CGT ATG GCA 6384
 Ser Glu Ser Ala Ile Glu Ser Gln Gly Ala Gln Ile Ser Arg Met Ala 2125
 2115 2120

50 GGC GCG GGT GTT GAT ATG GCA CCA AAT ATC TTC GGC CTG GCT GAT GGC 6432
 Gly Ala Gly Val Asp Met Ala Pro Asn Ile Phe Gly Leu Ala Asp Gly 2140
 2130 2135

55 GGC ATG CAT TAT GGT GCT ATT GCC TAT GCC ATC GCT GAC GGT ATT GAG 6480
 Gly Met His Tyr Gly Ala Ile Ala Tyr Ala Ile Ala Asp Gly Ile Glu 2160
 2145 2150 2155

60 TTG AGT GCT TCT GCC AAG ATG GTT GAT GCG GAG AAA GTT GCT CAG TCG 6528
 Leu Ser Ala Ser Ala Lys Met Val Asp Ala Glu Lys Val Ala Gln Ser 2175
 2165 2170

65 GAA ATA TAT CGC CGT CGC CGT CAA GAA TGG AAA ATT CAG CGT GAC AAC 6576
 Glu Ile Tyr Arg Arg Arg Arg Gln Glu Trp Lys Ile Gln Arg Asp Asn 2190
 2180 2185

70 GCA CAA GCG GAG ATT AAC CAG TTA AAC GCG CAA CTG GAA TCA CTG TCT 6624
 Ala Gln Ala Glu Ile Asn Gln Leu Asn Ala Gln Leu Glu Ser Leu Ser 2205
 2195 2200

75 ATT CGC CGT GAA GCC GCT GAA ATG CAA AAA GAG TAC CTG AAA ACC CAG 6672
 Ile Arg Arg Glu Ala Ala Glu Met Gln Lys Glu Tyr Leu Lys Thr Gln 2220
 2210 2215

80 CAA GCT CAG GCG CAG GCA CAA CTT ACT TTC TTA AGA AGC AAA TTC AGT 6720
 Gln Ala Gln Ala Gln Ala Gln Leu Thr Phe Leu Arg Ser Lys Phe Ser 2240
 2225 2230 2235

85 AAT CAA GCG TTA TAT AGT TGG TTA CGA GGG CGT TTG TCA GGT ATT TAT 6768
 Asn Gln Ala Leu Tyr Ser Trp Leu Arg Gly Arg Leu Ser Gly Ile Tyr 2255
 2245 2250

90 TTC CAG TTC TAT GAC TTG GCC GTA TCA CGT TGC CTG ATG GCA GAG CAA 6816
 Phe Gln Phe Tyr Asp Leu Ala Val Ser Arg Cys Leu Met Ala Glu Gln

2265 2270

5 TCC TAT CAA TGG GAA GCT AAT GAT AAT TCC ATT AGC TTT GTC AAA CCG 6864
 Ser Tyr Gln Trp Glu Ala Asn Asp Asn Ser Ile Ser Phe Val Lys Pro
 2275 2280 2285

10 GGT GCA TGG CAA GGA ACT TAC GCC GGC TTA TTG TGT GGA GAA GCT TTG 6912
 Gly Ala Trp Gln Gly Thr Tyr Ala Gly Leu Leu Cys Gly Glu Ala Leu
 2290 2295 2300

15 ATA CAA AAT CTG GCA CAA ATG GAA GAG GCA TAT CTG AAA TGG GAA TCT 6960
 Ile Gln Asn Leu Ala Gln Met Glu Glu Ala Tyr Leu Lys Trp Glu Ser
 2305 2310 2315 2320

20 CGC GCT TTG GAA GTA GAA CGC ACG GTT TCA TTG GCA GTG GTT TAT GAT 7008
 Arg Ala Leu Glu Val Glu Arg Thr Val Ser Leu Ala Val Val Tyr Asp
 2325 2330 2335

25 TCA CTG GAA GGT AAT GAT CGT TTT AAT TTA GCG GAA CAA ATA CCT GCA 7056
 Ser Leu Glu Gly Asn Asp Arg Phe Asn Leu Ala Glu Gln Ile Pro Ala
 2340 2345 2350

30 TTA TTG GAT AAG GGG GAG GGA ACA GCA GGA ACT AAA GAA AAT GGG TTA 7104
 Leu Leu Asp Lys Gly Glu Gly Thr Ala Gly Thr Lys Glu Asn Gly Leu
 2355 2360 2365

35 TCA TTG GCT AAT GCT ATC CTG TCA GCT TCG GTC AAA TTG TCC GAC TTG 7152
 Ser Leu Ala Asn Ala Ile Leu Ser Ala Ser Val Lys Leu Ser Asp Leu
 2370 2375 2380

40 AAA CTG GGA ACG GAT TAT CCA GAC AGT ATC GTT GGT AGC AAC AAG GTT 7200
 Lys Leu Gly Thr Asp Tyr Pro Asp Ser Ile Val Gly Ser Asn Lys Val
 2385 2390 2395 2400

45 CGT CGT ATT AAG CAA ATC AGT GTT TCG CTA CCT GCA TTG GTT GGG CCT 7248
 Arg Arg Ile Lys Gln Ile Ser Val Ser Leu Pro Ala Leu Val Gly Pro
 2405 2410 2415

50 TAT CAG GAT GTT CAG GCT ATG CTC AGC TAT GGT GGC AGT ACT CAA TTG 7296
 Tyr Gln Asp Val Gln Ala Met Leu Ser Tyr Gly Gly Ser Thr Gln Leu
 2420 2425 2430

55 CCG AAA GGT TGT TCA GCG TTG GCT GTG TCT CAT GGT ACC AAT GAT AGT 7344
 Pro Lys Gly Cys Ser Ala Leu Ala Val Ser His Gly Thr Asn Asp Ser
 2435 2440 2445

60 GGT CAG TTC CAG TTG GAT TTC AAT GAC GGC AAA TAC CTG CCA TTT GAA 7392
 Gly Gln Phe Gln Leu Asp Phe Asn Asp Gly Lys Tyr Leu Pro Phe Glu
~~2450~~ 2455 2460

GGT ATT GCT CTT GAT GAT CAG GGT ACA CTG AAT CTT CAA TTT CCG AAT 7440
 Gly Ile Ala Leu Asp Asp Gln Gly Thr Leu Asn Leu Gln Phe Pro Asn
 2465 2470 2475 2480

GCT ACC GAC AAG CAG AAA GCA ATA TTG CAA ACT ATG AGC GAT ATT ATT 7488
 Ala Thr Asp Lys Gln Lys Ala Ile Leu Gln Thr Met Ser Asp Ile Ile
 2485 2490 2495

60 TTG CAT ATT CGT TAT ACC ATC CGT TAA 7515
 Leu His Ile Arg Tyr Thr Ile Arg *
 2500 2505

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2504 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12 (TcbA protein):

5 Met Gln Asn Ser Leu Ser Ser Thr Ile Asp Thr Ile Cys Gln Lys Leu
 1 5 10 15
 15 Gln Leu Thr Cys Pro Ala Glu Ile Ala Leu Tyr Pro Phe Asp Thr Phe
 20 25 30
 20 Arg Glu Lys Thr Arg Gly Met Val Asn Trp Gly Glu Ala Lys Arg Ile
 35 40 45
 25 Tyr Glu Ile Ala Gln Ala Glu Gln Asp Arg Asn Leu Leu His Glu Lys
 50 55 60
 30 Arg Ile Phe Ala Tyr Ala Asn Pro Leu Leu Lys Asn Ala Val Arg Leu
 65 70 75 80
 35 Gly Thr Arg Gln Met Leu Gly Phe Ile Gln Gly Tyr Ser Asp Leu Phe
 85 90 95
 40 Gly Asn Arg Ala Asp Asn Tyr Ala Ala Pro Gly Ser Val Ala Ser Met
 100 105 110
 45 Phe Ser Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Lys Asn
 115 120 125
 50 Leu His Asp Ser Ser Ser Ile Tyr Tyr Leu Asp Lys Arg Arg Pro Asp
 130 135 140
 55 Leu Ala Ser Leu Met Leu Ser Gln Lys Asn Met Asp Glu Glu Ile Ser
 145 150 155 160
 60 Thr Leu Ala Leu Ser Asn Glu Leu Cys Leu Ala Gly Ile Glu Thr Lys
 165 170 175
 65 Thr Gly Lys Ser Gln Asp Glu Val Met Asp Met Leu Ser Thr Tyr Arg
 180 185 190
 70 Leu Ser Gly Glu Thr Pro Tyr His His Ala Tyr Glu Thr Val Arg Glu
 195 200 205
 75 Ile Val His Glu Arg Asp Pro Gly Phe Arg His Leu Ser Gln Ala Pro
 210 215 220
 80 Ile Val Ala Ala Lys Leu Asp Pro Val Thr Leu Leu Gly Ile Ser Ser
 225 230 235 240
 85 His Ile Ser Pro Glu Leu Tyr Asn Leu Leu Ile Glu Glu Ile Pro Glu
 245 250 255
 90 Lys Asp Glu Ala Ala Leu Asp Thr Leu Tyr Lys Thr Asn Phe Gly Asp
 260 265 270
 95 Ile Thr Thr Ala Gln Leu Met Ser Pro Ser Tyr Leu Ala Arg Tyr Tyr
 275 280 285
 100 Gly Val Ser Pro Glu Asp Ile Ala Tyr Val Thr Thr Ser Leu Ser His
 290 295 300
 105 Val Gly Tyr Ser Ser Asp Ile Leu Val Ile Pro Leu Val Asp Gly Val
 305 310 315 320

Gly Lys Met Gln Val Val Arg Val Thr Arg Thr Pro Ser Asp Asn Tyr
 325 330 335
 5 Thr Ser Gln Thr Asn Tyr Ile Glu Leu Tyr Pro Gln Gly Gly Asp Asn
 340 345 350
 Tyr Leu Ile Lys Tyr Asn Leu Ser Asn Ser Phe Gly Leu Asp Asp Phe
 355 360 365
 10 Tyr Leu Gln Tyr Lys Asp Gly Ser Ala Asp Trp Thr Glu Ile Ala His
 370 375 380
 Asn Pro Tyr Pro Asp Met Val Ile Asn Gln Lys Tyr Glu Ser Gln Ala
 385 390 395 400
 15 Thr Ile Lys Arg Ser Asp Ser Asp Asn Ile Leu Ser Ile Gly Leu Gln
 405 410 415
 20 Arg Trp His Ser Gly Ser Tyr Asn Phe Ala Ala Ala Asn Phe Lys Ile
 420 425 430
 Asp Gln Tyr Ser Pro Lys Ala Phe Leu Leu Lys Met Asn Lys Ala Ile
 435 440 445
 25 Arg Leu Leu Lys Ala Thr Gly Leu Ser Phe Ala Thr Leu Glu Arg Ile
 450 455 460
 Val Asp Ser Val Asn Ser Thr Lys Ser Ile Thr Val Glu Val Leu Asn
 465 470 475 480
 30 Lys Val Tyr Arg Val Lys Phe Tyr Ile Asp Arg Tyr Gly Ile Ser Glu
 485 490 495
 35 Glu Thr Ala Ala Ile Leu Ala Asn Ile Asn Ile Ser Gln Gln Ala Val
 500 505 510
 Gly Asn Gln Leu Ser Gln Phe Glu Gln Leu Phe Asn His Pro Pro Leu
 515 520 525
 40 Asn Gly Ile Arg Tyr Glu Ile Ser Glu Asp Asn Ser Lys His Leu Pro
 530 535 540
 Asn Pro Asp Leu Asn Leu Lys Pro Asp Ser Thr Gly Asp Asp Gln Arg
 545 550 555 560
 45 Lys Ala Val Leu Lys Arg Ala Phe Gln Val Asn Ala Ser Glu Leu Tyr
 565 570 575
 50 Gln Met Leu Leu Ile Thr Asp Arg Lys Glu Asp Gly Val Ile Lys Asn
 580 585 590
 Asn Leu Glu Asn Leu Ser Asp Leu Tyr Leu Val Ser Leu Leu Ala Gln
 595 600 605
 55 Ile His Asn Leu Thr Ile Ala Glu Leu Asn Ile Leu Leu Val Ile Cys
 610 615 620
 Gly Tyr Gly Asp Thr Asn Ile Tyr Gln Ile Thr Asp Asp Asn Leu Ala
 625 630 635 640
 60 Lys Ile Val Glu Thr Leu Leu Trp Ile Thr Gln Trp Leu Lys Thr Gln
 645 650 655
 65 Lys Trp Thr Val Thr Asp Leu Phe Leu Met Thr Thr Ala Thr Tyr Ser
 660 665 670
 Thr Thr Leu Thr Pro Glu Ile Ser Asn Leu Thr Ala Thr Leu Ser Ser
 675 680 685
 70 Thr Leu His Gly Lys Glu Ser Leu Ile Gly Glu Asp Leu Lys Arg Ala
 690 695 700

	Met	Ala	Pro	Cys	Ph	Thr	Ser	Ala	Leu	His	Leu	Thr	Ser	Gln	Glu	Val	
	705					710					715					720	
5	Ala	Tyr	Asp	Leu	Leu	Leu	Trp	Ile	Asp	Gln	Ile	Gln	Pro	Ala	Gln	Ile	
				725					730						735		
	Thr	Val	Asp	Gly	Phe	Trp	Glu	Glu	Val	Gln	Thr	Thr	Pro	Thr	Ser	Leu	
10				740					745					750			
	Lys	Val	Ile	Thr	Phe	Ala	Gln	Val	Leu	Ala	Gln	Leu	Ser	Leu	Ile	Tyr	
			755					760					765				
15	Arg	Arg	Ile	Gly	Leu	Ser	Glu	Thr	Glu	Leu	Ser	Leu	Ile	Val	Thr	Gln	
	770						775					780					
	Ser	Ser	Leu	Leu	Val	Ala	Gly	Lys	Ser	Ile	Leu	Asp	His	Gly	Leu	Leu	
	785					790					795					800	
20	Thr	Leu	Met	Ala	Leu	Glu	Gly	Phe	His	Thr	Trp	Val	Asn	Gly	Leu	Gly	
					805					810					815		
	Gln	His	Ala	Ser	Leu	Ile	Leu	Ala	Ala	Leu	Lys	Asp	Gly	Ala	Leu	Thr	
25				820					825					830			
	Val	Thr	Asp	Val	Ala	Gln	Ala	Met	Asn	Lys	Glu	Glu	Ser	Leu	Leu	Gln	
			835					840					845				
30	Met	Ala	Ala	Asn	Gln	Val	Glu	Lys	Asp	Leu	Thr	Lys	Leu	Thr	Ser	Trp	
	850						855					860					
	Thr	Gln	Ile	Asp	Ala	Ile	Leu	Gln	Trp	Leu	Gln	Met	Ser	Ser	Ala	Leu	
	865					870					875					880	
35	Ala	Val	Ser	Pro	Leu	Asp	Leu	Ala	Gly	Met	Met	Ala	Leu	Lys	Tyr	Gly	
					885				890						895		
	Ile	Asp	His	Asn	Tyr	Ala	Ala	Trp	Gln	Ala	Ala	Ala	Ala	Ala	Leu	Met	
40				900					905					910			
	Ala	Asp	His	Ala	Asn	Gln	Ala	Gln	Lys	Lys	Leu	Asp	Glu	Thr	Phe	Ser	
			915					920					925				
45	Lys	Ala	Leu	Cys	Asn	Tyr	Tyr	Ile	Asn	Ala	Val	Val	Asp	Ser	Ala	Ala	
	930						935					940					
	Gly	Val	Arg	Asp	Arg	Asn	Gly	Leu	Tyr	Thr	Tyr	Leu	Leu	Ile	Asp	Asn	
	945					950					955					960	
50	Gln	Val	Ser	Ala	Asp	Val	Ile	Thr	Ser	Arg	Ile	Ala	Glu	Ala	Ile	Ala	
					965					970					975		
	Gly	Ile	Gln	Leu	Tyr	Val	Asn	Arg	Ala	Leu	Asn	Arg	Asp	Glu	Gly	Gln	
55				980					985					990			
	Leu	Ala	Ser	Asp	Val	Ser	Thr	Arg	Gln	Phe	Phe	Thr	Asp	Trp	Glu	Arg	
			995					1000					1005				
60	Tyr	Asn	Lys	Arg	Tyr	Ser	Thr	Trp	Ala	Gly	Val	Ser	Glu	Leu	Val	Tyr	
	1010						1015					1020					
	Tyr	Pro	Glu	Asn	Tyr	Val	Asp	Pro	Thr	Gln	Arg	Ile	Gly	Gln	Thr	Lys	
	1025					1030					1035					1040	
65	Met	Met	Asp	Ala	Leu	Leu	Gln	Ser	Ile	Asn	Gln	Ser	Gln	Leu	Asn	Ala	
					1045					1050					1055		
	Asp	Thr	Val	Glu	Asp	Ala	Phe	Lys	Thr	Tyr	Leu	Thr	Ser	Phe	Glu	Gln	
70				1060					1065					1070			
	Val	Ala	Asn	Leu	Lys	Val	Ile	Ser	Ala	Tyr	His	Asp	Asn	Val	Asn	Val	

	1075	1080	1085
	Asp Gln Gly Leu Thr Tyr Phe Ile Gly Ile Asp Gln Ala Ala Pro Gly 1090	1095	1100
5	Thr Tyr Tyr Trp Arg Ser Val Asp His Ser Lys Cys Glu Asn Gly Lys 1105	1110	1115 1120
10	Phe Ala Ala Asn Ala Trp Gly Glu Trp Asn Lys Ile Thr Cys Ala Val 1125	1130	1135
	Asn Pro Trp Lys Asn Ile Ile Arg Pro Val Val Tyr Met Ser Arg Leu 1140	1145	1150
15	Tyr Leu Leu Trp Leu Glu Gln Gln Ser Lys Lys Ser Asp Asp Gly Lys 1155	1160	1165
	Thr Thr Ile Tyr Gln Tyr Asn Leu Lys Leu Ala His Ile Arg Tyr Asp 1170	1175	1180
20	Gly Ser Trp Asn Thr Pro Phe Thr Phe Asp Val Thr Glu Lys Val Lys 1185	1190	1195 1200
25	Asn Tyr Thr Ser Ser Thr Asp Ala Ala Glu Ser Leu Gly Leu Tyr Cys 1205	1210	1215
	Thr Gly Tyr Gln Gly Glu Asp Thr Leu Leu Val Met Phe Tyr Ser Met 1220	1225	1230
30	Gln Ser Ser Tyr Ser Ser Tyr Thr Asp Asn Asn Ala Pro Val Thr Gly 1235	1240	1245
	Leu Tyr Ile Phe Ala Asp Met Ser Ser Asp Asn Met Thr Asn Ala Gln 1250	1255	1260
35	Ala Thr Asn Tyr Trp Asn Asn Ser Tyr Pro Gln Phe Asp Thr Val Met 1265	1270	1275 1280
40	Ala Asp Pro Asp Ser Asp Asn Lys Lys Val Ile Thr Arg Arg Val Asn 1285	1290	1295
	Asn Arg Tyr Ala Glu Asp Tyr Glu Ile Pro Ser Ser Val Thr Ser Asn 1300	1305	1310
45	Ser Asn Tyr Ser Trp Gly Asp His Ser Leu Thr Met Leu Tyr Gly Gly 1315	1320	1325
	Ser Val Pro Asn Ile Thr Phe Glu Ser Ala Ala Glu Asp Leu Arg Leu 1330	1335	1340
50	Ser Thr Asn Met Ala Leu Ser Ile Ile His Asn Gly Tyr Ala Gly Thr 1345	1350	1355 1360
55	Arg Arg Ile Gln Cys Asn Leu Met Lys Gln Tyr Ala Ser Leu Gly Asp 1365	1370	1375
	Lys Phe Ile Ile Tyr Asp Ser Ser Phe Asp Asp Ala Asn Arg Phe Asn 1380	1385	1390
60	Leu Val Pro Leu Phe Lys Phe Gly Lys Asp Glu Asn Ser Asp Asp Ser 1395	1400	1405
	Ile Cys Ile Tyr Asn Glu Asn Pro Ser Ser Glu Asp Lys Lys Trp Tyr 1410	1415	1420
65	Phe Ser Ser Lys Asp Asp Asn Lys Thr Ala Asp Tyr Asn Gly Gly Thr 1425	1430	1435 1440
70	Gln Cys Ile Asp Ala Gly Thr Ser Asn Lys Asp Phe Tyr Tyr Asn Leu 1445	1450	1455

Gln Glu Ile Glu Val Ile Ser Val Thr Gly Gly Tyr Trp Ser Ser Tyr
 1460 1465 1470
 5 Lys Ile Ser Asn Pro Ile Asn Ile Asn Thr Gly Ile Asp Ser Ala Lys
 1475 1480 1485
 Val Lys Val Thr Val Lys Ala Gly Gly Asp Asp Gln Ile Phe Thr Ala
 1490 1495 1500
 10 Asp Asn Ser Thr Tyr Val Pro Gln Gln Pro Ala Pro Ser Phe Glu Glu
 1505 1510 1515 1520
 Met Ile Tyr Gln Phe Asn Asn Leu Thr Ile Asp Cys Lys Asn Leu Asn
 1525 1530 1535
 15 Phe Ile Asp Asn Gln Ala His Ile Glu Ile Asp Phe Thr Ala Thr Ala
 1540 1545 1550
 Gln Asp Gly Arg Phe Leu Gly Ala Glu Thr Phe Ile Ile Pro Val Thr
 1555 1560 1565
 Lys Lys Val Leu Gly Thr Glu Asn Val Ile Ala Leu Tyr Ser Glu Asn
 1570 1575 1580
 25 Asn Gly Val Gln Tyr Met Gln Ile Gly Ala Tyr Arg Thr Arg Leu Asn
 1585 1590 1595 1600
 Thr Leu Phe Ala Gln Gln Leu Val Ser Arg Ala Asn Arg Gly Ile Asp
 1605 1610 1615
 30 Ala Val Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro Gln Leu Gly
 1620 1625 1630
 Ala Gly Thr Tyr Val Gln Leu Val Leu Asp Lys Tyr Asp Glu Ser Ile
 1635 1640 1645
 35 His Gly Thr Asn Lys Ser Phe Ala Ile Glu Tyr Val Asp Ile Phe Lys
 1650 1655 1660
 40 Glu Asn Asp Ser Phe Val Ile Tyr Gln Gly Glu Leu Ser Glu Thr Ser
 1665 1670 1675 1680
 Gln Thr Val Val Lys Val Phe Leu Ser Tyr Phe Ile Glu Ala Thr Gly
 1685 1690 1695
 45 Asn Lys Asn His Leu Trp Val Arg Ala Lys Tyr Gln Lys Glu Thr Thr
 1700 1705 1710
 Asp Lys Ile Leu Phe Asp Arg Thr Asp Glu Lys Asp Pro His Gly Trp
 1715 1720 1725
 Phe Leu Ser Asp Asp His Lys Thr Phe Ser Gly Leu Ser Ser Ala Gln
 1730 1735 1740
 55 Ala Leu Lys Asn Asp Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ala
 1745 1750 1755 1760
 Leu Tyr Phe Trp Glu Leu Phe Tyr Tyr Thr Pro Met Met Met Ala His
 1765 1770 1775
 60 Arg Leu Leu Gln Glu Gln Asn Phe Asp Ala Ala Asn His Trp Phe Arg
 1780 1785 1790
 Tyr Val Trp Ser Pro Ser Gly Tyr Ile Val Asp Gly Lys Ile Ala Ile
 1795 1800 1805
 65 Tyr His Trp Asn Val Arg Pro Leu Glu Glu Asp Thr Ser Trp Asn Ala
 1810 1815 1820
 70 Gln Gln Leu Asp Ser Thr Asp Pro Asp Ala Val Ala Gln Asp Asp Pro
 1825 1830 1835 1840

Met His Tyr Lys Val Ala Thr Phe Met Ala Thr Leu Asp Leu Leu Met
1845 1850 1855

5 Ala Arg Gly Asp Ala Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Ala
1860 1865 1870

Glu Ala Lys Met Trp Tyr Thr Gln Ala Leu Asn Leu Leu Gly Asp Glu
1875 1880 1885

10 Pro Gln Val Met Leu Ser Thr Thr Trp Ala Asn Pro Thr Leu Gly Asn
1890 1895 1900

15 Ala Ala Ser Lys Thr Thr Gln Gln Val Arg Gln Gln Val Leu Thr Gln
1905 1910 1915 1920

Leu Arg Leu Asn Ser Arg Val Lys Thr Pro Leu Leu Gly Thr Ala Asn
1925 1930 1935

20 Ser Leu Thr Ala Leu Phe Leu Pro Gln Glu Asn Ser Lys Leu Lys Gly
1940 1945 1950

Tyr Trp Arg Thr Leu Ala Gln Arg Met Phe Asn Leu Arg His Asn Leu
1955 1960 1965

25 Ser Ile Asp Gly Gln Pro Leu Ser Leu Pro Leu Tyr Ala Lys Pro Ala
1970 1975 1980

30 Asp Pro Lys Ala Leu Leu Ser Ala Ala Val Ser Ala Ser Gln Gly Gly
1985 1990 1995 2000

Ala Asp Leu Pro Lys Ala Pro Leu Thr Ile His Arg Phe Pro Gln Met
2005 2010 2015

35 Leu Glu Gly Ala Arg Gly Leu Val Asn Gln Leu Ile Gln Phe Gly Ser
2020 2025 2030

Ser Leu Leu Gly Tyr Ser Glu Arg Gln Asp Ala Glu Ala Met Ser Gln
2035 2040 2045

40 Leu Leu Gln Thr Gln Ala Ser Glu Leu Ile Leu Thr Ser Ile Arg Met
2050 2055 2060

45 Gln Asp Asn Gln Leu Ala Glu Leu Asp Ser Glu Lys Thr Ala Leu Gln
2065 2070 2075 2080

Val Ser Leu Ala Gly Val Gln Gln Arg Phe Asp Ser Tyr Ser Gln Leu
2085 2090 2095

50 Tyr Glu Glu Asn Ile Asn Ala Gly Glu Gln Arg Ala Leu Ala Leu Arg
2100 2105 2110

Ser Glu Ser Ala Ile Glu Ser Gln Gly Ala Gln Ile Ser Arg Met Ala
2115 2120 2125

55 Gly Ala Gly Val Asp Met Ala Pro Asn Ile Phe Gly Leu Ala Asp Gly
2130 2135 2140

60 Gly Met His Tyr Gly Ala Ile Ala Tyr Ala Ile Ala Asp Gly Ile Glu
2145 2150 2155 2160

Leu Ser Ala Ser Ala Lys Met Val Asp Ala Glu Lys Val Ala Gln Ser
2165 2170 2175

65 Glu Ile Tyr Arg Arg Arg Arg Gln Glu Trp Lys Ile Gln Arg Asp Asn
2180 2185 2190

Ala Gln Ala Glu Ile Asn Gln Leu Asn Ala Gln Leu Glu Ser Leu Ser
2195 2200 2205

70 Ile Arg Arg Glu Ala Ala Glu Met Gln Lys Glu Tyr Leu Lys Thr Gln

(2) INFORMATION FOR SEQ ID NO:13:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13 (TcdA₁ N-terminus):

- 169 -

SDOCID: <WO__9808932A1_1_>

1 5 10

(2) INFORMATION FOR SEQ ID NO:14:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

10

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14 (TcdB N-terminus):

15

Met Gln Asn Ser Gln Thr Phe Ser Val Gly Glu Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

25

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15 (TcaA₁₁ N-terminus):

30

Ala Gln Asp Gly Asn Gln Asp Thr Phe Phe Ser Gly Asn Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

40

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16 (TcbA N-terminus):

45

Met Gln Asn Ser Leu
1 5

(2) INFORMATION FOR SEQ ID NO:17:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

55

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17 (TcdA₁₁-PT111 internal peptide):

60

Ala Phe Asn Ile Asp Asp Val Ser Leu Phe
1 5 10

(2) INFORMATION FOR SEQ ID NO:18: .

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18 (TcdA_{ii}- PT79 internal peptide):

Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn Ser Ser Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19 (TcaB_i- PT158 internal peptide):

Ile Ser Asp Leu Val Thr Thr Ser Pro Leu Ser Glu Ala Ile Gly Ser
1 5 10 15

Leu Gln Leu Phe Ile
20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20 (TcaB_i-PT 108 internal peptide):

Met Tyr Tyr Ile Gln Ala Gln Gln Leu Leu Gly Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21 (TcbA_{ii}- PT103 internal peptide):

Gly Ile Asp Ala Val Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro
 1 5 10 15
 5 Gln Leu Gly Ala Gly Thr Tyr Val Gln Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:22:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 15 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22 (TcbA_{ii}- PT56 internal peptide):

20 Ile Ser Asn Pro Ile Asn Ile Asn Thr Gly Ile Asp Ser Ala Lys
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:23:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23 (TcbA- PT81 (a) internal peptide):

35 Thr Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys
 1 5 10

40 (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 amino acids
 (B) TYPE: amino acid
 45 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24 (TcbA_{ii}- PT81 (b) internal peptide):

Val Leu Gly Thr Glu Asn Val Ile Ala Leu Tyr Ser Glu Asn Asn Gly
 1 5 10 15
 55 Val Gln Tyr Met Gln Ile
 20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6054 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..43
 (D) OTHER INFORMATION: /product= "end of TcaA_{iii}"

(ix) FEATURE:

- (A) NAME/KEY: RBS
 (B) LOCATION: 51 58

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 65 3634
 (D) OTHER INFORMATION: /product= "TcaB_i"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

A GTA GCC CAA AAC TTA AGT GCC GCA ATC AGC AAT CGT CAG TAACCGGATA 50
  Val Ala Gln Asn Leu Ser Ala Ala Ile Ser Asn Arg Gln ***

AAGAAGGAAT TGATT ATG TCT GAA TCT TTA TTT ACA CAA ACG TTG AAA GAA 100
          Met Ser Glu Ser Leu Phe Thr Gln Thr Leu Lys Glu
              1              5              10

GCG CGC CGT GAT GCA TTG GTT GCT CAT TAT ATT GCT ACT CAG GTG CCC 148
Ala Arg Arg Asp Ala Leu Val Ala His Tyr Ile Ala Thr Gln Val Pro
          15              20              25

GCA GAT TTA AAA GAG AGT ATC CAG ACC GCG GAT GAT CTG TAC GAA TAT 196
Ala Asp Leu Lys Glu Ser Ile Gln Thr Ala Asp Asp Leu Tyr Glu Tyr
          30              35              40

CTG TTG CTG GAT ACC AAA ATT AGC GAT CTG GTT ACT ACT TCA CCG CTG 244
Leu Leu Leu Asp Thr Lys Ile Ser Asp Leu Val Thr Thr Ser Pro Leu
          45              50              55

TCC GAA GCG ATT GGC AGT CTG CAA TTG TTT ATT CAT CGT GCG ATA GAG 292
Ser Glu Ala Ile Gly Ser Leu Gln Leu Phe Ile His Arg Ala Ile Glu
          65              70              75

GGC TAT GAC GGC ACG CTG GCA GAC TCA GCA AAA CCC TAT TTT GCC GAT 340
Gly Tyr Asp Gly Thr Leu Ala Asp Ser Ala Lys Pro Tyr Phe Ala Asp
          80              85              90

GAA CAG TTT TTA TAT AAC TGG GAT AGT TTT AAC CAC CGT TAT AGC ACT 388
Glu Gln Phe Leu Tyr Asn Trp Asp Ser Phe Asn His Arg Tyr Ser Thr
          95              100              105

TGG GCT GGC AAG GAA CGG TTG AAA TTC TAT GCC GGG GAT TAT ATT GAT 436
Trp Ala Gly Lys Glu Arg Leu Lys Phe Tyr Ala Gly Asp Tyr Ile Asp
          110              115              120

CCA ACA TTG CGA TTG AAT AAG ACC GAG ATA TTT ACC GCA TTT GAA CAA 484
Pro Thr Leu Arg Leu Asn Lys Thr Glu Ile Phe Thr Ala Phe Glu Gln
          125              130              135

GGT ATT TCT CAA GGG AAA TTA AAA AGT GAA TTA GTC GAA TCT AAA TTA 532
Gly Ile Ser Gln Gly Lys Leu Lys Ser Glu Leu Val Glu Ser Lys Leu
          145              150              155

CGT GAT TAT CTA ATT AGT TAT GAC ACT TTA GCC ACC CTT GAT TAT ATT 580

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	Arg	Asp	Tyr	Ile	Ser	Tyr	Asp	Thr	Leu	Ala	Thr	Leu	Asp	Tyr	Ile	
				160				165					170			
5	ACT	GCC	TGC	CAA	GGC	AAA	GAT	AAT	AAA	ACC	ATC	TTC	TTT	ATT	GGC	CGT 628
	Thr	Ala	Cys	Gln	Gly	Lys	Asp	Asn	Lys	Thr	Ile	Phe	Phe	Ile	Gly	Arg
			175					180					185			
10	ACA	CAG	AAT	GCA	CCC	TAT	GCA	TTT	TAT	TGG	CGA	AAA	TTA	ACT	TTA	GTC 676
	Thr	Gln	Asn	Ala	Pro	Tyr	Ala	Phe	Tyr	Trp	Arg	Lys	Leu	Thr	Leu	Val
			190				195					200				
15	ACT	GAT	GGC	GGT	AAG	TTG	AAA	CCA	GAT	CAA	TGG	TCA	GAG	TGG	CGA	GCA 724
	Thr	Asp	Gly	Gly	Lys	Leu	Lys	Pro	Asp	Gln	Trp	Ser	Glu	Trp	Arg	Ala
			205			210					215					220
	ATT	AAT	GCC	GGG	ATT	AGT	GAG	GCA	TAT	TCA	GGG	CAT	GTC	GAG	CCT	TTC 772
	Ile	Asn	Ala	Gly	Ile	Ser	Glu	Ala	Tyr	Ser	Gly	His	Val	Glu	Pro	Phe
					225					230					235	
20	TGG	GAA	AAT	AAC	AAG	CTG	CAC	ATC	CGT	TGG	TTT	ACT	ATC	TCG	AAA	GAA 820
	Trp	Glu	Asn	Asn	Lys	Leu	His	Ile	Arg	Trp	Phe	Thr	Ile	Ser	Lys	Glu
				240					245					250		
25	GAT	AAA	ATA	GAT	TTT	GTT	TAT	AAA	AAC	ATC	TGG	GTG	ATG	AGT	AGC	GAT 868
	Asp	Lys	Ile	Asp	Phe	Val	Tyr	Lys	Asn	Ile	Trp	Val	Met	Ser	Ser	Asp
			255					260					265			
30	TAT	AGC	TGG	GCA	TCA	AAG	AAA	AAA	ATC	TTG	GAA	CTT	TCT	TTT	ACT	GAC 916
	Tyr	Ser	Trp	Ala	Ser	Lys	Lys	Lys	Ile	Leu	Glu	Leu	Ser	Phe	Thr	Asp
			270				275					280				
35	TAC	AAT	AGA	GTT	GGA	GCA	ACA	GGA	TCA	TCA	AGC	CCG	ACT	GAA	GTA	GCT 964
	Tyr	Asn	Arg	Val	Gly	Ala	Thr	Gly	Ser	Ser		Pro	Thr	Glu	Val	Ala
			285			290					295					300
	TCA	CAA	TAT	GGT	TCT	GAT	GCT	CAG	ATG	AAT	ATT	TCT	GAT	GAT	GGG	ACT 1012
	Ser	Gln	Tyr	Gly	Ser	Asp	Ala	Gln	Met	Asn	Ile	Ser	Asp	Asp	Gly	Thr
					305					310					315	
40	GTA	CTT	ATT	TTT	CAG	AAT	GCC	GGC	GGA	GCT	ACT	CCC	AGT	ACT	GGA	GTG 1060
	Val	Leu	Ile	Phe	Gln	Asn	Ala	Gly	Gly	Ala	Thr	Pro	Ser	Thr	Gly	Val
				320					325					330		
45	ACG	TTA	TGT	TAT	GAC	TCT	GGC	AAC	GTG	ATT	AAG	AAC	CTA	TCT	AGT	ACA 1108
	Thr	Leu	Cys	Tyr	Asp	Ser	Gly	Asn	Val	Ile	Lys	Asn	Leu	Ser	Ser	Thr
			335					340					345			
50	GGA	AGT	GCA	AAT	TTA	TCG	TCA	AAG	GAT	TAT	GCC	ACA	ACT	AAA	TTA	CGC 1156
	Gly	Ser	Ala	Asn	Leu	Ser	Ser	Lys	Asp	Tyr	Ala	Thr	Thr	Lys	Leu	Arg
			350				355					360				
55	ATG	TGT	CAT	GGA	CAA	AGT	TAC	AAT	GAT	AAT	AAC	TAC	TGC	AAT	TTT	ACA 1204
	Met	Cys	His	Gly	Gln	Ser	Tyr	Asn	Asp	Asn	Tyr	Cys	Asn	Phe	Thr	
						370					375				380	
	CTC	TCT	ATT	AAT	ACA	ATA	GAA	TTC	ACC	TCC	TAC	GGC	ACA	TTC	TCA	TCA 1252
	Leu	Ser	Ile	Asn	Thr	Ile	Glu	Phe	Thr	Ser	Tyr	Gly	Thr	Phe	Ser	
						385				390					395	
60	GAT	GGA	AAA	CAA	TTT	ACA	CCA	CCT	TCT	GGT	TCT	GCC	ATT	GAT	TTA	CAC 1300
	Asp	Gly	Lys	Gln	Phe	Thr	Pro	Pro	Ser	Gly	Ser	Ala	Ile	Asp	Leu	His
				400					405					410		
65	CTC	CCT	AAT	TAT	GTA	GAT	CTC	AAC	GCG	CTA	TTA	GAT	ATT	AGC	CTC	GAT 1348
	Leu	Pro	Asn	Tyr	Val	Asp	Leu	Asn	Ala	Leu	Leu	Asp	Ile	Ser	Leu	Asp
				415				420					425			
70	TCA	CTA	CTT	AAT	TAT	GAC	GTT	CAG	GGG	CAG	TTT	GGC	GGA	TCT	AAT	CCG 1396
	Ser	Leu	Leu	Asn	Tyr	Asp	Val	Gln	Gly	Gln	Phe	Gly	Gly	Ser	Asn	Pro
				430			435					440				

	GTT Val 445	GAT Asp	AAT Asn	TTC Phe	AGT Ser	GGT Gly 450	CCC Pro	TAT Tyr	GGT Gly	ATT Ile	TAT Tyr 455	CTA Leu	TGG Trp	GAT Glu	ATC Ile	TTC Phe 460	1444
5	TTC Phe	CAT His	ATT Ile	CCG Pro	TTC Phe 465	CTT Leu	GTT Val	ACG Thr	GTC Val	CGT Arg 470	ATG Met	CAA Gln	ACC Thr	GAA Glu	CAA Gln 475	CGT Arg	1492
10	TAC Tyr	GAA Glu	GAC Asp	GCG Ala 480	GAC Asp	ACT Thr	TGG Trp	TAC Tyr	AAA Lys 485	TAT Tyr	ATT Ile	TTC Phe	CGC Arg	AGC Ser 490	GCC Ala	GGT Gly	1540
15	TAT Tyr	CGC Arg	GAT Asp 495	GCT Ala	AAT Asn	GGC Gly	CAG Gln	CTC Leu 500	ATT Ile	ATG Met	GAT Asp	GGC Gly	AGT Ser 505	AAA Lys	CCA Pro	CGT Arg	1588
20	TAT Tyr 510	TGG Trp	AAT Asn	GTG Val	ATG Met	CCA Pro	TTG Leu 515	CAA Gln	CTG Leu	GAT Asp	ACC Thr 520	GCA Ala	TGG Trp	GAT Asp	ACC Thr	ACA Thr	1636
25	CAG Gln 525	CCC Pro	GCC Ala	ACC Thr	ACT Thr	GAT Asp 530	CCA Pro	GAT Asp	GTG Val	ATC Ile	GCT Ala 535	ATG Met	GCG Ala	GAC Asp	CCG Pro	ATG Met 540	1684
30	CAT His	TAC Tyr	AAG Lys	CTG Leu	GCG Ala 545	ATA Ile	TTC Phe	CTG Leu	CAT His	ACC Thr 550	CTT Leu	GAT Asp	CTA Leu	TTG Leu	ATT Ile 555	GCC Ala	1732
35	CGA Arg	GGC Gly	GAC Asp	AGC Ser 560	GCT Ala	TAC Tyr	CGT Arg	CAA Gln	CTT Leu 565	GAA Glu	CGC Arg	GAT Asp	ACT Thr 570	CTA Leu	GTC Val	GAA Glu	1780
40	GCC Ala	AAA Lys	ATG Met 575	TAC Tyr	TAC Tyr	ATT Ile	CAG Gln 580	GCA Ala	CAA Gln	CAG Gln	CTA Leu	CTG Leu	GGA Gly 585	CCG Pro	CGC Arg	CCT Pro	1828
45	GAT Asp 590	ATC Ile	CAT His	ACC Thr	ACC Thr	AAT Asn	ACT Thr 595	TGG Trp	CCA Pro	AAT Asn	CCC Pro	ACC Thr 600	TTG Leu	AGT Ser	AAA Lys	GAA Glu	1876
50	GCT Ala 605	GGC Gly	GCT Ala	ATT Ile	GCC Ala	ACA Thr 610	CCG Pro	ACA Thr	TTC Phe	CTC Leu	AGT Ser 615	TCA Ser	CCG Pro	GAG Glu	GTG Val	ATG Met 620	1924
55	ACG Thr	TTC Phe	GCT Ala	GCC Ala	TGG Trp 625	CTA Leu	AGC Ser	GCA Ala	GGC Gly	GAT Asp 630	ACC Thr	GCA Ala	AAT Asn	ATT Ile	GGC Gly 635	GAC Asp	1972
60	GGT Gly	GAT Asp	TTC Phe	TTG Leu 640	CCA Pro	CCG Pro	TAC Tyr	AAC Asn 645	GAT Asp	GTA Val	CTA Leu	CTC Leu	GGT Gly	TAC Tyr 650	TGG Trp	GAT Asp	2020
65	AAA Lys	CTT Leu	GAG Glu 655	TTA Leu	CGC Arg	CTA Leu	TAC Tyr	AAC Asn 660	CTG Leu	CGC Arg	CAC His	AAT Asn	CTG Leu 665	AGT Ser	CTG Leu	GAT Asp	2068
70	GGT Gly 670	CAA Gln	CCG Pro	CTA Leu	AAT Asn	CTG Leu	CCA Pro 675	CTG Leu	TAT Tyr	GCC Ala	ACG Thr 680	CCG Pro	GTA Val	GAC Asp	CCG Pro	AAA Lys	2116
75	ACC Thr 685	CTG Leu	CAA Gln	CGC Arg	CAG Gln	CAA Gln 690	GCC Ala	GGA Gly	GGG Gly	GAC Asp	GGT Gly 695	ACA Thr	GGC Gly	AGT Ser	AGT Ser	CCG Pro 700	2164
80	GCT Ala	GGT Gly	GGT Gly	CAA Gln	GGC Gly 705	AGT Ser	GTT Val	CAG Gln	GGC Gly	TGG Trp 710	CGC Arg	TAT Tyr	CCG Pro	TTA Leu	TTG Leu 715	GTA Val	2212
85	GAA Glu	CGC Arg	GCC Ala	CGC Arg 720	TCT Ser	GCC Ala	GTG Val	AGT Ser	TTG Leu 725	TTG Leu	ACT Thr	CAG Gln	TTC Phe	GGC Gly 730	AAC Asn	AGC Ser	2260

5	TTA CAA ACA ACG TTA GAA CAT CAG GAT AAT GAA AAA ATG ACG ATA CTG 2308	
	Leu Gln Thr Thr Leu Glu His Gln Asp Asn Glu Lys Met Thr Ile Leu	735 740 745
10	TTG CAG ACT CAA CAG GAA GCC ATC CTG AAA CAT CAG CAC GAT ATA CAA 2356	
	Leu Gln Thr Gln Gln Glu Ala Ile Leu Lys His Gln His Asp Ile Gln	750 755 760
15	CAA AAT AAT CTA AAA GGA TTA CAA CAC AGC CTG ACC GCA TTA CAG GCT 2404	
	Gln Asn Asn Leu Lys Gly Leu Gln His Ser Leu Thr Ala Leu Gln Ala	765 770 775 780
20	AGC CGT GAT GGC GAC ACA TTG CGG CAA AAA CAT TAC AGC GAC CTG ATT 2452	
	Ser Arg Asp Gly Asp Thr Leu Arg Gln Lys His Tyr Ser Asp Leu Ile	785 790 795
25	AAC GGT GGT CTA TCT GCG GCA GAA ATC GCC GGT CTG ACA CTA CGC AGC 2500	
	Asn Gly Gly Leu Ser Ala Ala Glu Ile Ala Gly Leu Thr Leu Arg Ser	800 805 810
30	ACC GCC ATG ATT ACC AAT GGC GTT GCA ACG GGA TTG CTG ATT GCC GGC 2548	
	Thr Ala Met Ile Thr Asn Gly Val Ala Thr Gly Leu Leu Ile Ala Gly	815 820 825
35	GGA ATC GCC AAC GCG GTA CCT AAC GTC TTC GGG CTG GCT AAC GGT GGA 2596	
	Gly Ile Ala Asn Ala Val Pro Asn Val Phe Gly Leu Ala Asn Gly Gly	830 835 840
40	TCG GAA TGG GGA GCG CCA TTA ATT GGC TCC GGG CAA GCA ACC CAA GTT 2644	
	Ser Glu Trp Gly Ala Pro Leu Ile Gly Ser Gly Gln Ala Thr Gln Val	845 850 855 860
45	GGC GCC GGC ATC CAG GAT CAG AGC GCG GGC ATT TCA GAA GTG ACA GCA 2692	
	Gly Ala Gly Ile Gln Asp Gln Ser Ala Gly Ile Ser Glu Val Thr Ala	865 870 875
50	GGC TAT CAG CGT CGT CAG GAA GAA TGG GCA TTG CAA CGG GAT ATT GCT 2740	
	Gly Tyr Gln Arg Arg Gln Glu Glu Trp Ala Leu Gln Arg Asp Ile Ala	880 885 890
55	GAT AAC GAA ATA ACC CAA CTG GAT GCC CAG ATA CAA AGC CTG CAA GAG 2788	
	Asp Asn Glu Ile Thr Gln Leu Asp Ala Gln Ile Gln Ser Leu Gln Glu	895 900 905
60	CAA ATC ACG ATG GCA CAA AAA CAG ATC ACG CTC TCT GAA ACC GAA CAA 2836	
	Gln Ile Thr Met Ala Gln Lys Gln Ile Thr Leu Ser Glu Thr Glu Gln	910 915 920
65	GCG AAT GCC CAA GCG ATT TAT GAC CTG CAA ACC ACT CGT TTT ACC GGG 2884	
	Ala Asn Ala Gln Ala Ile Tyr Asp Leu Gln Thr Thr Arg Phe Thr Gly	925 930 935 940
70	CAG GCA CTG TAT AAC TGG ATG GCC GGT CGT CTC TCC GCG CTC TAT TAC 2932	
	Gln Ala Leu Tyr Asn Trp Met Ala Gly Arg Leu Ser Ala Leu Tyr Tyr	945 950 955
75	CAA ATG TAT GAT TCC ACT CTG CCA ATC TGT CTC CAG CCA AAA GCC GCA 2980	
	Gln Met Tyr Asp Ser Thr Leu Pro Ile Cys Leu Gln Pro Lys Ala Ala	960 965 970
80	TTA GTA CAG GAA TTA GGC GAG AAA GAG AGC GAC AGT CTT TTC CAG GTT 3028	
	Leu Val Gln Glu Leu Gly Glu Lys Glu Ser Asp Ser Leu Phe Gln Val	975 980 985
85	CCG GTG TGG AAT GAT CTG TGG CAA GGG CTG TTA GCA GGA GAA GGT TTA 3076	
	Pro Val Trp Asn Asp Leu Trp Gln Gly Leu Leu Ala Gly Glu Gly Leu	990 995 1000
90	AGT TCA GAG CTA CAG AAA CTG GAT GCC ATC TGG CTT GCA CGT GGT GGT 3124	
	Ser Ser Glu Leu Gln Lys Leu Asp Ala Ile Trp Leu Ala Arg Gly Gly	

	1005	1	1015	1020
5	ATT GGG CTA GAA GCC ATC CGC ACC GTG TCG CTG GAT ACC CTG TTT GGC 3172 Ile Gly Leu Glu Ala Ile Arg Thr Val Ser Leu Asp Thr Leu Phe Gly 1025 1030 1035			
10	ACA GGG ACG TTA AGT GAA AAT ATC AAT AAA GTG CTT AAC GGG GAA ACG 3220 Thr Gly Thr Leu Ser Glu Asn Ile Asn Lys Val Leu Asn Gly Glu Thr 1040 1045 1050			
	GTA TCT CCA TCC GGT GGC GTC ACT CTG GCG CTG ACA GGG GAT ATC TTC 3268 Val Ser Pro Ser Gly Gly Val Thr Leu Ala Leu Thr Gly Asp Ile Phe 1055 1060 1065			
15	CAA GCA ACA CTG GAT TTG AGT CAG CTA GGT TTG GAT AAC TCT TAC AAC 3316 Gln Ala Thr Leu Asp Leu Ser Gln Leu Gly Leu Asp Asn Ser Tyr Asn 1070 1075 1080			
20	TTG GGT AAC GAG AAG AAA CGT CGT ATT AAA CGT ATC GCC GTC ACC CTG 3364 Leu Gly Asn Glu Lys Lys Arg Arg Ile Lys Arg Ile Ala Val Thr Leu 1085 1090 1095 1100			
25	CCA ACA CTT CTG GGG CCA TAT CAA GAT CTT GAA GCC ACA CTG GTA ATG 3412 Pro Thr Leu Leu Gly Pro Tyr Gln Asp Leu Glu Ala Thr Leu Val Met 1105 1110 1115			
30	GGT GCG GAA ATC GCC GCC TTA TCA CAC GGT GTG AAT GAC GGA GGC CGG 3460 Gly Ala Glu Ile Ala Ala Leu Ser His Gly Val Asn Asp Gly Gly Arg 1120 1125 1130			
	TTT GTT ACC GAC TTT AAC GAC AGC CGT TTT CTG CCT TTT GAA GGT CGA 3508 Phe Val Thr Asp Phe Asn Asp Ser Arg Phe Leu Pro Phe Glu Gly Arg 1135 1140 1145			
35	GAT GCA ACA ACC GGC ACA CTG GAG CTC AAT ATT TTC CAT GCG GGT AAA 3556 Asp Ala Thr Thr Gly Thr Leu Glu Leu Asn Ile Phe His Ala Gly Lys 1150 1155 1160			
40	GAG GGA ACG CAA CAC GAG TTG GTC GCG AAT CTG AGT GAC ATC ATT GTG 3604 Glu Gly Thr Gln His Glu Leu Val Ala Asn Leu Ser Asp Ile Ile Val 1165 1170 1175 1180			
45	CAT CTG AAT TAC ATC ATT CGA GAC GCG TAA ATTTCTTTTC TTTGTCGATT 3654 His Leu Asn Tyr Ile Ile Arg Asp Ala * 1185 1190			
50	ACAGGTCCCT ATCAGGGGCC TGTTATTAAG GAGTACTTTA TGCAGGATTC ACCAGAAGTA 3714 TCGATTACAA CGCTGTCACT TCCCAAAGGT GGCGGTGCTA TCAATGGCAT GGGAGAAGCA 3774 CTGAATGCTG CCGGCCCTGA TGGAATGGCC TCCCTATCTC TGCCATTACC CCTTTGAC 3834 GGCAGAGGGA CGGCTCCTGG ATTATCGCTG ATTTACAGCA ACAGTGCAGG TAATGGGCCT 3894			
55	TTCGGCATCG GCTGGCAATG CGGTGTTATG TCCATTAGCC GACGCACCCA ACATGGCATT 3954 CCACAATACG GTAATGACGA CACGTTCCCTA TCCCCACAAG GCGAGGTCAT GAATATCGCC 4014 CTGAATGACC AAGGGCAACC TGATATCCGT CAAGACGTTA AAACGCTGCA AGGCGTTACC 4074 TTGCCAATTT CCTATACCGT GACCCGCTAT CAAGCCCGCC AGATCCTGGA TTTCAGTAAA 4134 ATCGAATACT GGCAACCTGC CTCCGGTCAA GAAGGACGCG CTTTCTGGCT GATATCGACA 4194			
60	CCGGACGGGC ATCTACACAT CTTAGGGAAA ACCGCGCAGG CTTGTCTGGC AAATCCGCAA 4254 AATGACCAAC AAATCGCCCA GTGGTTGCTG GAAGAACTG TGACGCCAGC CCGTGAACAT 4314 GTCAGCTATC AATATCGAGC CGAAGATGAA GCCCATGTG ACGACAATGA AAAAACCGCT 4374 CATCCCAATG TTACCGCACA GCGCTATCTG GTACAGGTGA ACTACAGGCA ACATCAAACC 4434			

5 ACAAGCCAGC CTGTTTCGTAC TGGATAACGC ACCTCCCAGCA CCGGAAGAGT GGCTGTTTCA 4494
 TCTGGTCTTT GACCACGGTG AGCGCGTACC TCACTTCATA CCGTGCCAAC ATGGGATGCA 4554
 GGTACAGCGC AATGGTCTGT ACGCCCGGAT ATCTTCTCTC GCTATGAATA TGGTTTGTAA 4614
 GTGCGTACTC GCCGCTTATG TCAACAAGTG CTGATGTTTC ACCGCACCGC GTCATGGCC 4674
 10 GGAGAAGCCA GTACCAATGA CGCCCCGAA CTGGTTGGAC GCTTAATACT GGAATATGAC 4634
 AAAAACGCCA GCGTCACCAC GTTGATTACC ATCCGTCAAT TAAGCCATGA ATCGGACGGG 4794
 AGGCCAGTCA CCCAGCCACC ACTAGAACTA GCCTGGCAAC GGTTTGATCT GGAGAAAATC 4854
 15 CCGACATGGC AACGCTTTGA CGCACTAGAT AATTTTAACT CGCAGCAACG TTATCAACTG 4865
 GTTGATCTGC GGGGAGAAGG GTTGCCAGGT ATGCTGTATC AAGATCGAGG CGCTTGGTGG 4914
 20 TATAAAGCTC CGCAACGTCA GGAAGACGGA GACAGCAATG CCGTCACTTA CGACAAAATC 4974
 GCCCCACTGC CTACCCTACC CAATTTGCAG GATAATGCCT CATTGATGGA TATCAACGGA 5034
 GACGGCCAAC TGGATTGGGT TGTTACCGCC TCCGGTATTC GCGGATACCA TAGTCAGCAA 5094
 25 CCCGATGGAA AGTGGACGCA CTTTACGCCA ATCAATGCCT TGCCCGTGA ATATTTTCAT 5214
 CCAAGCATCC AGTTCGCTGA CCTTACCGGG GCAGGCTTAT CTGATTTAGT GTTGATCGGG 5274
 30 CCGAAAAGCG TGCGTCTATA TGCCAACCAG CGAAACGGCT GGCGTAAAGG AGAAGATGTC 5334
 CCCCATCCA CAGGTATCAC CCTGCCTGTC ACAGGGACCG ATGCCCAGCA ACTGGTGGCT 5394
 TTCAGTGATA TGCTCGGTTT CCGTCAACAA CATCTGGTGG AAATCAAGGG TAATCGCGTC 5454
 35 ACCTGTTGGC CGAATCTAGG GCATGGCCGT TTCGGTCAAC CACTAACTCT GTCAGGATTT 5514
 AGCCAGCCCG AAAATAGCTT CAATCCCGAA CGGCTGTTTC TGGCGGATAT CGACGGCTCC 5574
 40 GGCACCACCG ACCTTATCTA TGCGCAATCC GGCTCTTTGC TCATTTATCT CAACCAAAGT 5634
 GGTAATCAGT TTGATGCCCC GTTGACATTA GCGTTGCCAG AAGGCGTACA ATTTGACAAC 5694
 ACTTGCCAAC TTCAAGTCGC CGATATTCAG GGATTAGGGA TAGCCAGCTT GATTCTGACT 5754
 45 GTGCCACATA TCGCGCCACA TCACTGGCGT TGTGACCTGT CACTGACCAA ACCCTGGTTG 5814
 TTGAATGTAA TGAACAATAA CCGGGGCGCA CATCACACGC TACATTATCG TAGTTCGCGC 5874
 50 CAATTCTGGT TGGATGAAAA ATTACAGCTC ACCAAAGCAG GCAAATCTCC GGCTTGTTAT 5934
 CTGCCGTTTC CAATGCATTT GCTATGGTAT ACCGAAATTC AGGATGAAAT CAGCGGCAAC 5994
 55 CGGCTCACCA GTGAAGTCAA CTACAGCCAC GGCGTCTGGG ATGGTAAAGA GCGGGAATTC 6054

(2) INFORMATION FOR SEQ ID NO:26:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1189 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26 (TcaB protein):

Met Ser Glu Ser Leu Phe Thr Gln Thr Leu Lys Glu Ala Arg Arg Asp
 1 5 10 15

Ala Leu Val Ala His Ile Ala Thr Gln Val Pro Ala Ala Leu Lys
 20 25 30

5 Glu Ser Ile Gln Thr Ala Asp Asp Leu Tyr Glu Tyr Leu Leu Leu Asp
 35 40 45

Thr Lys Ile Ser Asp Leu Val Thr Thr Ser Pro Leu Ser Glu Ala Ile
 50 55 60

10 Gly Ser Leu Gln Leu Phe Ile His Arg Ala Ile Glu Gly Tyr Asp Gly
 65 70 75 80

Thr Leu Ala Asp Ser Ala Lys Pro Tyr Phe Ala Asp Glu Gln Phe Leu
 85 90 95

15 Tyr Asn Trp Asp Ser Phe Asn His Arg Tyr Ser Thr Trp Ala Gly Lys
 100 105 110

20 Glu Arg Leu Lys Phe Tyr Ala Gly Asp Tyr Ile Asp Pro Thr Leu Arg
 115 120 125

Leu Asn Lys Thr Glu Ile Phe Thr Ala Phe Glu Gln Gly Ile Ser Gln
 130 135 140

25 Gly Lys Leu Lys Ser Glu Leu Val Glu Ser Lys Leu Arg Asp Tyr Leu
 145 150 155 160

Ile Ser Tyr Asp Thr Leu Ala Thr Leu Asp Tyr Ile Thr Ala Cys Gln
 165 170 175

30 Gly Lys Asp Asn Lys Thr Ile Phe Phe Ile Gly Arg Thr Gln Asn Ala
 180 185 190

Pro Tyr Ala Phe Tyr Trp Arg Lys Leu Thr Leu Val Thr Asp Gly Gly
 195 200 205

Lys Leu Lys Pro Asp Gln Trp Ser Glu Trp Arg Ala Ile Asn Ala Gly
 210 215 220

40 Ile Ser Glu Ala Tyr Ser Gly His Val Glu Pro Phe Trp Glu Asn Asn
 225 230 235 240

Lys Leu His Ile Arg Trp Phe Thr Ile Ser Lys Glu Asp Lys Ile Asp
 245 250 255

45 Phe Val Tyr Lys Asn Ile Trp Val Met Ser Ser Asp Tyr Ser Trp Ala
 260 265 270

Ser Lys Lys Lys Ile Leu Glu Leu Ser Phe Thr Asp Tyr Asn Arg Val
 275 280 285

Gly Ala Thr Gly Ser Ser Ser Pro Thr Glu Val Ala Ser Gln Tyr Gly
 290 295 300

55 Ser Asp Ala Gln Met Asn Ile Ser Asp Asp Gly Thr Val Leu Ile Phe
 305 310 315 320

Gln Asn Ala Gly Gly Ala Thr Pro Ser Thr Gly Val Thr Leu Cys Tyr
 325 330 335

60 Asp Ser Gly Asn Val Ile Lys Asn Leu Ser Ser Thr Gly Ser Ala Asn
 340 345 350

Leu Ser Ser Lys Asp Tyr Ala Thr Thr Lys Leu Arg Met Cys His Gly
 355 360 365

Gln Ser Tyr Asn Asp Asn Asn Tyr Cys Asn Phe Thr Leu Ser Ile Asn
 370 375 380

70 Thr Ile Glu Phe Thr Ser Tyr Gly Thr Phe Ser Ser Asp Gly Lys Gln
 385 390 395 400

Phe Thr Pro Pro Ser Gly Ser Ala Ile Asp Leu His Leu Pro Asn Tyr
 405 410 415
 5 Val Asp Leu Asn Ala Leu Leu Asp Ile Ser Leu Asp Ser Leu Leu Asn
 420 425 430
 Tyr Asp Val Gln Gly Gln Phe Gly Gly Ser Asn Pro Val Asp Asn Phe
 435 440 445
 10 Ser Gly Pro Tyr Gly Ile Tyr Leu Trp Glu Ile Phe Phe His Ile Pro
 450 455 460
 15 Phe Leu Val Thr Val Arg Met Gln Thr Glu Gln Arg Tyr Glu Asp Ala
 465 470 475 480
 Asp Thr Trp Tyr Lys Tyr Ile Phe Arg Ser Ala Gly Tyr Arg Asp Ala
 485 490 495
 20 Asn Gly Gln Leu Ile Met Asp Gly Ser Lys Pro Arg Tyr Trp Asn Val
 500 505 510
 Met Pro Leu Gln Leu Asp Thr Ala Trp Asp Thr Thr Gln Pro Ala Thr
 515 520 525
 25 Thr Asp Pro Asp Val Ile Ala Met Ala Asp Pro Met His Tyr Lys Leu
 530 535 540
 30 Ala Ile Phe Leu His Thr Leu Asp Leu Leu Ile Ala Arg Gly Asp Ser
 545 550 555 560
 Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Val Glu Ala Lys Met Tyr
 565 570 575
 35 Tyr Ile Gln Ala Gln Gln Leu Leu Gly Pro Arg Pro Asp Ile His Thr
 580 585 590
 Thr Asn Thr Trp Pro Asn Pro Thr Leu Ser Lys Glu Ala Gly Ala Ile
 595 600 605
 40 Ala Thr Pro Thr Phe Leu Ser Ser Pro Glu Val Met Thr Phe Ala Ala
 610 615 620
 45 Trp Leu Ser Ala Gly Asp Thr Ala Asn Ile Gly Asp Gly Asp Phe Leu
 625 630 635 640
 Pro Pro Tyr Asn Asp Val Leu Leu Gly Tyr Trp Asp Lys Leu Glu Leu
 645 650 655
 50 Arg Leu Tyr Asn Leu Arg His Asn Leu Ser Leu Asp Gly Gln Pro Leu
 660 665 670
 Asn Leu Pro Leu Tyr Ala Thr Pro Val Asp Pro Lys Thr Leu Gln Arg
 675 680 685
 55 Gln Gln Ala Gly Gly Asp Gly Thr Gly Ser Ser Pro Ala Gly Gly Gln
 690 695 700
 60 Gly Ser Val Gln Gly Trp Arg Tyr Pro Leu Leu Val Glu Arg Ala Arg
 705 710 715 720
 Ser Ala Val Ser Leu Leu Thr Gln Phe Gly Asn Ser Leu Gln Thr Thr
 725 730 735
 65 Leu Glu His Gln Asp Asn Glu Lys Met Thr Ile Leu Leu Gln Thr Gln
 740 745 750
 Gln Glu Ala Ile Leu Lys His Gln His Asp Ile Gln Gln Asn Asn Leu
 755 760 765
 70 Lys Gly Leu Gln His Ser Leu Thr Ala Leu Gln Ala Ser Arg Asp Gly

	770	775	780
5	Asp Thr Leu Arg Gln Lys His Tyr Ser Asp Leu Ile Asn Gly Gly Leu 785 790 795 800		
	Ser Ala Ala Glu Ile Ala Gly Leu Thr Leu Arg Ser Thr Ala Met Ile 805 810 815		
10	Thr Asn Gly Val Ala Thr Gly Leu Leu Ile Ala Gly Gly Ile Ala Asn 820 825 830		
	Ala Val Pro Asn Val Phe Gly Leu Ala Asn Gly Gly Ser Glu Trp Gly 835 840 845		
15	Ala Pro Leu Ile Gly Ser Gly Gln Ala Thr Gln Val Gly Ala Gly Ile 850 855 860		
	Gln Asp Gln Ser Ala Gly Ile Ser Glu Val Thr Ala Gly Tyr Gln Arg 865 870 875 880		
20	Arg Gln Glu Glu Trp Ala Leu Gln Arg Asp Ile Ala Asp Asn Glu Ile 885 890 895		
	Thr Gln Leu Asp Ala Gln Ile Gln Ser Leu Gln Glu Gln Ile Thr Met 900 905 910		
25	Ala Gln Lys Gln Ile Thr Leu Ser Glu Thr Glu Gln Ala Asn Ala Gln 915 920 925		
30	Ala Ile Tyr Asp Leu Gln Thr Thr Arg Phe Thr Gly Gln Ala Leu Tyr 930 935 940		
	Asn Trp Met Ala Gly Arg Leu Ser Ala Leu Tyr Tyr Gln Met Tyr Asp 945 950 955 960		
35	Ser Thr Leu Pro Ile Cys Leu Gln Pro Lys Ala Ala Leu Val Gln Glu 965 970 975		
	Leu Gly Glu Lys Glu Ser Asp Ser Leu Phe Gln Val Pro Val Trp Asn 980 985 990		
40	Asp Leu Trp Gln Gly Leu Leu Ala Gly Glu Gly Leu Ser Ser Glu Leu 995 1000 1005		
45	Gln Lys Leu Asp Ala Ile Trp Leu Ala Arg Gly Gly Ile Gly Leu Glu 1010 1015 1020		
	Ala Ile Arg Thr Val Ser Leu Asp Thr Leu Phe Gly Thr Gly Thr Leu 1025 1030 1035 1040		
50	Ser Glu Asn Ile Asn Lys Val Leu Asn Gly Glu Thr Val Ser Pro Ser 1045 1050 1055		
	Gly Gly Val Thr Leu Ala Leu Thr Gly Asp Ile Phe Gln Ala Thr Leu 1060 1065 1070		
55	Asp Leu Ser Gln Leu Gly Leu Asp Asn Ser Tyr Asn Leu Gly Asn Glu 1075 1080 1085		
60	Lys Lys Arg Arg Ile Lys Arg Ile Ala Val Thr Leu Pro Thr Leu Leu 1090 1095 1100		
	Gly Pro Tyr Gln Asp Leu Glu Ala Thr Leu Val Met Gly Ala Glu Ile 1105 1110 1115 1120		
65	Ala Ala Leu Ser His Gly Val Asn Asp Gly Gly Arg Phe Val Thr Asp 1125 1130 1135		
	Phe Asn Asp Ser Arg Phe Leu Pro Phe Glu Gly Arg Asp Ala Thr Thr 1140 1145 1150		

Gly Thr Leu Glu Leu Asn Ile Phe His Ala Gly Lys Glu Gly Thr Gln
 1155 1160 1165

5 His Glu Leu Val Ala Asn Leu Ser Asp Ile Ile Val His Leu Asn Tyr
 1170 1175 1180

Ile Ile Arg Asp Ala *
 1185 1190

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(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 1881 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..1881
 (D) OTHER INFORMATION: tcaB_i

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27 (tcaB_i coding region):

30

ATG TCT GAA TCT TTA TTT ACA CAA ACG TTG AAA GAA GCG CGC CGT GAT 48
 Met Ser Glu Ser Leu Phe Thr Gln Thr Leu Lys Glu Ala Arg Arg Asp
 1 5 10 15

35

GCA TTG GTT GCT CAT TAT ATT GCT ACT CAG GTG CCC GCA GAT TTA AAA 96
 Ala Leu Val Ala His Tyr Ile Ala Thr Gln Val Pro Ala Asp Leu Lys
 20 25 30

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GAG AGT ATC CAG ACC GCG GAT GAT CTG TAC GAA TAT CTG TTG CTG GAT 144
 Glu Ser Ile Gln Thr Ala Asp Asp Leu Tyr Glu Tyr Leu Leu Leu Asp
 35 40 45

45

ACC AAA ATT AGC GAT CTG GTT ACT ACT TCA CCG CTG TCC GAA GCG ATT 192
 Thr Lys Ile Ser Asp Leu Val Thr Thr Ser Pro Leu Ser Glu Ala Ile
 50 55 60

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GGC AGT CTG CAA TTG TTT ATT CAT CGT GCG ATA GAG GGC TAT GAC GGC 240
 Gly Ser Leu Gln Leu Phe Ile His Arg Ala Ile Glu Gly Tyr Asp Gly
 65 70 75 80

55

ACG CTG GCA GAC TCA GCA AAA CCC TAT TTT GCC GAT GAA CAG TTT TTA 288
 Thr Leu Ala Asp Ser Ala Lys Pro Tyr Phe Ala Asp Glu Gln Phe Leu
 85 90 95

60

TAT AAC TGG GAT AGT TTT AAC CAC CGT TAT AGC ACT TGG GCT GGC AAG 336
 Tyr Asn Trp Asp Ser Phe Asn His Arg Tyr Ser Thr Trp Ala Gly Lys
 100 105 110

65

GAA CGG TTG AAA TTC TAT GCC GGG GAT TAT ATT GAT CCA ACA TTG CGA 384
 Glu Arg Leu Lys Phe Tyr Ala Gly Asp Tyr Ile Asp Pro Thr Leu Arg
 115 120 125

TTG AAT AAG ACC GAG ATA TTT ACC GCA TTT GAA CAA GGT ATT TCT CAA 432
 Leu Asn Lys Thr Glu Ile Phe Thr Ala Phe Glu Gln Gly Ile Ser Gln
 130 135 140

GGG AAA TTA AAA AGT GAA TTA GTC GAA TCT AAA TTA CGT GAT TAT CTA 480
 Gly Lys Leu Lys Ser Glu Leu Val Glu Ser Lys Leu Arg Asp Tyr Leu
 145 150 155 160

ATT AGT TAT GAC ACT TTA GCC ACC CTT GAT TAT ATT ACT GCC TGC CAA 528
 Ile Ser Tyr Asp Thr Leu Ala Thr Leu Asp Tyr Ile Thr Ala Cys Gln
 165 170 175

5	GGC AAA GAT AAT AAA ACC ATC TTC TTT ATT GGC CGT ACA CAG AAT GCA 576 Gly Lys Asp Asn Lys Thr Ile Phe Phe Ile Gly Arg Thr Gln Asn Ala 180 185 190
10	CCC TAT GCA TTT TAT TGG CGA AAA TTA ACT TTA GTC ACT GAT GGC GGT 624 Pro Tyr Ala Phe Tyr Trp Arg Lys Leu Thr Leu Val Thr Asp Gly Gly 195 200 205
15	AAG TTG AAA CCA GAT CAA TGG TCA GAG TGG CGA GCA ATT AAT GCC GGG 672 Lys Leu Lys Pro Asp Gln Trp Ser Glu Trp Arg Ala Ile Asn Ala Gly 210 215 220
20	ATT AGT GAG GCA TAT TCA GGG CAT GTC GAG CCT TTC TGG GAA AAT AAC 720 Ile Ser Glu Ala Tyr Ser Gly His Val Glu Pro Phe Trp Glu Asn Asn 225 230 235 240
25	AAG CTG CAC ATC CGT TGG TTT ACT ATC TCG AAA GAA GAT AAA ATA GAT 768 Lys Leu His Ile Arg Trp Phe Thr Ile Ser Lys Glu Asp Lys Ile Asp 245 250 255
30	TTT GTT TAT AAA AAC ATC TGG GTG ATG AGT AGC GAT TAT AGC TGG GCA 816 Phe Val Tyr Lys Asn Ile Trp Val Met Ser Ser Asp Tyr Ser Trp Ala 260 265 270
35	TCA AAG AAA AAA ATC TTG GAA CTT TCT TTT ACT GAC TAC AAT AGA GTT 864 Ser Lys Lys Lys Ile Leu Glu Leu Ser Phe Thr Asp Tyr Asn Arg Val 275 280 285
40	GGA GCA ACA GGA TCA TCA AGC CCG ACT GAA GTA GCT TCA CAA TAT GGT 912 Gly Ala Thr Gly Ser Ser Ser Pro Thr Glu Val Ala Ser Gln Tyr Gly 290 295 300
45	TCT GAT GCT CAG ATG AAT ATT TCT GAT GAT GGG ACT GTA CTT ATT TTT 960 Ser Asp Ala Gln Met Asn Ile Ser Asp Asp Gly Thr Val Leu Ile Phe 305 310 315 320
50	CAG AAT GCC GGC GGA GCT ACT CCC AGT ACT GGA GTG ACG TTA TGT TAT 1008 Gln Asn Ala Gly Gly Ala Thr Pro Ser Thr Gly Val Thr Leu Cys Tyr 325 330 335
55	GAC TCT GGC AAC GTG ATT AAG AAC CTA TCT AGT ACA GGA AGT GCA AAT 1056 Asp Ser Gly Asn Val Ile Lys Asn Leu Ser Ser Thr Gly Ser Ala Asn 340 345 350
60	TTA TCG TCA AAG GAT TAT GCC ACA ACT AAA TTA CGC ATG TGT CAT GGA 1104 Leu Ser Ser Lys Asp Tyr Ala Thr Thr Lys Leu Arg Met Cys His Gly 355 360 365
65	CAA AGT TAC AAT GAT AAT AAC TAC TGC AAT TTT ACA CTC TCT ATT AAT 1152 Gln Ser Tyr Asn Asp Asn Asn Tyr Cys Asn Phe Thr Leu Ser Ile Asn 370 375 380
70	ACA ATA GAA TTC ACC TCC TAC GGC ACA TTC TCA TCA GAT GGA AAA CAA 1200 Thr Ile Glu Phe Thr Ser Tyr Gly Thr Phe Ser Ser Asp Gly Lys Gln 385 390 395 400
75	TTT ACA CCA CCT TCT GGT TCT GCC ATT GAT TTA CAC CTC CCT AAT TAT 1248 Phe Thr Pro Pro Ser Gly Ser Ala Ile Asp Leu His Leu Pro Asn Tyr 405 410 415
80	GTA GAT CTC AAC GCG CTA TTA GAT ATT AGC CTC GAT TCA CTA CTT AAT 1296 Val Asp Leu Asn Ala Leu Leu Asp Ile Ser Leu Asp Ser Leu Leu Asn 420 425 430
85	TAT GAC GTT CAG GGG CAG TTT GGC GGA TCT AAT CCG GTT GAT AAT TTC 1344 Tyr Asp Val Gln Gly Gln Phe Gly Gly Ser Asn Pro Val Asp Asn Phe 435 440 445
90	AGT GGT CCC TAT GGT ATT TAT CTA TGG GAA ATC TTC TTC CAT ATT CCG 1392 Ser Gly Pro Tyr Gly Ile Tyr Leu Trp Glu Ile Phe Phe His Ile Pro

	450		455		460	
	TTC CTT GTT ACG GTC CGT ATG CAA ACC GAA CAA CGT TAC GAA GAC GCG	1440				
5	Phe Leu Val Thr Val Arg Met Gln Thr Glu Gln Arg Tyr Glu Asp Ala	480				
	465 470 475 480					
	GAC ACT TGG TAC AAA TAT ATT TTC CGC AGC GCC GGT TAT CGC GAT GCT	1488				
10	Asp Thr Trp Tyr Lys Tyr Ile Phe Arg Ser Ala Gly Tyr Arg Asp Ala	495				
	485 490 495					
	AAT GGC CAG CTC ATT ATG GAT GGC AGT AAA CCA CGT TAT TGG AAT GTG	1536				
	Asn Gly Gln Leu Ile Met Asp Gly Ser Lys Pro Arg Tyr Trp Asn Val	510				
	500 505 510					
15	ATG CCA TTG CAA CTG GAT ACC GCA TGG GAT ACC ACA CAG CCC GCC ACC	1584				
	Met Pro Leu Gln Leu Asp Thr Ala Trp Asp Thr Thr Gln Pro Ala Thr	525				
	515 520 525					
20	ACT GAT CCA GAT GTG ATC GCT ATG GCG GAC CCG ATG CAT TAC AAG CTG	1632				
	Thr Asp Pro Asp Val Ile Ala Met Ala Asp Pro Met His Tyr Lys Leu	540				
	530 535 540					
	GCG ATA TTC CTG CAT ACC CTT GAT CTA TTG ATT GCC CGA GGC GAC AGC	1680				
25	Ala Ile Phe Leu His Thr Leu Asp Leu Leu Ile Ala Arg Gly Asp Ser	560				
	545 550 555 560					
	GCT TAC CGT CAA CTT GAA CGC GAT ACT CTA GTC GAA GCC AAA ATG TAC	1728				
	Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Val Glu Ala Lys Met Tyr	575				
	565 570 575					
30	TAC ATT CAG GCA CAA CAG CTA CTG GGA CCG CGC CCT GAT ATC CAT ACC	1776				
	Tyr Ile Gln Ala Gln Gln Leu Leu Gly Pro Arg Pro Asp Ile His Thr	590				
	580 585 590					
35	ACC AAT ACT TGG CCA AAT CCC ACC TTG AGT AAA GAA GCT GGC GCT ATT	1824				
	Thr Asn Thr Trp Pro Asn Pro Thr Leu Ser Lys Glu Ala Gly Ala Ile	605				
	595 600 605					
40	GCC ACA CCG ACA TTC CTC AGT TCA CCG GAG GTG ATG ACG TTC GCT GCC	1872				
	Ala Thr Pro Thr Phe Leu Ser Ser Pro Glu Val Met Thr Phe Ala Ala	620				
	610 615 620					
45	TGG CTA AGC	1881				
	Trp Leu Ser					
	625					

(2) INFORMATION FOR SEQ ID NO:28:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 627 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28 (TcaB₁ protein):

Met Ser Glu Ser Leu Phe Thr Gln Thr Leu Lys Glu Ala Arg Asp
1 5 10 15
Ala Leu Val Ala His Tyr Ile Ala Thr Gln Val Pro Ala Asp Leu Lys
20 25 30
Glu Ser Ile Gln Thr Ala Asp Asp Leu Tyr Glu Tyr Leu Leu Asp
35 40 45
Thr Lys Ile Ser Asp Leu Val Thr Thr Ser Pro Leu Ser Glu Ala Ile
50 55 60

Gly Ser Leu Gln Leu Ile His Arg Ala Ile Glu Gly Tyr Asp Gly
 65 70 75 80
 5 Thr Leu Ala Asp Ser Ala Lys Pro Tyr Phe Ala Asp Glu Gln Phe Leu
 85 90 95
 Tyr Asn Trp Asp Ser Phe Asn His Arg Tyr Ser Thr Trp Ala Gly Lys
 100 105 110
 10 Glu Arg Leu Lys Phe Tyr Ala Gly Asp Tyr Ile Asp Pro Thr Leu Arg
 115 120 125
 Leu Asn Lys Thr Glu Ile Phe Thr Ala Phe Glu Gln Gly Ile Ser Gln
 130 135 140
 15 Gly Lys Leu Lys Ser Glu Leu Val Glu Ser Lys Leu Arg Asp Tyr Leu
 145 150 155 160
 20 Ile Ser Tyr Asp Thr Leu Ala Thr Leu Asp Tyr Ile Thr Ala Cys Gln
 165 170 175
 Gly Lys Asp Asn Lys Thr Ile Phe Phe Ile Gly Arg Thr Gln Asn Ala
 180 185 190
 25 Pro Tyr Ala Phe Tyr Trp Arg Lys Leu Thr Leu Val Thr Asp Gly Gly
 195 200 205
 Lys Leu Lys Pro Asp Gln Trp Ser Glu Trp Arg Ala Ile Asn Ala Gly
 210 215 220
 30 Ile Ser Glu Ala Tyr Ser Gly His Val Glu Pro Phe Trp Glu Asn Asn
 225 230 235 240
 35 Lys Leu His Ile Arg Trp Phe Thr Ile Ser Lys Glu Asp Lys Ile Asp
 245 250 255
 Phe Val Tyr Lys Asn Ile Trp Val Met Ser Ser Asp Tyr Ser Trp Ala
 260 265 270
 40 Ser Lys Lys Lys Ile Leu Glu Leu Ser Phe Thr Asp Tyr Asn Arg Val
 275 280 285
 Gly Ala Thr Gly Ser Ser Ser Pro Thr Glu Val Ala Ser Gln Tyr Gly
 290 295 300
 45 Ser Asp Ala Gln Met Asn Ile Ser Asp Asp Gly Thr Val Leu Ile Phe
 305 310 315 320
 50 Gln Asn Ala Gly Gly Ala Thr Pro Ser Thr Gly Val Thr Leu Cys Tyr
 325 330 335
 Asp Ser Gly Asn Val Ile Lys Asn Leu Ser Ser Thr Gly Ser Ala Asn
 340 345 350
 55 Leu Ser Ser Lys Asp Tyr Ala Thr Thr Lys Leu Arg Met Cys His Gly
 355 360 365
 Gln Ser Tyr Asn Asp Asn Asn Tyr Cys Asn Phe Thr Leu Ser Ile Asn
 370 375 380
 60 Thr Ile Glu Phe Thr Ser Tyr Gly Thr Phe Ser Ser Asp Gly Lys Gln
 385 390 395 400
 65 Phe Thr Pro Pro Ser Gly Ser Ala Ile Asp Leu His Leu Pro Asn Tyr
 405 410 415
 Val Asp Leu Asn Ala Leu Leu Asp Ile Ser Leu Asp Ser Leu Leu Asn
 420 425 430
 70 Tyr Asp Val Gln Gly Gln Phe Gly Gly Ser Asn Pro Val Asp Asn Phe
 435 440 445

Ser Gly Pro Tyr Gly Ile Tyr Leu Trp Glu Ile Phe Phe His Ile Pro
 450 455 460

5 Phe Leu Val Thr Val Arg Met Gln Thr Glu Gln Arg Tyr Glu Asp Ala
 465 470 475 480

Asp Thr Trp Tyr Lys Tyr Ile Phe Arg Ser Ala Gly Tyr Arg Asp Ala
 485 490 495

10 Asn Gly Gln Leu Ile Met Asp Gly Ser Lys Pro Arg Tyr Trp Asn Val
 500 505 510

15 Met Pro Leu Gln Leu Asp Thr Ala Trp Asp Thr Thr Gln Pro Ala Thr
 515 520 525

Thr Asp Pro Asp Val Ile Ala Met Ala Asp Pro Met His Tyr Lys Leu
 530 535 540

20 Ala Ile Phe Leu His Thr Leu Asp Leu Leu Ile Ala Arg Gly Asp Ser
 545 550 555 560

Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Val Glu Ala Lys Met Tyr
 565 570 575

25 Tyr Ile Gln Ala Gln Gln Leu Leu Gly Pro Arg Pro Asp Ile His Thr
 580 585 590

30 Thr Asn Thr Trp Pro Asn Pro Thr Leu Ser Lys Glu Ala Gly Ala Ile
 595 600 605

Ala Thr Pro Thr Phe Leu Ser Ser Pro Glu Val Met Thr Phe Ala Ala
 610 615 620

35 Trp Leu Ser
 625

(2) INFORMATION FOR SEQ ID NO:29:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1689 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1689

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(D) OTHER INFORMATION: tcaB_{ii}(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29 (tcaB_{ii} coding region):

55 GCA GGC GAT ACC GCA AAT ATT GGC GAC GGT GAT TTC TTG CCA CCG TAC 48
 Ala Gly Asp Thr Ala Asn Ile Gly Asp Gly Asp Phe Leu Pro Pro Tyr
 1 5 10 15

60 AAC GAT GTA CTA CTC GGT TAC TGG GAT AAA CTT GAG TTA CGC CTA TAC 96
 Asn Asp Val Leu Leu Gly Tyr Trp Asp Lys Leu Glu Leu Arg Leu Tyr
 20 25 30

AAC CTG CGC CAC AAT CTG AGT CTG GAT GGT CAA CCG CTA AAT CTG CCA 144
 Asn Leu Arg His Asn Leu Ser Leu Asp Gly Gln Pro Leu Asn Leu Pro
 35 40 45

65 CTG TAT GCC ACG CCG GTA GAC CCG AAA ACC CTG CAA CGC CAG CAA GCC 192
 Leu Tyr Ala Thr Pro Val Asp Pro Lys Thr Leu Gln Arg Gln Gln Ala
 50 55 60

	GGA GGG GAC GGT ACA GGC AGT AGT CCG GCT GGT GGT CAA GGC AGT GTT	240
	Gly Gly Asp Gly Thr Gly Ser Ser Pro Ala Gly Gly Gln Gly Ser Val	
	65 70 75 80	
5	CAG GGC TGG CGC TAT CCG TTA TTG GTA GAA CGC GCC CGC TCT GCC GTG	288
	Gln Gly Trp Arg Tyr Pro Leu Leu Val Glu Arg Ala Arg Ser Ala Val	
	85 90 95	
10	AGT TTG TTG ACT CAG TTC GGC AAC AGC TTA CAA ACA ACG TTA GAA CAT	336
	Ser Leu Leu Thr Gln Phe Gly Asn Ser Leu Gln Thr Thr Leu Glu His	
	100 105 110	
15	CAG GAT AAT GAA AAA ATG ACG ATA CTG TTG CAG ACT CAA CAG GAA GCC	384
	Gln Asp Asn Glu Lys Met Thr Ile Leu Leu Gln Thr Gln Gln Glu Ala	
	115 120 125	
20	ATC CTG AAA CAT CAG CAC GAT ATA CAA CAA AAT AAT CTA AAA GGA TTA	432
	Ile Leu Lys His Gln His Asp Ile Gln Gln Asn Asn Leu Lys Gly Leu	
	130 135 140	
25	CAA CAC AGC CTG ACC GCA TTA CAG GCT AGC CGT GAT GGC GAC ACA TTG	480
	Gln His Ser Leu Thr Ala Leu Gln Ala Ser Arg Asp Gly Asp Thr Leu	
	145 150 155	
30	CGG CAA AAA CAT TAC AGC GAC CTG ATT AAC GGT GGT CTA TCT GCG GCA	528
	Arg Gln Lys His Tyr Ser Asp Leu Ile Asn Gly Gly Leu Ser Ala Ala	
	165 170 175	
35	GAA ATC GCC GGT CTG ACA CTA CGC AGC ACC GCC ATG ATT ACC AAT GGC	576
	Glu Ile Ala Gly Leu Thr Leu Arg Ser Thr Ala Met Ile Thr Asn Gly	
	180 185 190	
40	GTT GCA ACG GGA TTG CTG ATT GCC GGC GGA ATC GCC AAC GCG GTA CCT	624
	Val Ala Thr Gly Leu Leu Ile Ala Gly Gly Ile Ala Asn Ala Val Pro	
	195 200 205	
45	AAC GTC TTC GGG CTG GCT AAC GGT GGA TCG GAA TGG GGA GCG CCA TTA	672
	Asn Val Phe Gly Leu Ala Asn Gly Gly Ser Glu Trp Gly Ala Pro Leu	
	210 215 220	
50	ATT GGC TCC GGG CAA GCA ACC CAA GTT GGC GCC GGC ATC CAG GAT CAG	720
	Ile Gly Ser Gly Gln Ala Thr Gln Val Gly Ala Gly Ile Gln Asp Gln	
	225 230 235 240	
55	AGC GCG GGC ATT TCA GAA GTG ACA GCA GGC TAT CAG CGT CGT CAG GAA	768
	Ser Ala Gly Ile Ser Glu Val Thr Ala Gly Tyr Gln Arg Arg Gln Glu	
	245 250 255	
60	GAA TGG GCA TTG CAA CGG GAT ATT GCT GAT AAC GAA ATA ACC CAA CTG	816
	Glu Trp Ala Leu Gln Arg Asp Ile Ala Asp Asn Glu Ile Thr Gln Leu	
	260 265 270	
65	GAT GCC CAG ATA CAA AGC CTG CAA GAG CAA ATC ACG ATG GCA CAA AAA	864
	Asp Ala Gln Ile Gln Ser Leu Gln Glu Gln Ile Thr Met Ala Gln Lys	
	275 280 285	
70	CAG ATC ACG CTC TCT GAA ACC GAA CAA GCG AAT GCC CAA GCG ATT TAT	912
	Gln Ile Thr Leu Ser Glu Thr Glu Gln Ala Asn Ala Gln Ala Ile Tyr	
	290 295 300	
75	GAC CTG CAA ACC ACT CGT TTT ACC GGG CAG GCA CTG TAT AAC TGG ATG	960
	Asp Leu Gln Thr Thr Arg Phe Thr Gly Gln Ala Leu Tyr Asn Trp Met	
	305 310 315 320	
80	GCC GGT CGT CTC TCC GCG CTC TAT TAC CAA ATG TAT GAT TCC ACT CTG	1008
	Ala Gly Arg Leu Ser Ala Leu Tyr Tyr Gln Met Tyr Asp Ser Thr Leu	
	325 330 335	
85	CCA ATC TGT CTC CAG CCA AAA GCC GCA TTA GTA CAG GAA TTA GGC GAG	1056
	Pro Ile Cys Leu Gln Pro Lys Ala Ala Leu Val Gln Glu Leu Gly Glu	

			340				345				350						
5	AAA	GAG	AGC	GAC	AGT	CTT	TTC	CAG	GTT	CCG	GTG	TGG	AAT	GAT	CTG	TGG	1104
	Lys	Glu	Ser	Asp	Ser	Leu	Phe	Gln	Val	Pro	Val	Trp	Asn	Asp	Leu	Trp	
			355					360					365				
10	CAA	GGG	CTG	TTA	GCA	GGA	GAA	GGT	TTA	AGT	TCA	GAG	CTA	CAG	AAA	CTG	1152
	Gln	Gly	Leu	Leu	Ala	Gly	Glu	Gly	Leu	Ser	Ser	Glu	Leu	Gln	Lys	Leu	
			370				375					380					
15	GAT	GCC	ATC	TGG	CTT	GCA	CGT	GGT	GGT	ATT	GGG	CTA	GAA	GCC	ATC	CGC	1200
	Asp	Ala	Ile	Trp	Leu	Ala	Arg	Gly	Gly	Ile	Gly	Leu	Glu	Ala	Ile	Arg	
	385					390					395					400	
20	ACC	GTG	TCG	CTG	GAT	ACC	CTG	TTT	GGC	ACA	GGG	ACG	TTA	AGT	GAA	AAT	1248
	Thr	Val	Ser	Leu	Asp	Thr	Leu	Phe	Gly	Thr	Gly	Thr	Leu	Ser	Glu	Asn	
					405					410					415		
25	ATC	AAT	AAA	GTG	CTT	AAC	GGG	GAA	ACG	GTA	TCT	CCA	TCC	GGT	GGC	GTC	1296
	Ile	Asn	Lys	Val	Leu	Asn	Gly	Glu	Thr	Val	Ser	Pro	Ser	Gly	Gly	Val	
				420					425					430			
30	ACT	CTG	GCG	CTG	ACA	GGG	GAT	ATC	TTC	CAA	GCA	ACA	CTG	GAT	TTG	AGT	1344
	Thr	Leu	Ala	Leu	Thr	Gly	Asp	Ile	Phe	Gln	Ala	Thr	Leu	Asp	Leu	Ser	
			435					440					445				
35	CAG	CTA	GGT	TTG	GAT	AAC	TCT	TAC	AAC	TTG	GGT	AAC	GAG	AAG	AAA	CGT	1392
	Gln	Leu	Gly	Leu	Asp	Asn	Ser	Tyr	Asn	Leu	Gly	Asn	Glu	Lys	Lys	Arg	
		450				455					460						
40	CGT	ATT	AAA	CGT	ATC	GCC	GTC	ACC	CTG	CCA	ACA	CTT	CTG	GGG	CCA	TAT	1440
	Arg	Ile	Lys	Arg	Ile	Ala	Val	Thr	Leu	Pro	Thr	Leu	Leu	Gly	Pro	Tyr	
	465					470				475						480	
45	CAA	GAT	CTT	GAA	GCC	ACA	CTG	GTA	ATG	GGT	GCG	GAA	ATC	GCC	GCC	TTA	1488
	Gln	Asp	Leu	Glu	Ala	Thr	Leu	Val	Met	Gly	Ala	Glu	Ile	Ala	Ala	Leu	
					485					490				495			
50	TCA	CAC	GGT	GTG	AAT	GAC	GGA	GGC	CGG	TTT	GTT	ACC	GAC	TTT	AAC	GAC	1536
	Ser	His	Gly	Val	Asn	Asp	Gly	Gly	Arg	Phe	Val	Thr	Asp	Phe	Asn	Asp	
				500					505					510			
55	AGC	CGT	TTT	CTG	CCT	TTT	GAA	GGT	CGA	GAT	GCA	ACA	ACC	GGC	ACA	CTG	1584
	Ser	Arg	Phe	Leu	Pro	Phe	Glu	Gly	Arg	Asp	Ala	Thr	Thr	Gly	Thr	Leu	
			515					520					525				
60	GAG	CTC	AAT	ATT	TTC	CAT	GCG	GGT	AAA	GAG	GGA	ACG	CAA	CAC	GAG	TTG	1632
	Glu	Leu	Asn	Ile	Phe	His	Ala	Gly	Lys	Glu	Gly	Thr	Gln	His	Glu	Leu	
		530					535					540					
65	GTC	GCG	AAT	CTG	AGT	GAC	ATC	ATT	GTG	CAT	CTG	AAT	TAC	ATC	ATT	CGA	1680
	Val	Ala	Asn	Leu	Ser	Asp	Ile	Ile	Val	His	Leu	Asn	Tyr	Ile	Ile	Arg	
	545					550					555					560	
70	GAC	GCG	TAA														1689
	Asp	Ala	*														

60 (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 562 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30 (Tcab₁₁ protein):

1	Ala	Gly	Asp	Thr	Ala	Asn	Ile	Gly	Asp	Gly	Asp	Phe	Leu	Pro	Pro	Tyr
5	Asn	Asp	Val	Leu	Leu	Gly	Tyr	Trp	Asp	Lys	Leu	Glu	Leu	Arg	Leu	Tyr
10	Asn	Leu	Arg	His	Asn	Leu	Ser	Leu	Asp	Gly	Gln	Pro	Leu	Asn	Leu	Pro
	Leu	Tyr	Ala	Thr	Pro	Val	Asp	Pro	Lys	Thr	Leu	Gln	Arg	Gln	Gln	Ala
15	Gly	Gly	Asp	Gly	Thr	Gly	Ser	Ser	Pro	Ala	Gly	Gly	Gln	Gly	Ser	Val
20	Gln	Gly	Trp	Arg	Tyr	Pro	Leu	Leu	Val	Glu	Arg	Ala	Arg	Ser	Ala	Val
	Ser	Leu	Leu	Thr	Gln	Phe	Gly	Asn	Ser	Leu	Gln	Thr	Thr	Leu	Glu	His
25	Gln	Asp	Asn	Glu	Lys	Met	Thr	Ile	Leu	Leu	Gln	Thr	Gln	Gln	Glu	Ala
	Ile	Leu	Lys	His	Gln	His	Asp	Ile	Gln	Gln	Asn	Asn	Leu	Lys	Gly	Leu
30	Gln	His	Ser	Leu	Thr	Ala	Leu	Gln	Ala	Ser	Arg	Asp	Gly	Asp	Thr	Leu
35	Arg	Gln	Lys	His	Tyr	Ser	Asp	Leu	Ile	Asn	Gly	Gly	Leu	Ser	Ala	Ala
	Glu	Ile	Ala	Gly	Leu	Thr	Leu	Arg	Ser	Thr	Ala	Met	Ile	Thr	Asn	Gly
40	Val	Ala	Thr	Gly	Leu	Leu	Ile	Ala	Gly	Gly	Ile	Ala	Asn	Ala	Val	Pro
	Asn	Val	Phe	Gly	Leu	Ala	Asn	Gly	Gly	Ser	Glu	Trp	Gly	Ala	Pro	Leu
45	Ile	Gly	Ser	Gly	Gln	Ala	Thr	Gln	Val	Gly	Ala	Gly	Ile	Gln	Asp	Gln
50	Ser	Ala	Gly	Ile	Ser	Glu	Val	Thr	Ala	Gly	Tyr	Gln	Arg	Arg	Gln	Glu
	Glu	Trp	Ala	Leu	Gln	Arg	Asp	Ile	Ala	Asp	Asn	Glu	Ile	Thr	Gln	Leu
55	Asp	Ala	Gln	Ile	Gln	Ser	Leu	Gln	Glu	Gln	Ile	Thr	Met	Ala	Gln	Lys
	Gln	Ile	Thr	Leu	Ser	Glu	Thr	Glu	Gln	Ala	Asn	Ala	Gln	Ala	Ile	Tyr
60	Asp	Leu	Gln	Thr	Thr	Arg	Phe	Thr	Gly	Gln	Ala	Leu	Tyr	Asn	Trp	Met
	Ala	Gly	Arg	Leu	Ser	Ala	Leu	Tyr	Tyr	Gln	Met	Tyr	Asp	Ser	Thr	Leu
65	Pro	Ile	Cys	Leu	Gln	Pro	Lys	Ala	Ala	Leu	Val	Gln	Glu	Leu	Gly	Glu
	Lys	Glu	Ser	Asp	Ser	Leu	Phe	Gln	Val	Pro	Val	Trp	Asn	Asp	Leu	Trp

Gln Gly Leu Leu Ala Gly Glu Gly Leu Ser Ser Glu Leu Gln Lys Leu
 370 375 380

5 Asp Ala Ile Trp Leu Ala Arg Gly Gly Ile Gly Leu Glu Ala Ile Arg
 385 390 395 400

Thr Val Ser Leu Asp Thr Leu Phe Gly Thr Gly Thr Leu Ser Glu Asn
 405 410 415

10 Ile Asn Lys Val Leu Asn Gly Glu Thr Val Ser Pro Ser Gly Gly Val
 420 425 430

15 Thr Leu Ala Leu Thr Gly Asp Ile Phe Gln Ala Thr Leu Asp Leu Ser
 435 440 445

Gln Leu Gly Leu Asp Asn Ser Tyr Asn Leu Gly Asn Glu Lys Lys Arg
 450 455 460

20 Arg Ile Lys Arg Ile Ala Val Thr Leu Pro Thr Leu Leu Gly Pro Tyr
 465 470 475 480

Gln Asp Leu Glu Ala Thr Leu Val Met Gly Ala Glu Ile Ala Ala Leu
 485 490 495

25 Ser His Gly Val Asn Asp Gly Gly Arg Phe Val Thr Asp Phe Asn Asp
 500 505 510

30 Ser Arg Phe Leu Pro Phe Glu Gly Arg Asp Ala Thr Thr Gly Thr Leu
 515 520 525

Glu Leu Asn Ile Phe His Ala Gly Lys Glu Gly Thr Gln His Glu Leu
 530 535 540

35 Val Ala Asn Leu Ser Asp Ile Ile Val His Leu Asn Tyr Ile Ile Arg
 545 550 555 560

Asp Ala *

40

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 4458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50 (ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 1..4458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31 (tcac gene):

55 ATG CAG GAT TCA CCA GAA GTA TCG ATT ACA ACG CTG TCA CTT CCC AAA 48
 Met Gln Asp Ser Pro Glu Val Ser Ile Thr Thr Thr Leu Ser Leu Pro Lys
 1 5 10 15

60 GGT GGC GGT GCT ATC AAT GGC ATG GGA GAA GCA CTG AAT GCT GCC GGC 96
 Gly Gly Gly Ala Ile Asn Gly Met Gly Glu Ala Leu Asn Ala Ala Gly
 20 25 30

65 CCT GAT GGA ATG GCC TCC CTA TCT CTG CCA TTA CCC CTT TCG ACC GGC 144
 Pro Asp Gly Met Ala Ser Leu Ser Leu Pro Leu Pro Leu Ser Thr Gly
 35 40 45

AGA GGG ACG GCT CCT GGA TTA TCG CTG ATT TAC AGC AAC AGT GCA GGT 192
 Arg Gly Thr Ala Pro Gly Leu Ser Leu Ile Tyr Ser Asn Ser Ala Gly

	50	55	60	
5	AAT GGG CCT TTC GGC ATC GGC TGG CAA TGC GGT GTT ATG TCC ATT AGC 240 Asn Gly Pro Phe Gly Ile Gly Trp Gln Cys Gly Val Met Ser Ile Ser 80 65 70 75 80			
10	CGA CGC ACC CAA CAT GGC ATT CCA CAA TAC GGT AAT GAC GAC ACG TTC 288 Arg Arg Thr Gln His Gly Ile Pro Gln Tyr Gly Asn Asp Asp Thr Phe 95 85 90 95			
15	CTA TCC CCA CAA GGC GAG GTC ATG AAT ATC GCC CTG AAT GAC CAA GGG 336 Leu Ser Pro Gln Gly Glu Val Met Asn Ile Ala Leu Asn Asp Gln Gly 110 100 105 110			
20	CAA CCT GAT ATC CGT CAA GAC GTT AAA ACG CTG CAA GGC GTT ACC TTG 384 Gln Pro Asp Ile Arg Gln Asp Val Lys Thr Leu Gln Gly Val Thr Leu 125 115 120 125			
25	CCA ATT TCC TAT ACC GTG ACC CGC TAT CAA GCC CGC CAG ATC CTG GAT 432 Pro Ile Ser Tyr Thr Val Thr Arg Tyr Gln Ala Arg Gln Ile Leu Asp 140 130 135 140			
30	TTC AGT AAA ATC GAA TAC TGG CAA CCT GCC TCC GGT CAA GAA GGA CGC 480 Phe Ser Lys Ile Glu Tyr Trp Gln Pro Ala Ser Gly Gln Glu Gly Arg 160 145 150 155			
35	GCT TTC TGG CTG ATA TCG ACA CCG GAC GGG CAT CTA CAC ATC TTA GGG 528 Ala Phe Trp Leu Ile Ser Thr Pro Asp Gly His Leu His Ile Leu Gly 175 165 170 175			
40	AAA ACC GCG CAG GCT TGT CTG GCA AAT CCG CAA AAT GAC CAA CAA ATC 576 Lys Thr Ala Gln Ala Cys Leu Ala Asn Pro Gln Asn Asp Gln Gln Ile 190 180 185 190			
45	GCC CAG TGG TTG CTG GAA GAA ACT GTG ACG CCA GCC GGT GAA CAT GTC 624 Ala Gln Trp Leu Leu Glu Glu Thr Val Thr Pro Ala Gly Glu His Val 205 195 200 205			
50	AGC TAT CAA TAT CGA GCC GAA GAT GAA GCC CAT TGT GAC GAC AAT GAA 672 Ser Tyr Gln Tyr Arg Ala Glu Asp Glu Ala His Cys Asp Asp Asn Glu 220 210 215 220			
55	AAA ACC GCT CAT CCC AAT GTT ACC GCA CAG CGC TAT CTG GTA CAG GTG 720 Lys Thr Ala His Pro Asn Val Thr Ala Gln Arg Tyr Leu Val Gln Val 240 225 230 235 240			
60	AAC TAC GGC AAC ATC AAA CCA CAA GCC AGC CTG TTC GTA CTG GAT AAC 768 Asn Tyr Gly Asn Ile Lys Pro Gln Ala Ser Leu Phe Val Leu Asp Asn 255 245 250 255			
65	GCA CCT CCC GCA CCG GAA GAG TGG CTG TTT CAT CTG GTC TTT GAC CAC 816 Ala Pro Pro Ala Pro Glu Glu Trp Leu Phe His Leu Val Phe Asp His 270 260 265 270			
70	GGT GAG CGC GAT ACC TCA CTT CAT ACC GTG CCA ACA TGG GAT GCA GGT 864 Gly Glu Arg Asp Thr Ser Leu His Thr Val Pro Thr Trp Asp Ala Gly 285 275 280 285			
75	ACA GCG CAA TGG TCT GTA CGC CCG GAT ATC TTC TCT CGC TAT GAA TAT 912 Thr Ala Gln Trp Ser Val Arg Pro Asp Ile Phe Ser Arg Tyr Glu Tyr 300 290 295 300			
80	GGT TTT GAA GTG CGT ACT CGC CGC TTA TGT CAA CAA GTG CTG ATG TTT 960 Gly Phe Glu Val Arg Thr Arg Arg Leu Cys Gln Gln Val Leu Met Phe 320 305 310 315 320			
85	CAC CGC ACC GCG CTC ATG GCC GGA GAA GCC AGT ACC AAT GAC GCC CCG 1008 His Arg Thr Ala Leu Met Ala Gly Glu Ala Ser Thr Asn Asp Ala Pro 335 325 330 335			
90	GAA CTG GTT GGA CGC TTA ATA CTG GAA TAT GAC AAA AAC GCC AGC GTC 1056			

	Glu	Leu	Val	Gly	Arg	Leu	Ile	Leu	Glu	Tyr	Asp	Lys	Asn	Ala	Ser	Val	
				340					345					350			
5	ACC	ACG	TTG	ATT	ACC	ATC	CGT	CAA	TTA	AGC	CAT	GAA	TCG	GAC	GGG	AGG	1104
	Thr	Thr	Leu	Ile	Thr	Ile	Arg	Gln	Leu	Ser	His	Glu	Ser	Asp	Gly	Arg	
			355				360					365					
10	CCA	GTC	ACC	CAG	CCA	CCA	CTA	GAA	CTA	GCC	TGG	CAA	CGG	TTT	GAT	CTG	1152
	Pro	Val	Thr	Gln	Pro	Pro	Leu	Glu	Leu	Ala	Trp	Gln	Arg	Phe	Asp	Leu	
		370					375					380					
15	GAG	AAA	ATC	CCG	ACA	TGG	CAA	CGC	TTT	GAC	GCA	CTA	GAT	AAT	TTT	AAC	1200
	Glu	Lys	Ile	Pro	Thr	Trp	Gln	Arg	Phe	Asp	Ala	Leu	Asp	Asn	Phe	Asn	
	385					390				395						400	
20	TCG	CAG	CAA	CGT	TAT	CAA	CTG	GTT	GAT	CTG	CGG	GGA	GAA	GGG	TTG	CCA	1248
	Ser	Gln	Gln	Arg	Tyr	Gln	Leu	Val	Asp	Leu	Arg	Gly	Glu	Gly	Leu	Pro	
				405					410						415		
25	GGT	ATG	CTG	TAT	CAA	GAT	CGA	GGC	GCT	TGG	TGG	TAT	AAA	GCT	CCG	CAA	1296
	Gly	Met	Leu	Tyr	Gln	Asp	Arg	Gly	Ala	Trp	Trp	Tyr	Lys	Ala	Pro	Gln	
				420				425						430			
30	CGT	CAG	GAA	GAC	GGA	GAC	AGC	AAT	GCC	GTC	ACT	TAC	GAC	AAA	ATC	GCC	1344
	Arg	Gln	Glu	Asp	Gly	Asp	Ser	Asn	Ala	Val	Thr	Tyr	Asp	Lys	Ile	Ala	
			435					440					445				
35	CCA	CTG	CCT	ACC	CTA	CCC	AAT	TTG	CAG	GAT	AAT	GCC	TCA	TTG	ATG	GAT	1392
	Pro	Leu	Pro	Thr	Leu	Pro	Asn	Leu	Gln	Asp	Asn	Ala	Ser	Leu	Met	Asp	
		450					455					460					
40	ATC	AAC	GGA	GAC	GGC	CAA	CTG	GAT	TGG	GTT	GTT	ACC	GCC	TCC	GGT	ATT	1440
	Ile	Asn	Gly	Asp	Gly	Gln	Leu	Asp	Trp	Val	Val	Thr	Ala	Ser	Gly	Ile	
	465				470				475						480		
45	CGC	GGA	TAC	CAT	AGT	CAG	CAA	CCC	GAT	GGA	AAG	TGG	ACG	CAC	TTT	ACG	1488
	Arg	Gly	Tyr	His	Ser	Gln	Gln	Pro	Asp	Gly	Lys	Trp	Thr	His	Phe	Thr	
				485					490						495		
50	CCA	ATC	AAT	GCC	TTG	CCC	GTG	GAA	TAT	TTT	CAT	CCA	AGC	ATC	CAG	TTC	1536
	Pro	Ile	Asn	Ala	Leu	Pro	Val	Glu	Tyr	Phe	His	Pro	Ser	Ile	Gln	Phe	
				500				505						510			
55	GCT	GAC	CTT	ACC	GGG	GCA	GGC	TTA	TCT	GAT	TTA	GTG	TTG	ATC	GGG	CCG	1584
	Ala	Asp	Leu	Thr	Gly	Ala	Gly	Leu	Ser	Asp	Leu	Val	Leu	Ile	Gly	Pro	
			515				520						525				
60	AAA	AGC	GTG	CGT	CTA	TAT	GCC	AAC	CAG	CGA	AAC	GGC	TGG	CGT	AAA	GGA	1632
	Lys	Ser	Val	Arg	Leu	Tyr	Ala	Asn	Gln	Arg	Asn	Gly	Trp	Arg	Lys	Gly	
		530					535					540					
65	GAA	GAT	GTC	CCC	CAA	TCC	ACA	GGT	ATC	ACC	CTG	CCT	GTC	ACA	GGG	ACC	1680
	Glu	Asp	Val	Pro	Gln	Ser	Thr	Gly	Ile	Thr	Leu	Pro	Val	Thr	Gly	Thr	
	545					550					555					560	
70	GAT	GCC	CGC	AAA	CTG	GTG	GCT	TTC	AGT	GAT	ATG	CTC	GGT	TCC	GGT	CAA	1728
	Asp	Ala	Arg	Lys	Leu	Val	Ala	Phe	Ser	Asp	Met	Leu	Gly	Ser	Gly	Gln	
				565				570							575		
75	CAA	CAT	CTG	GTG	GAA	ATC	AAG	GGT	AAT	CGC	GTC	ACC	TGT	TGG	CCG	AAT	1776
	Gln	His	Leu	Val	Glu	Ile	Lys	Gly	Asn	Arg	Val	Thr	Cys	Trp	Pro	Asn	
				580				585						590			
80	CTA	GGG	CAT	GGC	CGT	TTC	GGT	CAA	CCA	CTA	ACT	CTG	TCA	GGA	TTT	AGC	1824
	Leu	Gly	His	Gly	Arg	Phe	Gly	Gln	Pro	Leu	Thr	Leu	Ser	Gly	Phe	Ser	
			595				600					605					
85	CAG	CCC	GAA	AAT	AGC	TTC	AAT	CCC	GAA	CGG	CTG	TTT	CTG	GCG	GAT	ATC	1872
	Gln	Pro	Glu	Asn	Ser	Phe	Asn	Pro	Glu	Arg	Leu	Phe	Leu	Ala	Asp	Ile	
		610					615					620					

	GAC	GGC	TCC	GGC	ACC	GAC	CTT	ATC	TAT	GCG	CAA	TCC	TCT	TTG	1920
	Asp	Gly	Ser	Gly	Thr	Asp	Leu	Ile	Tyr	Ala	Gln	Ser	Gly	Ser	Leu
	625				630					635					640
5	CTC	ATT	TAT	CTC	AAC	CAA	AGT	GGT	AAT	CAG	TTT	GAT	GCC	CCG	TTG
	Leu	Ile	Tyr	Leu	Asn	Gln	Ser	Gly	Asn	Gln	Phe	Asp	Ala	Pro	Leu
					645					650					655
10	TTA	GCG	TTG	CCA	GAA	GGC	GTA	CAA	TTT	GAC	AAC	ACT	TGC	CAA	CTT
	Leu	Ala	Leu	Pro	Glu	Gly	Val	Gln	Phe	Asp	Asn	Thr	Cys	Gln	Leu
				660					665					670	
15	GTC	GCC	GAT	ATT	CAG	GGA	TTA	GGG	ATA	GCC	AGC	TTG	ATT	CTG	ACT
	Val	Ala	Asp	Ile	Gln	Gly	Leu	Gly	Ile	Ala	Ser	Leu	Ile	Leu	Thr
			675					680					685		
20	CCA	CAT	ATC	GCG	CCA	CAT	CAC	TGG	CGT	TGT	GAC	CTG	TCA	CTG	ACC
	Pro	His	Ile	Ala	Pro	His	His	Trp	Arg	Cys	Asp	Leu	Ser	Leu	Thr
		690					695					700			
	CCC	TGG	TTG	TTG	AAT	GTA	ATG	AAC	AAT	AAC	CGG	GGC	GCA	CAT	CAC
	Pro	Trp	Leu	Leu	Asn	Val	Met	Asn	Asn	Asn	Arg	Gly	Ala	His	His
		705				710					715				720
25	CTA	CAT	TAT	CGT	AGT	TCC	GCG	CAA	TTC	TGG	TTG	GAT	GAA	AAA	TTA
	Leu	His	Tyr	Arg	Ser	Ser	Ala	Gln	Phe	Trp	Leu	Asp	Glu	Lys	Leu
					725					730					735
30	CTC	ACC	AAA	GCA	GGC	AAA	TCT	CCG	GCT	TGT	TAT	CTG	CCG	TTT	CCA
	Leu	Thr	Lys	Ala	Gly	Lys	Ser	Pro	Ala	Cys	Tyr	Leu	Pro	Phe	Pro
				740					745					750	
35	CAT	TTG	CTA	TGG	TAT	ACC	GAA	ATT	CAG	GAT	GAA	ATC	AGC	GGC	AAC
	His	Leu	Leu	Trp	Tyr	Thr	Glu	Ile	Gln	Asp	Glu	Ile	Ser	Gly	Asn
			755					760				765			
40	CTC	ACC	AGT	GAA	GTC	AAC	TAC	AGC	CAC	GGC	GTC	TGG	GAT	GGT	AAA
	Leu	Thr	Ser	Glu	Val	Asn	Tyr	Ser	His	Gly	Val	Trp	Asp	Gly	Lys
		770					775					780			
	CGG	GAA	TTC	AGA	GGA	TTT	GGC	TGC	ATC	AAA	CAG	ACA	GAT	ACC	ACA
	Arg	Glu	Phe	Arg	Gly	Phe	Gly	Cys	Ile	Lys	Gln	Thr	Asp	Thr	Thr
		785				790					795				800
45	TTT	TCT	CAC	GGC	ACC	GCC	CCC	GAA	CAG	GCG	GCA	CCG	TCG	CTG	AGT
	Phe	Ser	His	Gly	Thr	Ala	Pro	Glu	Gln	Ala	Ala	Pro	Ser	Leu	Ser
					805					810					815
50	AGC	TGG	TTT	GCC	ACC	GGC	ATG	GAT	GAA	GTA	GAC	AGC	CAA	TTA	GCT
	Ser	Trp	Phe	Ala	Thr	Gly	Met	Asp	Glu	Val	Asp	Ser	Gln	Leu	Ala
				820					825					830	
55	GAA	TAT	TGG	CAG	GCA	GAC	ACG	CAA	GCT	TAT	AGC	GGA	TTT	GAA	ACC
	Glu	Tyr	Trp	Gln	Ala	Asp	Thr	Gln	Ala	Tyr	Ser	Gly	Phe	Glu	Thr
			835					840					845		
60	TAT	ACC	GTC	TGG	GAT	CAC	ACC	AAC	CAG	ACA	GAC	CAA	GCA	TTT	ACC
	Tyr	Thr	Val	Trp	Asp	His	Thr	Asn	Gln	Thr	Asp	Gln	Ala	Phe	Thr
		850					855					860			
	AAT	GAG	ACA	CAA	CGT	AAC	TGG	CTG	ACG	CGA	GCG	CTT	AAA	GGC	CAA
	Asn	Glu	Thr	Gln	Arg	Asn	Trp	Leu	Thr	Arg	Ala	Leu	Lys	Gly	Gln
		865				870					875				880
65	CTA	CGC	ACT	GAG	CTC	TAC	GGT	CTG	GAC	GGA	ACA	GAT	AAG	CAA	ACA
	Leu	Arg	Thr	Glu	Leu	Tyr	Gly	Leu	Asp	Gly	Thr	Asp	Lys	Gln	Thr
					885					890					895
70	CCT	TAT	ACC	GTC	AGT	GAA	TCG	CGC	TAT	CAG	GTA	CGC	TCT	ATT	CCC
	Pro	Tyr	Thr	Val	Ser	Glu	Ser	Arg	Tyr	Gln	Val	Arg	Ser	Ile	Pro
				900					905					910	

5 AAT AAA GAA ACT GAA TTA TCT GCC TGG GTG ACT GCT ATT GAA AAT CGC 2784
 Asn Lys Glu Thr Glu Leu Ser Ala Trp Val Thr Ala Ile Glu Asn Arg
 915 920 925

10 AGC TAC CAC TAT GAA CGT ATC ATC ACT GAC CCA CAG TTC AGC CAG AGT 2832
 Ser Tyr His Tyr Glu Arg Ile Ile Thr Asp Pro Gln Phe Ser Gln Ser
 930 935 940

15 ATC AAG TTG CAA CAC GAT ATC TTT GGT CAA TCA CTG CAA AGT GTC GAT 2880
 Ile Lys Leu Gln His Asp Ile Phe Gly Gln Ser Leu Gln Ser Val Asp
 945 950 955 960

20 ATT GCC TGG CCG CGC CGC GAA AAA CCA GCA GTG AAT CCC TAC CCG CCT 2928
 Ile Ala Trp Pro Arg Arg Glu Lys Pro Ala Val Asn Pro Tyr Pro Pro
 965 970 975

25 ACC CTG CCG GAA ACG CTA TTT GAC AGC AGC TAT GAT GAT CAA CAA CAA 2976
 Thr Leu Pro Glu Thr Leu Phe Asp Ser Ser Tyr Asp Asp Gln Gln Gln
 980 985 990

30 CTA TTA CGT CTG GTG AGA CAA AAA AAT AGC TGG CAT CAC CTG ACT GAT 3024
 Leu Leu Arg Leu Val Arg Gln Lys Asn Ser Trp His His Leu Thr Asp
 995 1000 1005

35 GGG GAA AAC TGG CGA TTA GGT TTA CCG AAT GCA CAA CGC CGT GAT GTT 3072
 Gly Glu Asn Trp Arg Leu Gly Leu Pro Asn Ala Gln Arg Arg Asp Val
 1010 1015 1020

40 TAT ACT TAT GAC CGG AGC AAA ATT CCA ACC GAA GGG ATT TCC CTT GAA 3120
 Tyr Thr Tyr Asp Arg Ser Lys Ile Pro Thr Glu Gly Ile Ser Leu Glu
 1025 1030 1035 1040

45 ATC TTG CTG AAA GAT GAT GGC CTG CTA GCA GAT GAA AAA GCG GCC GTT 3168
 Ile Leu Leu Lys Asp Asp Gly Leu Leu Ala Asp Glu Lys Ala Ala Val
 1045 1050 1055

50 TAT CTG GGA CAA CAA CAG ACG TTT TAC ACC GCC GGT CAA GCG GAA GTC 3216
 Tyr Leu Gly Gln Gln Gln Thr Phe Tyr Thr Ala Gly Gln Ala Glu Val
 1060 1065 1070

55 ACT CTA GAA AAA CCC ACG TTA CAA GCA CTG GTC GCG TTC CAA GAA ACC 3264
 Thr Leu Glu Lys Pro Thr Leu Gln Ala Leu Val Ala Phe Gln Glu Thr
 1075 1080 1085

60 GCC ATG ATG GAC GAT ACC TCA TTA CAG GCG TAT GAA GGC GTG ATT GAA 3312
 Ala Met Met Asp Asp Thr Ser Leu Gln Ala Tyr Glu Gly Val Ile Glu
 1090 1095 1100

65 GAG CAA GAG TTG AAT ACC GCG CTG ACA CAG GCC GGT TAT CAG CAA GTC 3360
 Glu Gln Glu Leu Asn Thr Ala Leu Thr Gln Ala Gly Tyr Gln Gln Val
 1105 1110 1115 1120

70 GCG CGG TTG TTT AAT ACC AGA TCA GAA AGC CCG GTA TGG GCG GCA CGG 3408
 Ala Arg Leu Phe Asn Thr Arg Ser Glu Ser Pro Val Trp Ala Ala Arg
 1125 1130 1135

75 CAA GGT TAT ACC GAT TAC GGT GAC GCC GCA CAG TTC TGG CGG CCT CAG 3456
 Gln Gly Tyr Thr Asp Tyr Gly Asp Ala Ala Gln Phe Trp Arg Pro Gln
 1140 1145 1150

80 GCT CAG CGT AAC TCG TTG CTG ACA GGG AAA ACC ACA CTG ACC TGG GAT 3504
 Ala Gln Arg Asn Ser Leu Leu Thr Gly Lys Thr Thr Leu Thr Trp Asp
 1155 1160 1165

85 ACC CAT CAT TGT GTA ATA ATA CAG ACT CAA GAT GCC GCT GGA TTA ACG 3552
 Thr His His Cys Val Ile Ile Gln Thr Gln Asp Ala Ala Gly Leu Thr
 1170 1175 1180

90 ACG CAA GCC CAT TAC GAT TAT CGT TTC CTT ACA CCG GTA CAA CTG ACA 3600
 Thr Gln Ala His Tyr Asp Tyr Arg Phe Leu Thr Pro Val Gln Leu Thr

	1185	1190	1195	1200
5	GAT ATT AAT GAT AAT CAA CAT ATT GTG ACT CTG GAC GCG CTA GGT CGC 3648 Asp Ile Asn Asp Asn Gln His Ile Val Thr Leu Asp Ala Leu Gly Arg 1205 1210 1215			
10	GTA ACC ACC AGC CGG TTC TGG GGC ACA GAG GCA GGA CAA GCC GCA GGC 3696 Val Thr Thr Ser Arg Phe Trp Gly Thr Glu Ala Gly Gln Ala Ala Gly 1220 1225 1230			
15	TAT TCC AAC CAG CCC TTC ACA CCA CCG GAC TCC GTA GAT AAA GCG CTG 3744 Tyr Ser Asn Gln Pro Phe Thr Pro Pro Asp Ser Val Asp Lys Ala Leu 1235 1240 1245			
20	GCA TTA ACC GGC GCA CTC CCT GTT GCC CAA TGT TTA GTC TAT GCC GTT 3792 Ala Leu Thr Gly Ala Leu Pro Val Ala Gln Cys Leu Val Tyr Ala Val 1250 1255 1260			
25	GAT AGC TGG ATG CCG TCG TTA TCT TTG TCT CAG CTT TCT CAG TCA CAA 3840 Asp Ser Trp Met Pro Ser Leu Ser Leu Ser Gln Leu Ser Gln Ser Gln 1265 1270 1275 1280			
30	GAA GAG GCA GAA GCG CTA TGG GCG CAA CTG CGT GCC GCT CAT ATG ATT 3888 Glu Glu Ala Glu Ala Leu Trp Ala Gln Leu Arg Ala Ala His Met Ile 1285 1290 1295			
35	ACC GAA GAT GGG AAA GTG TGT GCG TTA AGC GGG AAA CGA GGA ACA AGC 3936 Thr Glu Asp Gly Lys Val Cys Ala Leu Ser Gly Lys Arg Gly Thr Ser 1300 1305 1310			
40	CAT CAG AAC CTG ACG ATT CAA CTT ATT TCG CTA TTG GCA AGT ATT CCC 3984 His Gln Asn Leu Thr Ile Gln Leu Ile Ser Leu Leu Ala Ser Ile Pro 1315 1320 1325			
45	CGT TTA CCG CCA CAT GTA CTG GGG ATC ACC ACT GAT CGC TAT GAT AGC 4032 Arg Leu Pro Pro His Val Leu Gly Ile Thr Thr Asp Arg Tyr Asp Ser 1330 1335 1340			
50	GAT CCG CAA CAG CAG CAC CAA CAG ACG GTG AGC TTT AGT GAC GGT TTT 4080 Asp Pro Gln Gln Gln His Gln Gln Thr Val Ser Phe Ser Asp Gly Phe 1345 1350 1355 1360			
55	GGC CGG TTA CTC CAG AGT TCA GCT CGT CAT GAG TCA GGT GAT GCC TGG 4128 Gly Arg Leu Leu Gln Ser Ser Ala Arg His Glu Ser Gly Asp Ala Trp 1365 1370 1375			
60	CAA CGT AAA GAG GAT GGC GGG CTG GTC GTG GAT GCA AAT GGC GTT CTG 4176 Gln Arg Lys Glu Asp Gly Gly Leu Val Val Asp Ala Asn Gly Val Leu 1380 1385 1390			
65	GTC AGT GCC CCT ACA GAC ACC CGA TGG GCC GTT TCC GGT CGC ACA GAA 4224 Val Ser Ala Pro Thr Asp Thr Arg Trp Ala Val Ser Gly Arg Thr Glu 1395 1400 1405			
70	TAT GAC GAC AAA GGC CAA CCT GTG CGT ACT TAT CAA CCC TAT TTT CTA 4272 Tyr Asp Asp Lys Gly Gln Pro Val Arg Thr Tyr Gln Pro Tyr Phe Leu 1410 1415 1420			
75	AAT GAC TGG CGT TAC GTT AGT GAT GAC AGC GCA CGA GAT GAC CTG TTT 4320 Asn Asp Trp Arg Tyr Val Ser Asp Asp Ser Ala Arg Asp Asp Leu Phe 1425 1430 1435 1440			
80	GCC GAT ACC CAC CTT TAT GAT CCA TTG GGA CGG GAA TAC AAA GTC ATC 4368 Ala Asp Thr His Leu Tyr Asp Pro Leu Gly Arg Glu Tyr Lys Val Ile 1445 1450 1455			
85	ACT GCT AAG AAA TAT TTG CGA GAA AAG CTG TAC ACC CCG TGG TTT ATT 4416 Thr Ala Lys Lys Tyr Leu Arg Glu Lys Leu Tyr Thr Pro Trp Phe Ile 1460 1465 1470			
90	GTC AGT GAG GAT GAA AAC GAT ACA GCA TCA AGA ACC CCA TAG 4458			

Val Ser Glu Asp Glu Asn Asp Thr Ala Ser Arg Thr Pro *
 1475 1480 1485

5 (2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1485 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear


10

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32 (TcaC protein):

15 Met Gln Asp Ser Pro Glu Val Ser Ile Thr Thr Leu Ser Leu Pro Lys
 1 5 10 15
 Gly Gly Gly Ala Ile Asn Gly Met Gly Glu Ala Leu Asn Ala Ala Gly
 20 20 25 30
 Pro Asp Gly Met Ala Ser Leu Ser Leu Pro Leu Pro Leu Ser Thr Gly
 35 40 45
 Arg Gly Thr Ala Pro Gly Leu Ser Leu Ile Tyr Ser Asn Ser Ala Gly
 50 55 60
 Asn Gly Pro Phe Gly Ile Gly Trp Gln Cys Gly Val Met Ser Ile Ser
 65 70 75 80
 Arg Arg Thr Gln His Gly Ile Pro Gln Tyr Gly Asn Asp Asp Thr Phe
 85 90 95
 Leu Ser Pro Gln Gly Glu Val Met Asn Ile Ala Leu Asn Asp Gln Gly
 100 105 110
 Gln Pro Asp Ile Arg Gln Asp Val Lys Thr Leu Gln Gly Val Thr Leu
 115 120 125
 Pro Ile Ser Tyr Thr Val Thr Arg Tyr Gln Ala Arg Gln Ile Leu Asp
 130 135 140
 Phe Ser Lys Ile Glu Tyr Trp Gln Pro Ala Ser Gly Gln Glu Gly Arg
 145 150 155 160
 Ala Phe Trp Leu Ile Ser Thr Pro Asp Gly His Leu His Ile Leu Gly
 165 170 175
 Lys Thr Ala Gln Ala Cys Leu Ala Asn Pro Gln Asn Asp Gln Gln Ile
 180 185 190
 Ala Gln Trp Leu Leu Glu Glu Thr Val Thr Pro Ala Gly Glu His Val
 195 200 205
 Ser Tyr Gln Tyr Arg Ala Glu Asp Glu Ala His Cys Asp Asp Asn Glu
 210 215 220
 Lys Thr Ala His Pro Asn Val Thr Ala Gln Arg Tyr Leu Val Gln Val
 225 230 235 240
 Asn Tyr Gly Asn Ile Lys Pro Gln Ala Ser Leu Phe Val Leu Asp Asn
 245 250 255
 Ala Pro Pro Ala Pro Glu Glu Trp Leu Phe His Leu Val Phe Asp His
 260 265 270
 Gly Glu Arg Asp Thr Ser Leu His Thr Val Pro Thr Trp Asp Ala Gly
 275 280 285
 Thr Ala Gln Trp Ser Val Arg Pro Asp Ile Phe Ser Arg Tyr Glu Tyr

	290		295		300												
	Gly	Phe	Glu	Val	Arg	Thr	Arg	Arg	Leu	Cys	Gln	Gln	Val	Leu	Met	Phe	
	305					310					315					320	
5	His	Arg	Thr	Ala	Leu	Met	Ala	Gly	Glu	Ala	Ser	Thr	Asn	Asp	Ala	Pro	
					325					330					335		
	Glu	Leu	Val	Gly	Arg	Leu	Ile	Leu	Glu	Tyr	Asp	Lys	Asn	Ala	Ser	Val	
10				340					345					350			
	Thr	Thr	Leu	Ile	Thr	Ile	Arg	Gln	Leu	Ser	His	Glu	Ser	Asp	Gly	Arg	
			355					360					365				
15	Pro	Val	Thr	Gln	Pro	Pro	Leu	Glu	Leu	Ala	Trp	Gln	Arg	Phe	Asp	Leu	
		370					375					380					
	Glu	Lys	Ile	Pro	Thr	Trp	Gln	Arg	Phe	Asp	Ala	Leu	Asp	Asn	Phe	Asn	
20		385				390					395					400	
	Ser	Gln	Gln	Arg	Tyr	Gln	Leu	Val	Asp	Leu	Arg	Gly	Glu	Gly	Leu	Pro	
				405					410						415		
25	Gly	Met	Leu	Tyr	Gln	Asp	Arg	Gly	Ala	Trp	Trp	Tyr	Lys	Ala	Pro	Gln	
				420					425					430			
	Arg	Gln	Glu	Asp	Gly	Asp	Ser	Asn	Ala	Val	Thr	Tyr	Asp	Lys	Ile	Ala	
			435					440					445				
30	Pro	Leu	Pro	Thr	Leu	Pro	Asn	Leu	Gln	Asp	Asn	Ala	Ser	Leu	Met	Asp	
		450					455					460					
	Ile	Asn	Gly	Asp	Gly	Gln	Leu	Asp	Trp	Val	Val	Thr	Ala	Ser	Gly	Ile	
35		465				470					475					480	
	Arg	Gly	Tyr	His	Ser	Gln	Gln	Pro	Asp	Gly	Lys	Trp	Thr	His	Phe	Thr	
				485					490						495		
40	Pro	Ile	Asn	Ala	Leu	Pro	Val	Glu	Tyr	Phe	His	Pro	Ser	Ile	Gln	Phe	
			500					505						510			
	Ala	Asp	Leu	Thr	Gly	Ala	Gly	Leu	Ser	Asp	Leu	Val	Leu	Ile	Gly	Pro	
			515				520					525					
45	Lys	Ser	Val	Arg	Leu	Tyr	Ala	Asn	Gln	Arg	Asn	Gly	Trp	Arg	Lys	Gly	
		530					535					540					
	Glu	Asp	Val	Pro	Gln	Ser	Thr	Gly	Ile	Thr	Leu	Pro	Val	Thr	Gly	Thr	
50		545				550					555					560	
	Asp	Ala	Arg	Lys	Leu	Val	Ala	Phe	Ser	Asp	Met	Leu	Gly	Ser	Gly	Gln	
				565					570					575			
55	Gln	His	Leu	Val	Glu	Ile	Lys	Gly	Asn	Arg	Val	Thr	Cys	Trp	Pro	Asn	
			580					585					590				
	Leu	Gly	His	Gly	Arg	Phe	Gly	Gln	Pro	Leu	Thr	Leu	Ser	Gly	Phe	Ser	
			595				600					605					
60	Gln	Pro	Glu	Asn	Ser	Phe	Asn	Pro	Glu	Arg	Leu	Phe	Leu	Ala	Asp	Ile	
		610					615					620					
	Asp	Gly	Ser	Gly	Thr	Thr	Asp	Leu	Ile	Tyr	Ala	Gln	Ser	Gly	Ser	Leu	
65		625				630					635					640	
	Leu	Ile	Tyr	Leu	Asn	Gln	Ser	Gly	Asn	Gln	Phe	Asp	Ala	Pro	Leu	Thr	
				645				650						655			
70	Leu	Ala	Leu	Pro	Glu	Gly	Val	Gln	Phe	Asp	Asn	Thr	Cys	Gln	Leu	Gln	
			660					665					670				

Val Ala Asp Ile  Gly Leu Gly Ile Ala Ser Leu Leu Thr Val
675 680 685

5 Pro His Ile Ala Pro His His Trp Arg Cys Asp Leu Ser Leu Thr Lys
690 695 700

Pro Trp Leu Leu Asn Val Met Asn Asn Asn Arg Gly Ala His His Thr
705 710 715 720

10 Leu His Tyr Arg Ser Ser Ala Gln Phe Trp Leu Asp Glu Lys Leu Gln
725 730 735

Leu Thr Lys Ala Gly Lys Ser Pro Ala Cys Tyr Leu Pro Phe Pro Met
740 745 750

15 His Leu Leu Trp Tyr Thr Glu Ile Gln Asp Glu Ile Ser Gly Asn Arg
755 760 765

20 Leu Thr Ser Glu Val Asn Tyr Ser His Gly Val Trp Asp Gly Lys Glu
770 775 780

Arg Glu Phe Arg Gly Phe Gly Cys Ile Lys Gln Thr Asp Thr Thr Thr
785 790 795 800

25 Phe Ser His Gly Thr Ala Pro Glu Gln Ala Ala Pro Ser Leu Ser Ile
805 810 815

Ser Trp Phe Ala Thr Gly Met Asp Glu Val Asp Ser Gln Leu Ala Thr
820 825 830

30 Glu Tyr Trp Gln Ala Asp Thr Gln Ala Tyr Ser Gly Phe Glu Thr Arg
835 840 845

Tyr Thr Val Trp Asp His Thr Asn Gln Thr Asp Gln Ala Phe Thr Pro
850 855 860

35 Asn Glu Thr Gln Arg Asn Trp Leu Thr Arg Ala Leu Lys Gly Gln Leu
865 870 875 880

40 Leu Arg Thr Glu Leu Tyr Gly Leu Asp Gly Thr Asp Lys Gln Thr Val
885 890 895

Pro Tyr Thr Val Ser Glu Ser Arg Tyr Gln Val Arg Ser Ile Pro Val
900 905 910

45 Asn Lys Glu Thr Glu Leu Ser Ala Trp Val Thr Ala Ile Glu Asn Arg
915 920 925

Ser ~~Tyr His Tyr~~ Glu Arg Ile Ile Thr Asp Pro Gln Phe Ser Gln Ser
930 935 940

Ile Lys Leu Gln His Asp Ile Phe Gly Gln Ser Leu Gln Ser Val Asp
945 950 955 960

55 Ile Ala Trp Pro Arg Arg Glu Lys Pro Ala Val Asn Pro Tyr Pro Pro
965 970 975

Thr Leu Pro Glu Thr Leu Phe Asp Ser Ser Tyr Asp Asp Gln Gln Gln
980 985 990

60 Leu Leu Arg Leu Val Arg Gln Lys Asn Ser Trp His His Leu Thr Asp
995 1000 1005

Gly Glu Asn Trp Arg Leu Gly Leu Pro Asn Ala Gln Arg Arg Asp Val
1010 1015 1020

65 Tyr Thr Tyr Asp Arg Ser Lys Ile Pro Thr Glu Gly Ile Ser Leu Glu
1025 1030 1035 1040

70 Ile Leu Leu Lys Asp Asp Gly Leu Leu Ala Asp Glu Lys Ala Ala Val
1045 1050 1055

Tyr Leu Gly Gln Gln Thr Phe Tyr Thr Ala Gly Gln Ala Glu Val
 1060 1065 1070
 5 Thr Leu Glu Lys Pro Thr Leu Gln Ala Leu Val Ala Phe Gln Glu Thr
 1075 1080 1085
 Ala Met Met Asp Asp Thr Ser Leu Gln Ala Tyr Glu Gly Val Ile Glu
 1090 1095 1100
 10 Glu Gln Glu Leu Asn Thr Ala Leu Thr Gln Ala Gly Tyr Gln Gln Val
 1105 1110 1115 1120
 Ala Arg Leu Phe Asn Thr Arg Ser Glu Ser Pro Val Trp Ala Ala Arg
 1125 1130 1135
 15 Gln Gly Tyr Thr Asp Tyr Gly Asp Ala Ala Gln Phe Trp Arg Pro Gln
 1140 1145 1150
 20 Ala Gln Arg Asn Ser Leu Leu Thr Gly Lys Thr Thr Leu Thr Trp Asp
 1155 1160 1165
 Thr His His Cys Val Ile Ile Gln Thr Gln Asp Ala Ala Gly Leu Thr
 1170 1175 1180
 25 Thr Gln Ala His Tyr Asp Tyr Arg Phe Leu Thr Pro Val Gln Leu Thr
 1185 1190 1195 1200
 Asp Ile Asn Asp Asn Gln His Ile Val Thr Leu Asp Ala Leu Gly Arg
 1205 1210 1215
 30 Val Thr Thr Ser Arg Phe Trp Gly Thr Glu Ala Gly Gln Ala Ala Gly
 1220 1225 1230
 35 Tyr Ser Asn Gln Pro Phe Thr Pro Pro Asp Ser Val Asp Lys Ala Leu
 1235 1240 1245
 Ala Leu Thr Gly Ala Leu Pro Val Ala Gln Cys Leu Val Tyr Ala Val
 1250 1255 1260
 40 Asp Ser Trp Met Pro Ser Leu Ser Leu Ser Gln Leu Ser Gln Ser Gln
 1265 1270 1275 1280
 Glu Glu Ala Glu Ala Leu Trp Ala Gln Leu Arg Ala Ala His Met Ile
 1285 1290 1295
 45 Thr Glu Asp Gly Lys Val Cys Ala Leu Ser Gly Lys Arg Gly Thr Ser
 1300 1305 1310
 50 His Gln Asn Leu Thr Ile Gln Leu Ile Ser Leu Leu Ala Ser Ile Pro
 1315 1320 1325
 Arg Leu Pro Pro His Val Leu Gly Ile Thr Thr Asp Arg Tyr Asp Ser
 1330 1335 1340
 55 Asp Pro Gln Gln Gln His Gln Gln Thr Val Ser Phe Ser Asp Gly Phe
 1345 1350 1355 1360
 60 Gly Arg Leu Leu Gln Ser Ser Ala Arg His Glu Ser Gly Asp Ala Trp
 1365 1370 1375
 Gln Arg Lys Glu Asp Gly Gly Leu Val Val Asp Ala Asn Gly Val Leu
 1380 1385 1390
 65 Val Ser Ala Pro Thr Asp Thr Arg Trp Ala Val Ser Gly Arg Thr Glu
 1395 1400 1405
 Tyr Asp Asp Lys Gly Gln Pro Val Arg Thr Tyr Gln Pro Tyr Phe Leu
 1410 1415 1420
 70 Asn Asp Trp Arg Tyr Val Ser Asp Asp Ser Ala Arg Asp Asp Leu Phe

1425 1430 . 1435 1440

Ala Asp Thr His Leu Tyr Asp Pro Leu Gly Arg Glu Tyr Lys Val Ile
 1445 1450 1455

5 Thr Ala Lys Lys Tyr Leu Arg Glu Lys Leu Tyr Thr Pro Trp Phe Ile
 1460 1465 1470

10 Val Ser Glu Asp Glu Asn Asp Thr Ala Ser Arg Thr Pro *
 1475 1480 1485

(2) INFORMATION FOR SEQ ID NO:33:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3288 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33 (tcaA gene):

25 ATG GTG ACT GTT ATG CAA AAT AAA ATA TCA TTT TTA TCA GGT ACA TCC 48
 Met Val Thr Val Met Gln Asn Lys Ile Ser Phe Leu Ser Gly Thr Ser
 1 5 10 15

30 GAA CAG CCC CTG CTT GAC GCC GGT TAT CAA AAC GTA TTT GAT ATC GCA 96
 Glu Gln Pro Leu Leu Asp Ala Gly Tyr Gln Asn Val Phe Asp Ile Ala
 20 25 30

35 TCA ATC AGC CGG GCT ACT TTC GTT CAA TCC GTT CCC ACC CTG CCC GTT 144
 Ser Ile Ser Arg Ala Thr Phe Val Gln Ser Val Pro Thr Leu Pro Val
 35 40 45

40 AAA GAG GCT CAT ACC GTC TAT CGT CAG GCG CGG CAA CGT GCG GAA AAT 192
 Lys Glu Ala His Thr Val Tyr Arg Gln Ala Arg Gln Arg Ala Glu Asn
 50 55 60

45 CTG AAA TCC CTC TAC CGA GCC TGG CAA TTG CGT CAG GAG CCG GTT ATT 240
 Leu Lys Ser Leu Tyr Arg Ala Trp Gln Leu Arg Gln Glu Pro Val Ile
 65 70 75 80

50 AAA GGG CTG GCT AAA CTT AAC CTA CAA TCC AAC GTT TCT GTG CTT CAA 288
 Lys Gly Leu Ala Lys Leu Asn Leu Gln Ser Asn Val Ser Val Leu Gln
 85 90 95

55 GAT GCT TTG GTA GAG AAT ATT GGC GGT GAT GGG GAT TTC AGC GAT TTA 336
 Asp Ala Leu Val Glu Asn Ile Gly Gly Asp Gly Asp Phe Ser Asp Leu
 100 105 110

60 ATG AAC CGT GCC AGT CAA TAT GCT GAC GCT GCC TCT ATT CAA TCC CTA 384
 Met Asn Arg Ala Ser Gln Tyr Ala Asp Ala Ala Ser Ile Gln Ser Leu
 115 120 125

65 TTT TCA CCG GGC CGT TAT GCT TCC GCA CTC TAC AGA GTT GCT AAA GAT 432
 Phe Ser Pro Gly Arg Tyr Ala Ser Ala Leu Tyr Arg Val Ala Lys Asp
 130 135 140

70 CTG CAT AAA TCA GAT TCC AGT TTG CAT ATT GAT AAT CGC CGC GCT GAT 480
 Leu His Lys Ser Asp Ser Ser Leu His Ile Asp Asn Arg Arg Ala Asp
 145 150 155 160

75 CTG AAG GAT CTG ATA TTA AGC GAA ACG ACG ATG AAT AAA GAG GTC ACT 528
 Leu Lys Asp Leu Ile Leu Ser Glu Thr Thr Met Asn Lys Glu Val Thr
 165 170 175

80 TCC CTT GAT ATC TTG TTG GAT GTG CTA CAA AAA GGC GGT AAA GAT ATT 576
 Ser Leu Asp Ile Leu Leu Asp Val Leu Gln Lys Gly Gly Lys Asp Ile

	180								185								
5	ACT Thr	GAG Glu	CTG Leu 195	TCC Ser	GGC Gly	GCA Ala	TTC Phe	TTC Phe 200	CCA Pro	ATG Met	ACG Thr	TTA Leu 205	CCT Pro	TAT Tyr	GAC Asp	GAT Asp	624
10	CAT His 210	CTG Leu	TCG Ser	CAA Gln	ATC Ile	GAT Asp	TCC Ser 215	GCT Ala	TTA Leu	TCG Ser	GCA Ala	CAA Gln 220	GCC Ala	AGA Arg	ACG Thr	CTG Leu	672
15	AAC Asn 225	GGT Gly	GTG Val	TGG Trp	AAT Asn 230	ACT Thr	TTG Leu 235	ACA Thr	GAT Asp	ACC Thr	ACG Thr 235	GCA Ala	CAA Gln	GCG Ala	GTT Val	TCA Ser 240	720
20	GAA Glu	CAA Gln	ACC Thr	AGT Ser 245	AAT Asn	ACG Thr	AAT Asn	ACA Thr	CGC Arg 250	AAA Lys	CTG Leu	TTC Phe	GCT Ala	GCC Ala	CAA Gln 255	GAT Asp	768
25	GGT Gly	AAT Asn	CAA Gln	GAT Asp 260	ACA Thr	TTT Phe	TTT Phe	TCC Ser 265	GGA Gly	AAC Asn	ACT Thr	TTT Phe	TAT Tyr	TTC Phe 270	AAA Lys	GCG Ala	816
30	GTG Val	GGA Gly	TTC Phe 275	AGC Ser	GGG Gly	CAA Gln	CCT Pro	ATG Met 280	GTT Val	TAC Tyr	CTG Leu	TCA Ser 285	CAG Gln	TAC Tyr	ACC Thr	AGC Ser	864
35	GGG Gly 290	AAC Asn	GGC Gly	ATT Ile	GTC Val	GGC Gly	GCA Ala 295	CAA Gln	TTG Leu	ATT Ile	GCA Ala 300	GGT Gly 305	AAT Asn	CCA Pro	GAC Asp	CAA Gln	912
40	GCC Ala 305	GCC Ala	GCC Ala	GCA Ala	ATA Ile 310	GTC Val	GCA Ala 315	CCG Pro	TTG Leu	AAA Lys	CTC Leu 315	ACT Thr	TGG Trp	TCA Ser	ATG Met	GCA Ala 320	960
45	AAA Lys	CAG Gln	TGT Cys	TAC Tyr 325	CTC Leu	GTC Val	GCT Ala	CCC Pro	GAT Asp 330	GGT Gly	ACA Thr	ACG Thr	ATG Met	GGA Gly 335	GAC Asp		1008
50	GGT Gly	AAT Asn	GTT Val 340	CTG Leu	ACC Thr	GGC Gly	TGT Cys	TTC Phe 345	TTA Leu	AGA Arg	GGC Gly	AAC Asn	AGC Ser	CCA Pro 350	ACT Thr	AAC Asn	1056
55	CCG Pro	GAT Asp	AAA Lys 355	GAC Asp	GGT Gly	ATT Ile	TTT Phe 360	GCT Ala	CAG Gln	GTA Val	GCC Ala	AAC Asn	AAA Lys 365	TCA Ser	GGC Gly	AGT Ser	1104
60	ACT Thr 370	CAG Gln	CCT Pro	TTG Leu	CCA Pro	AGC Ser	TTC Phe 375	CAT His	CTG Leu	CCG Pro	GTC Val 380	ACA Thr	CTG Leu	GAA Glu	CAC His	AGC Ser	1152
65	GAG Glu 385	AAT Asn	AAA Lys	GAT Asp	CAG Gln	TAC Tyr 390	TAT Tyr	CTG Leu	AAA Lys	ACA Thr	GAG Glu 395	CAG Gln	GGT Gly	TAT Tyr	ATC Ile	ACG Thr 400	1200
70	GTA Val	GAT Asp	AGT Ser	TCC Ser 405	GGA Gly	CAG Gln	TCA Ser	AAT Asn	TGG Trp 410	AAA Lys	AAC Asn	GCG Ala	CTG Leu	GTT Val 415	ATC Ile	AAT Asn	1248
75	GGG Gly	ACA Thr	AAA Lys	GAC Asp 420	AAG Lys	GGG Gly	CTG Leu	TTA Leu 425	TTA Leu	ACC Thr	TTT Phe	TGC Cys	AGC Ser	GAT Asp 430	AGC Ser	TCA Ser	1296
80	GGC Gly	ACT Thr	CCG Pro 435	ACA Thr	AAC Asn	CCT Pro	GAT Asp 440	GAT Asp	GTG Val	ATT Ile	CCT Pro	CCC Pro	GCT Ala 445	ATC Ile	AAT Asn	GAT Asp	1344
85	ATT Ile 450	CCA Pro	TCG Ser	CCG Pro	CCA Pro	GCC Ala	CGC Arg 455	GAA Glu	ACA Thr	CTG Leu	TCA Ser	CTG Leu 460	ACG Thr	CCG Pro	GTC Val	AGT Ser	1392
90	TAT	CAA	TTG	ATG	ACC	AAT	CCG	GCA	CCG	ACA	GAA	GAT	GAT	ATT	ACC	AAC	1440

	Tyr	Gln	Leu	Met	Thr	Asn	Pro	Ala	Pro	Thr	Glu	Asp	Asp	Ile	Thr	Asn	
	465					470					475					480	
5	CAT	TAT	GGT	TTT	AAC	GGC	GCT	AGC	TTA	CGG	GCT	TCT	CCA	TTG	TCA	ACC	1488
	His	Tyr	Gly	Phe	Asn	Gly	Ala	Ser	Leu	Arg	Ala	Ser	Pro	Leu	Ser	Thr	
					485					490				495			
10	AGC	GAG	TTG	ACC	AGC	AAA	CTG	AAT	TCT	ATC	GAT	ACT	TTC	TGT	GAG	AAG	1536
	Ser	Glu	Leu	Thr	Ser	Lys	Leu	Asn	Ser	Ile	Asp	Thr	Phe	Cys	Glu	Lys	
				500					505					510			
15	ACC	CGG	TTA	AGC	TTC	AAT	CAG	TTA	ATG	GAT	TTG	ACC	GCT	CAG	CAA	TCT	1584
	Thr	Arg	Leu	Ser	Phe	Asn	Gln	Leu	Met	Asp	Leu	Thr	Ala	Gln	Gln	Ser	
				515				520					525				
20	TAC	AGT	CAA	AGC	AGC	ATT	GAT	GCG	AAA	GCA	GCC	AGC	CGC	TAT	GTT	CGT	1632
	Tyr	Ser	Gln	Ser	Ser	Ile	Asp	Ala	Lys	Ala	Ala	Ser	Arg	Tyr	Val	Arg	
				530			535					540					
25	TTT	GGG	GAA	ACC	ACC	CCA	ACC	CGC	GTC	AAT	GTC	TAC	GGT	GCC	GCT	TAT	1680
	Phe	Gly	Glu	Thr	Thr	Pro	Thr	Arg	Val	Asn	Val	Tyr	Gly	Ala	Ala	Tyr	
						550					555					560	
30	CTG	AAC	AGC	ACA	CTG	GCA	GAC	GCG	GCT	GAT	GGT	CAA	TAT	CTG	TGG	ATT	1728
	Leu	Asn	Ser	Thr	Leu	Ala	Asp	Ala	Ala	Asp	Gly	Gln	Tyr	Leu	Trp	Ile	
					565					570					575		
35	CAG	ACT	GAT	GGC	AAG	AGC	CTA	AAT	TTC	ACT	GAC	GAT	ACG	GTA	GTC	GCC	1776
	Gln	Thr	Asp	Gly	Lys	Ser	Leu	Asn	Phe	Thr	Asp	Asp	Thr	Val	Val	Ala	
				580					585					590			
40	TTA	GCC	GGT	CGC	GCT	GAA	AAG	CTG	GTA	CGT	TTA	TCA	TCC	CAG	ACC	GGG	1824
	Leu	Ala	Gly	Arg	Ala	Glu	Lys	Leu	Val	Arg	Leu	Ser	Ser	Gln	Thr	Gly	
				595				600					605				
45	CTA	TCA	TTT	GAA	GAA	TTG	GAC	TGG	CTG	ATT	GCC	AAT	GCC	AGT	CGT	AGT	1872
	Leu	Ser	Phe	Glu	Glu	Leu	Asp	Trp	Leu	Ile	Ala	Asn	Ala	Ser	Arg	Ser	
				610			615					620					
50	GTG	CCG	GAC	CAC	CAC	GAC	AAA	ATT	GTG	CTG	GAT	AAG	CCG	GTC	CTT	GAA	1920
	Val	Pro	Asp	His	His	Asp	Lys	Ile	Val	Leu	Asp	Lys	Pro	Val	Leu	Glu	
						630					635					640	
55	GCA	CTG	GCA	GAG	TAT	GTC	AGC	CTA	AAA	CAG	CGC	TAT	GGG	CTT	GAT	GCC	1968
	Ala	Leu	Ala	Glu	Val	Ser	Leu	Lys	Gln	Arg	Tyr	Gly	Leu	Asp	Ala		
					645				650					655			
60	AAT	ACC	TTT	GCG	ACC	TTC	ATT	AGT	GCA	GTA	AAT	CCT	TAT	ACG	CCA	GAT	2016
	Asn	Thr	Phe	Ala	Thr	Phe	Ile	Ser	Ala	Val	Asn	Pro	Tyr	Thr	Pro	Asp	
				660					665					670			
65	CAG	ACA	CCC	AGT	TTC	TAT	GAA	ACC	GCT	TTC	CGC	TCT	GCC	GAC	GGT	AAT	2064
	Gln	Thr	Pro	Ser	Phe	Tyr	Glu	Thr	Ala	Phe	Arg	Ser	Ala	Asp	Gly	Asn	
				675				680					685				
70	CAT	GTC	ATT	GCG	CTA	GGT	ACA	GAG	GTG	AAA	TAT	GCA	GAA	AAT	GAG	CAG	2112
	His	Val	Ile	Ala	Leu	Gly	Thr	Glu	Val	Lys	Tyr	Ala	Glu	Asn	Glu	Gln	
						695						700					
75	GAT	GAG	TTA	GCC	GCC	ATA	TGC	TGC	AAA	GCA	TTG	GGT	GTC	ACC	AGT	GAT	2160
	Asp	Glu	Leu	Ala	Ala	Ile	Cys	Cys	Lys	Ala	Leu	Gly	Val	Thr	Ser	Asp	
						710					715					720	
80	GAA	CTG	CTC	CGT	ATT	GGT	CGC	TAT	TGC	TTC	GGT	AAT	GCA	GGC	AGT	TTT	2208
	Glu	Leu	Leu	Arg	Ile	Gly	Arg	Tyr	Cys	Phe	Gly	Asn	Ala	Gly	Ser	Phe	
					725					730					735		
85	ACC	TTG	GAT	GAA	TAT	ACC	GCC	AGT	CAG	TTG	TAT	CGC	TTC	GGC	GCC	ATT	2256
	Thr	Leu	Asp	Glu	Tyr	Thr	Ala	Ser	Gln	Leu	Tyr	Arg	Phe	Gly	Ala	Ile	
					740				745					750			

	CCC Pro	CGT Arg	TTG Leu 755	TTT Phe	GGG Gly	GGG Leu	ACA Thr	TTT Phe 760	GCC Ala	CAA Gln	GCC Ala	GAA Glu	ATT Ile 765	TTT Leu	TGG Trp	CGT Arg	2304
5	CTG Leu 770	ATG Met	GAA Glu 770	GGC Gly	GGA Gly	AAA Lys	GAT Asp 775	ATC Ile	TTA Leu	TTG Leu	CAA Gln	CAG Gln 780	TTA Leu	GGT Gly	CAG Gln	GCA Ala	2352
10	AAA Lys 785	TCC Ser	CTG Leu	CAA Gln	CCA Pro	CTG Leu 790	GCT Ala	ATT Ile	TTA Leu	CGC Arg	CGT Arg 795	ACC Thr	GAG Glu	CAG Gln	GTG Val	CTG Leu 800	2400
15	GAT Asp	TGG Trp	ATG Met	TCG Ser	TCC Ser 805	GTA Val	AAT Asn	CTA Leu	AGT Ser	CTG Leu 810	ACT Thr	TAT Tyr	CTG Leu	CAA Gln	GGG Gly 815	ATG Met	2448
20	GTA Val	AGT Ser	ACG Thr	CAA Gln 820	TGG Trp	AGC Ser	GGT Gly	ACC Thr	GCC Ala 825	ACC Thr	GCT Ala	GAG Glu	ATG Met	TTC Phe 830	AAT Asn	TTC Phe	2496
25	TTG Leu	GAA Glu 835	AAC Asn	GTT Val	TGT Cys	GAC Asp	AGC Ser	GTG Val 840	AAT Asn	AGT Ser	CAA Gln	GCT Ala 845	GCC Ala	ACT Thr	AAA Lys	GAA Glu	2544
30	ACA Thr 850	ATG Met	GAT Asp	TCG Ser	GCG Ala	TTA Leu 855	CAG Gln	CAG Gln	AAA Lys	GTG Val	CTG Leu	CGG Arg 860	GCG Ala	CTA Leu	AGC Ser	GCC Ala	2592
35	GGT Gly 865	TTC Phe	GGC Gly	ATT Ile	AAG Lys 870	AGC Ser	AAT Asn	GTG Val	ATG Met	GGT Gly 875	ATC Ile	GTC Val	ACC Thr	TTC Phe	TGG Trp	CTG Leu 880	2640
40	GAG Glu	AAA Lys	ATC Ile	ACA Thr	ATC Ile 885	GGT Gly	AGT Ser	GAT Asp	AAT Asn	CCT Pro 890	TTT Phe	ACA Thr	TTG Leu	GCA Ala	AAC Asn 895	TAC Tyr	2688
45	TGG Trp	CAT His	GAT Asp	ATT Ile 900	CAA Gln	ACC Thr	CTG Leu	TTT Phe	AGC Ser 905	CAT His	GAC Asp	AAT Asn	GCC Ala	ACG Thr 910	TTA Leu	GAG Glu	2736
50	TCC Ser	TTA Leu 915	CAA Gln	ACC Thr	GAC Asp	ACT Thr	TCT Ser	CTG Leu 920	GTA Val	ATT Ile	GCT Ala	ACT Thr	CAG Gln 925	CAA Gln	CTT Leu	AGC Ser	2784
55	CAG Gln 930	CTA Leu	GTG Val	TTA Leu	ATT Ile	GTG Val	AAA Lys 935	TGG Trp	CTG Leu	AGC Ser	CTG Leu	ACC Thr 940	GAG Glu	CAG Gln	GAT Asp	CTG Leu	2832
60	CAA Gln 945	TTA Leu	CTG Leu	ACA Thr	ACC Thr	TAT Tyr 950	CCC Pro	GAA Glu	CGT Arg	TTA Leu	ATC Ile 955	AAC Asn	GGC Gly	ATC Ile	ACG Thr	AAT Asn 960	2880
65	GTT Val	CCT Pro	GTA Val	CCC Pro	AAT Asn 965	CCG Pro	GAG Glu	CTA Leu	TTA Leu	CTC Leu 970	ACG Thr	CTA Leu	TCA Ser	CGT Arg	TTT Phe 975	AAG Lys	2928
70	CAG Gln	TGG Trp	GAA Glu 980	ACT Thr	CAA Gln	GTC Val	ACC Thr	GTT Val	TCC Ser 985	CGT Arg	GAT Asp	GAA Glu	GCG Ala	ATG Met 990	CGC Arg	TGT Cys	2976
75	TTC Phe	GAT Asp 995	CAA Gln	TTA Leu	AAT Asn	GCC Ala	AAT Asn	GAT Asp 1000	ATG Met	ACG Thr	ACT Thr	GAA Glu 1005	AAT Asn	GCA Ala	GGT Gly	TCA Ser	3024
80	CTG Leu 1010	ATC Ile	GCC Ala	ACA Thr	TTG Leu	TAT Tyr	GAG Glu 1015	ATG Met	GAT Asp	AAA Lys	GGT Gly 1020	ACG Thr	GGA Gly	GCG Ala	CAA Gln	GTT Val	3072
85	AAT Asn 1025	ACC Thr	TTG Leu	CTA Leu	TTA Leu	GGT Gly 1030	GAA Glu	AAT Asn	AAC Asn	TGG Trp	CCG Pro 1035	AAA Lys	AGT Ser	TTT Phe	ACC Thr	TCT Ser 1040	3120

CTC TGG CAA CTT CTG ACC TGG TTA CGC GTC GGG CAA AGA CTG AAT GTC 3168
 Leu Trp Gln Leu Leu Thr Trp Leu Arg Val Gly Gln Arg Leu Asn Val 1055
 5
 GGT AGT ACC ACT CTG GGC AAT CTG TTG TCC ATG ATG CAA GCA GAC CCT 3216
 Gly Ser Thr Thr Leu Gly Asn Leu Leu Ser Met Met Gln Ala Asp Pro 1070
 10
 GCT GCC GAG AGT AGC GCT TTA TTG GCA TCA GTA GCC CAA AAC TTA AGT 3264
 Ala Ala Glu Ser Ser Ala Leu Leu Ala Ser Val Ala Gln Asn Leu Ser 1085
 15
 GCC GCA ATC AGC AAT CGT CAG TAA 3288
 Ala Ala Ile Ser Asn Arg Gln *** 1095
 1090

(2) INFORMATION FOR SEQ ID NO:34:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34 (TcaA protein):

Features	From	To	Description
	254	267	SEQ ID NO:15
	254	492	TcaA ₁₁ peptide

30

Met Val Thr Val Met Gln Asn Lys Ile Ser Phe Leu Ser Gly Thr Ser
 1 5 10 15
 35
 Glu Gln Pro Leu Leu Asp Ala Gly Tyr Gln Asn Val Phe Asp Ile Ala
 20 25 30
 40
 Ser Ile Ser Arg Ala Thr Phe Val Gln Ser Val Pro Thr Leu Pro Val
 35 40 45
 Lys Glu Ala His Thr Val Tyr Arg Gln Ala Arg Gln Arg Ala Glu Asn
 50 55 60
 45
 Leu Lys Ser Leu Tyr Arg Ala Trp Gln Leu Arg Gln Glu Pro Val Ile
 65 70 75 80
 Lys Gly Leu Ala Lys Leu Asn Leu Gln Ser Asn Val Ser Val Leu Gln
 85 90 95
 50
 Asp Ala Leu Val Glu Asn Ile Gly Gly Asp Gly Asp Phe Ser Asp Leu
 100 105 110
 55
 Met Asn Arg Ala Ser Gln Tyr Ala Asp Ala Ala Ser Ile Gln Ser Leu
 115 120 125
 Phe Ser Pro Gly Arg Tyr Ala Ser Ala Leu Tyr Arg Val Ala Lys Asp
 130 135 140
 60
 Leu His Lys Ser Asp Ser Ser Leu His Ile Asp Asn Arg Arg Ala Asp
 145 150 155 160
 Leu Lys Asp Leu Ile Leu Ser Glu Thr Thr Met Asn Lys Glu Val Thr
 165 170 175
 65
 Ser Leu Asp Ile Leu Leu Asp Val Leu Gln Lys Gly Gly Lys Asp Ile
 180 185 190
 Thr Glu Leu Ser Gly Ala Phe Phe Pro Met Thr Leu Pro Tyr Asp Asp

	195						200						205					
5	His	Leu	Ser	Gln	Ile	Asp	Ser	Ala	Leu	Ser	Ala	Gln	Ala	Arg	Thr	Leu		
	210						215					220						
	Asn	Gly	Val	Trp	Asn	Thr	Leu	Thr	Asp	Thr	Thr	Ala	Gln	Ala	Val	Ser		
	225					230					235					240		
10	Glu	Gln	Thr	Ser	Asn	Thr	Asn	Thr	Arg	Lys	Leu	Phe	Ala	Ala	Gln	Asp		
					245					250					255			
	Gly	Asn	Gln	Asp	Thr	Phe	Phe	Ser	Gly	Asn	Thr	Phe	Tyr	Phe	Lys	Ala		
				260					265					270				
15	Val	Gly	Phe	Ser	Gly	Gln	Pro	Met	Val	Tyr	Leu	Ser	Gln	Tyr	Thr	Ser		
			275					280					285					
	Gly	Asn	Gly	Ile	Val	Gly	Ala	Gln	Leu	Ile	Ala	Gly	Asn	Pro	Asp	Gln		
	290						295					300						
20	Ala	Ala	Ala	Ala	Ile	Val	Ala	Pro	Leu	Lys	Leu	Thr	Trp	Ser	Met	Ala		
	305					310					315					320		
	Lys	Gln	Cys	Tyr	Tyr	Leu	Val	Ala	Pro	Asp	Gly	Thr	Thr	Met	Gly	Asp		
					325					330					335			
	Gly	Asn	Val	Leu	Thr	Gly	Cys	Phe	Leu	Arg	Gly	Asn	Ser	Pro	Thr	Asn		
				340					345					350				
30	Pro	Asp	Lys	Asp	Gly	Ile	Phe	Ala	Gln	Val	Ala	Asn	Lys	Ser	Gly	Ser		
			355					360					365					
	Thr	Gln	Pro	Leu	Pro	Ser	Phe	His	Leu	Pro	Val	Thr	Leu	Glu	His	Ser		
							375					380						
35	Glu	Asn	Lys	Asp	Gln	Tyr	Tyr	Leu	Lys	Thr	Glu	Gln	Gly	Tyr	Ile	Thr		
	385					390					395					400		
	Val	Asp	Ser	Ser	Gly	Gln	Ser	Asn	Trp	Lys	Asn	Ala	Leu	Val	Ile	Asn		
					405					410					415			
	Gly	Thr	Lys	Asp	Lys	Gly	Leu	Leu	Leu	Thr	Phe	Cys	Ser	Asp	Ser	Ser		
				420					425					430				
45	Gly	Thr	Pro	Thr	Asn	Pro	Asp	Asp	Val	Ile	Pro	Pro	Ala	Ile	Asn	Asp		
			435					440					445					
	Ile	Pro	Ser	Pro	Pro	Ala	Arg	Glu	Thr	Leu	Ser	Leu	Thr	Pro	Val	Ser		
							455					460						
50	Tyr	Gln	Leu	Met	Thr	Asn	Pro	Ala	Pro	Thr	Glu	Asp	Asp	Ile	Thr	Asn		
	465					470					475					480		
	His	Tyr	Gly	Phe	Asn	Gly	Ala	Ser	Leu	Arg	Ala	Ser	Pro	Leu	Ser	Thr		
					485					490			W4 »		495			
	Ser	Glu	Leu	Thr	Ser	Lys	Leu	Asn	Ser	Ile	Asp	Thr	Phe	Cys	Glu	Lys		
				500					505					510				
60	Thr	Arg	Leu	Ser	Phe	Asn	Gln	Leu	Met	Asp	Leu	Thr	Ala	Gln	Gln	Ser		
			515					520					525					
	Tyr	Ser	Gln	Ser	Ser	Ile	Asp	Ala	Lys	Ala	Ala	Ser	Arg	Tyr	Val	Arg		
			530				535					540						
65	Phe	Gly	Glu	Thr	Thr	Pro	Thr	Arg	Val	Asn	Val	Tyr	Gly	Ala	Ala	Tyr		
	545					550					555					560		
	Leu	Asn	Ser	Thr	Leu	Ala	Asp	Ala	Ala	Asp	Gly	Gln	Tyr	Leu	Trp	Ile		
					565					570					575			

	Gln	Thr	Asp	Gly	Lys	Ser	Leu	Asn	Phe	Thr	Asp	Asp	Thr	Val	Val	Ala	
				580					585					590			
5	Leu	Ala	Gly	Arg	Ala	Glu	Lys	Leu	Val	Arg	Leu	Ser	Ser	Gln	Thr	Gly	
			595					600					605				
	Leu	Ser	Phe	Glu	Glu	Leu	Asp	Trp	Leu	Ile	Ala	Asn	Ala	Ser	Arg	Ser	
		610					615					620					
10	Val	Pro	Asp	His	His	Asp	Lys	Ile	Val	Leu	Asp	Lys	Pro	Val	Leu	Glu	
		625				630					635					640	
	Ala	Leu	Ala	Glu	Tyr	Val	Ser	Leu	Lys	Gln	Arg	Tyr	Gly	Leu	Asp	Ala	
					645					650					655		
15	Asn	Thr	Phe	Ala	Thr	Phe	Ile	Ser	Ala	Val	Asn	Pro	Tyr	Thr	Pro	Asp	
				660					665					670			
20	Gln	Thr	Pro	Ser	Phe	Tyr	Glu	Thr	Ala	Phe	Arg	Ser	Ala	Asp	Gly	Asn	
			675					680					685				
	His	Val	Ile	Ala	Leu	Gly	Thr	Glu	Val	Lys	Tyr	Ala	Glu	Asn	Glu	Gln	
		690					695					700					
25	Asp	Glu	Leu	Ala	Ala	Ile	Cys	Cys	Lys	Ala	Leu	Gly	Val	Thr	Ser	Asp	
		705				710					715					720	
	Glu	Leu	Leu	Arg	Ile	Gly	Arg	Tyr	Cys	Phe	Gly	Asn	Ala	Gly	Ser	Phe	
					725					730					735		
30	Thr	Leu	Asp	Glu	Tyr	Thr	Ala	Ser	Gln	Leu	Tyr	Arg	Phe	Gly	Ala	Ile	
				740					745					750			
35	Pro	Arg	Leu	Phe	Gly	Leu	Thr	Phe	Ala	Gln	Ala	Glu	Ile	Leu	Trp	Arg	
			755					760					765				
	Leu	Met	Glu	Gly	Gly	Lys	Asp	Ile	Leu	Leu	Gln	Gln	Leu	Gly	Gln	Ala	
		770					775					780					
40	Lys	Ser	Leu	Gln	Pro	Leu	Ala	Ile	Leu	Arg	Arg	Thr	Glu	Gln	Val	Leu	
		785				790					795					800	
	Asp	Trp	Met	Ser	Ser	Val	Asn	Leu	Ser	Leu	Thr	Tyr	Leu	Gln	Gly	Met	
					805					810					815		
45	Val	Ser	Thr	Gln	Trp	Ser	Gly	Thr	Ala	Thr	Ala	Glu	Met	Phe	Asn	Phe	
				820					825					830			
50	Leu	Glu	Asn	Val	Cys	Asp	Ser	Val	Asn	Ser	Gln	Ala	Ala	Thr	Lys	Glu	
			835					840				845					
	Thr	Met	Asp	Ser	Ala	Leu	Gln	Gln	Lys	Val	Leu	Arg	Ala	Leu	Ser	Ala	
		850					855					860					
55	Gly	Phe	Gly	Ile	Lys	Ser	Asn	Val	Met	Gly	Ile	Val	Thr	Phe	Trp	Leu	
		865				870					875					880	
	Glu	Lys	Ile	Thr	Ile	Gly	Ser	Asp	Asn	Pro	Phe	Thr	Leu	Ala	Asn	Tyr	
					885					890					895		
60	Trp	His	Asp	Ile	Gln	Thr	Leu	Phe	Ser	His	Asp	Asn	Ala	Thr	Leu	Glu	
				900					905					910			
65	Ser	Leu	Gln	Thr	Asp	Thr	Ser	Leu	Val	Ile	Ala	Thr	Gln	Gln	Leu	Ser	
			915					920					925				
	Gln	Leu	Val	Leu	Ile	Val	Lys	Trp	Leu	Ser	Leu	Thr	Glu	Gln	Asp	Leu	
			930				935					940					
70	Gln	Leu	Leu	Thr	Thr	Tyr	Pro	Glu	Arg	Leu	Ile	Asn	Gly	Ile	Thr	Asn	
						950					955					960	

30 (2) INFORMATION FOR SEQ ID NO:35

35 (C) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

40	Pro 1	Leu	Ser	Thr	Ser 5	Glu	Leu	Thr	Ser	Lys 10	Leu	Asn	Ser	Ile	Asp 15	Thr
	Phe	Cys	Glu	Lys 20	Thr	Arg	Leu	Ser	Phe 25	Asn	Gln	Leu	Met	Asp 30	Leu	Thr
45	Ala	Gln	Gln 35	Ser	Tyr	Ser	Gln	Ser 40	Ser	Ile	Asp	Ala	Lys 45	Ala	Ala	Ser
	Arg	Tyr 50	Val	Arg	Phe	Gly	Glu 55	Thr	Thr	Pro	Thr	Arg 60	Val	Asn	Val	Tyr
	Gly 65	Ala	Ala	Tyr	Leu	Asn 70	Ser	Thr	Leu	Ala	Asp 75	Ala	Ala	Asp	Gly	Gln 80
55	Tyr	Leu	Trp	Ile 85	Gln	Thr	Asp	Gly	Lys	Ser 90	Leu	Asn	Phe	Thr	Asp 95	Asp
	Thr	Val	Val	Ala 100	Leu	Ala	Gly	Arg	Ala 105	Glu	Lys	Leu	Val	Arg 110	Leu	Ser
60	Ser	Gln	Thr 115	Gly	Leu	Ser	Phe	Glu 120	Glu	Leu	Asp	Trp	Leu 125	Ile	Ala	Asn
	Ala	Ser 130	Arg	Ser	Val	Pro	Asp 135	His	His	Asp	Lys	Ile 140	Val	Leu	Asp	Lys
65	Pro 145	Val	Leu	Glu	Ala	Leu 150	Ala	Glu	Tyr	Val	Ser 155	Leu	Lys	Gln	Arg	Tyr 160

	Gly	Leu	Asp	Ala	Asn	Thr	Phe	Ala	Thr	Phe	Ile	Ser	Ala	Val	Asn	Pro	
					165					170					175		
5	Tyr	Thr	Pro	Asp	Gln	Thr	Pro	Ser	Phe	Tyr	Glu	Thr	Ala	Phe	Arg	Ser	
				180					185					190			
	Ala	Asp	Gly	Asn	His	Val	Ile	Ala	Leu	Gly	Thr	Glu	Val	Lys	Tyr	Ala	
			195					200					205				
10	Glu	Asn	Glu	Gln	Asp	Glu	Leu	Ala	Ala	Ile	Cys	Cys	Lys	Ala	Leu	Gly	
		210					215					220					
	Val	Thr	Ser	Asp	Glu	Leu	Leu	Arg	Ile	Gly	Arg	Tyr	Cys	Phe	Gly	Asn	
15		225				230				235						240	
	Ala	Gly	Arg	Phe	Thr	Leu	Asp	Glu	Tyr	Thr	Ala	Ser	Gln	Leu	Tyr	Arg	
					245					250					255		
20	Phe	Gly	Ala	Ile	Pro	Arg	Leu	Phe	Gly	Leu	Thr	Phe	Ala	Gln	Ala	Glu	
				260					265					270			
	Ile	Leu	Trp	Arg	Leu	Met	Glu	Gly	Gly	Lys	Asp	Ile	Leu	Leu	Gln	Gln	
		275						280					285				
25	Xxx	Gly	Gln	Ala	Lys	Ser	Leu	Gln	Pro	Leu	Ala	Ile	Leu	Arg	Arg	Thr	
		290					295					300					
	Glu	Gln	Val	Leu	Asp	Trp	Met	Ser	Pro	Val	Asn	Leu	Ser	Leu	Thr	Tyr	
30		305				310					315					320	
	Leu	Gln	Gly	Met	Val	Ser	Thr	Gln	Trp	Ser	Gly	Thr	Ala	Thr	Ala	Glu	
				325						330					335		
35	Met	Phe	Asn	Phe	Leu	Glu	Asn	Val	Cys	Asp	Ser	Val	Asn	Ser	Gln	Ala	
				340					345					350			
	Xxx	Thr	Lys	Glu	Thr	Met	Asp	Ser	Ala	Leu	Gln	Gln	Lys	Val	Leu	Arg	
		355						360					365				
40	Ala	Leu	Ser	Ala	Gly	Phe	Gly	Ile	Lys	Ser	Asn	Val	Met	Gly	Ile	Val	
		370					375					380					
	Thr	Phe	Trp	Leu	Glu	Lys	Ile	Thr	Ile	Gly	Arg	Asp	Asn	Pro	Phe	Thr	
45		385				390					395					400	
	Leu	Ala	Asn	Tyr	Trp	His	Asp	Ile	Gln	Thr	Leu	Phe	Ser	His	Asp	Asn	
				405					410						415		
50	Ala	Thr	Leu	Glu	Ser	Leu	Gln	Thr	Asp	Thr	Ser	Leu	Val	Ile	Ala	Thr	
				420					425					430			
	Gln	Gln	Leu	Ser	Gln	Leu	Val	Leu	Ile	Val	Lys	Trp	Val	Ser	Leu	Thr	
			435					440					445				
55	Glu	Gln	Asp	Leu	Gln	Leu	Leu	Thr	Thr	Tyr	Pro	Glu	Arg	Leu	Ile	Asn	
		450					455					460					
	Gly	Ile	Thr	Asn	Val	Pro	Val	Pro	Asn	Pro	Glu	Leu	Leu	Leu	Thr	Leu	
60		465				470					475					480	
	Ser	Arg	Phe	Lys	Gln	Trp	Glu	Thr	Gln	Val	Thr	Val	Ser	Arg	Asp	Glu	
				485						490					495		
65	Ala	Met	Arg	Cys	Phe	Asp	Gln	Leu	Asn	Ala	Asn	Asp	Met	Thr	Thr	Glu	
				500					505					510			
	Asn	Ala	Gly	Ser	Leu	Ile	Ala	Thr	Leu	Tyr	Glu	Met	Asp	Lys	Gly	Thr	
			515					520					525				
70	Gly	Ala	Gln	Val	Asn	Thr	Leu	Leu	Leu	Gly	Glu	Asn	Asn	Trp	Pro	Lys	
		530					535					540					

Ser Phe Thr Ser Leu Trp Gln Leu Leu Thr Trp Leu Arg Val Gly Gln
 545 550 555 560

5 Arg Leu Asn Val Gly Ser Thr Thr Leu Gly Asn Leu Leu Ser Met Met
 565 570 575

Gln Ala Asp Pro Ala Ala Glu Ser Ser Ala Leu Leu Ala Ser Val Ala
 580 585 590

10 Gln Asn Leu Ser Ala Ala Ile Ser Asn Arg Gln *
 595 600

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2557 base pairs

(B) TYPE: nucleic acid

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36 (*tcdA* internal fragment):

GAATTCGGCT TGC GTTTAAT ATTGATGATG TCTCGCTCTT CCGCCTGCTT AAAATTACCG 60
 ACCATGATAA TAAAGATGGA AAAATTAAAA ATAACCTAAA GAATCTTTCC AATTTATATA 120
 TTGGAAAATT ACTGGCAGAT ATTCATCAAT TAACCATTGA TGAAGTGGAT TTATTACTGA 180
 TTGCCGTAGG TGAAGGAAAA ACTAATTTAT CCGCTATCAG TGATAAGCAA TTGGCTACCC 240
 30 TGATCAGAAA ACTCAATACT ATTACCAGCT GGCTACATAC ACAGAAAGTGG AGTGTTATCC 300
 AGCTATTTAT CATGACCTCC ACCAGCTATA ACAAACGCT AACGCCTGAA ATTAAGAATT 360
 TGCTGGATAC CGTCTACCAC GGTTTACAAG GTTTTGATAA AGACAAAGCA GATTTGCTAC 420
 ATGTCATGGC GCCCTATATT GCGGCCACCT TGCAATTATC ATCGGAAAAAT GTCGCCCCACT 480
 CGGTACTCCT TTGGGCAGAT AAGTTACAGC CCGGCGACGG CGCAATGACA GCAGAGGGAN 540
 35 TCTGGGACTG GTTGAATACT AAGTATACGC CGGGTTTCATC GGAAGCCGTA GAAACGCAGG 600
 AACATATCGT TCAGTATTGT CAGGCTCTGG CACAATTGGA AATGGTTTAC CATTCCACCG 660
 GCATCAACGA AAACGCCTTC CGTCTATTTG TGACAAAACC AGAGATGTTT GCGGCTGCAA 720
 CTGGAGCAGC GCCCGCGCAT GATGCCCTTT CACTGATTAT GCTGACACGT TTTGCGGATT 780
 GGGTGAACGC ACTAGGCGAA AAAGCGTCCT CGGTGCTAGC GGCATTTGAA GCTAACTCGT 840
 40 TAACGGCAGA ACAACTGGCT GATGCCATGA ATCTTGATGC TAATTTGCTG TTGCAAGCCA 900
 GTATTCAAGC ACAAATCAT CAACATCTTC CCCCAGTAAC TCCAGAAAAT GCGTTCTCCT 960
 GTTGGACATC TATCAATACT ATCCTGCAAT GGGTTAATGT CGCACACAA TTGAAATGTC 1020
 GCCCCACAGG GCGTTTCCGC TTTGGTCCGG CTGGATTATA TTCAATCAAT GAAAGAGACA 1080
 CCGACCTATG CCCAGTGGGA AAACGCGGCA GGCGTATTAA CCGCCGGGTT GAATTCAACA 1140
 45 ACAGGCTAAT ACATTACAAC GCTTTTCTGG ATGAATCTCG CAGTGCCGCA TTAAGCACCT 1200
 ACTATATCCG TCAAGTCGCC AAGGCAGCGG CGGCTATTAA AAGCCGTGAT GACTTGATC 1260
 AATACTTACT GATTGATAAT CAGGTTTCTG CCGCAATAAA AACCACCCGG ATCGCCGAAG 1320
 CCATTGCCAG TATTCAACTG TACGTCAACC GGGCATTGGA AAATGTGGAA GAAAATGCCA 1380
 ATTCGGGGGT TATCAGCCGC CAATTCTTTA TCGACTGGGA CAAATACAAT AAACGCTACA 1440
 50 GCACTTGGGC GGGTGTTTCT CAATTAGTTT ACTACCCGGA AAATATATT GATCCGACCA 1500
 TCGGTATCGG ACAAACCAA ATGATGGACG CATTACTGCA ATCCGTCAGC CAAAGCCAAT 1560
 TAAACGCCGA TACCGTCGAA GATGCCTTTA TGTCTTATCT GACATCGTTT GAACAAGTGG 1620
 CTAATCTTAA AGTTATTAGC GCATATCACG ATAATATTAA TAACGATCAA GGGCTGACCT 1680
 ATTTTATCGG ACTCAGTGAA ACTGATGCCG GTGAATATTA TTGGCGCAGT GTCGATCACA 1740
 55 GTAAATTCAA CGACGGTAAA TTCGCGGCTA ATGCCTGGAG TGAATGGCAT AAAATTGATT 1800

GTCCAATTAA CCCAATAAA AGCACTATCC GTCCAGTGAT ATATATATCC CGCCTGTATC 1860
 TGCTCTGGTT GGAACAAAAG GAGATCACCA AACAGACAGG AAATAGTAAA GATGGCTATC 1920
 AAAGTGAAC GGATTATCGT TATGAACTAA AATTGGCGCA TATCCGCTAT GATGGCACTT 1980
 GGAATACGCC AATCACCTTT GATGTCAATA AAAAAATATC CGAGCTAAAA CTGGAAAAAA 2040
 5 ATAGAGCGCC CGGACTCTAT TGTGCCGGTT ATCAAGGTGA AGATACGTTG CTGGTGATGT 2100
 TTTATAACCA ACAAGACACA CTAGATAGTT ATAAAAACGC TTCAATGCAA GGACTATATA 2160
 TCTTTGCTGA TATGGCATCC AAAGATATGA CCCCAGAACA GAGCAATGTT TATCGGGATA 2220
 ATAGCTATCA ACAATTTGAT ACCAATAATG TCAGAAGAGT GAATAACCGC TATGCAGAGG 2280
 ATTATGAGAT TCCTTCTTCG GTAAGTAGCC GTAAAGACTA TGGTTGGGGA GATTATTACC 2340
 10 TCAGCATGGT ATATAACGGA GATATTCCAA CTATCAATTA CAAAGCCGCA TCAAGTGATT 2400
 TAAAAATTTA TATTTACCA AAATTAAGAA TTATTCATAA TGGATATGAA GGACAGAAGC 2460
 GCAATCAATG CAATTTGATG AATAAATATG GCAAACCTAGG TGATAAATTT ATTGTGTATA 2520
 CCAGCCTGGG CGTTAATCCG AATAATAAGC CGAATTC 2557

15

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 845 amino acids
 (B) TYPE: amino acids
 (C) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein (partial)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37 (TcdA internal peptide):

Ala Phe Asn Ile Asp Asp Val Ser Leu Phe Arg Leu Leu Lys Ile Thr
 1 5 10 15
 30 Asp His Asp Asn Lys Asp Gly Lys Ile Lys Asn Asn Leu Lys Asn Leu
 20 25 30
 Ser Asn Leu Tyr Ile Gly Lys Leu Leu Ala Asp Ile His Gln Leu Thr
 35 40 45
 Ile Asp Glu Leu Asp Leu Leu Leu Ile Ala Val Gly Glu Gly Lys Thr
 50 55 60
 Asn Leu Ser Ala Ile Ser Asp Lys Gln Leu Ala Thr Leu Ile Arg Lys
 65 70 75 80
 Leu Asn Thr Ile Thr Ser Trp Leu His Thr Gln Lys Trp Ser Val Phe
 85 90 95
 45 Gln Leu Phe Ile Met Thr Ser Thr Ser Tyr Asn Lys Thr Leu Thr Pro
 100 105 110
 Glu Ile Lys Asn Leu Leu Asp Thr Val Tyr His Gly Leu Gln Gly Phe
 115 120 125
 50 Asp Lys Asp Lys Ala Asp Leu Leu His Val Met Ala Pro Tyr Ile Ala
 130 135 140
 Ala Thr Leu Gln Leu Ser Ser Glu Asn Val Ala His Ser Val Leu Leu
 145 150 155 160
 Trp Ala Asp Lys Leu Gln Pro Gly Asp Gly Ala Met Thr Ala Glu Gly
 165 170 175
 60 Phe Trp Asp Trp Leu Asn Thr Lys Tyr Thr Pro Gly Ser Ser Glu Ala
 180 185 190
 Val Glu Thr Gln Glu His Ile Val Gln Tyr Cys Gln Ala Leu Ala Gln

	195	200	205	
5	Leu Glu Met Val Tyr His Ser Thr Gly Ile Asn Glu Asn Ala Phe Arg 210 215 220			
10	Leu Phe Val Thr Lys Pro Glu Met Phe Gly Ala Ala Thr Gly Ala Ala 225 230 235 240			
15	Pro Ala His Asp Ala Leu Ser Leu Ile Met Leu Thr Arg Phe Ala Asp 245 250 255			
20	Trp Val Asn Ala Leu Gly Glu Lys Ala Ser Ser Val Leu Ala Ala Phe 260 265 270			
25	Glu Ala Asn Ser Leu Thr Ala Glu Gln Leu Ala Asp Ala Met Asn Leu 275 280 285			
30	Asp Ala Asn Leu Leu Leu Gln Ala Ser Ile Gln Ala Gln Asn His Gln 290 295 300			
35	His Leu Pro Pro Val Thr Pro Glu Asn Ala Phe Ser Cys Trp Thr Ser 305 310 315 320			
40	Ile Asn Thr Ile Leu Gln Trp Val Asn Val Ala Gln Gln Leu Lys Cys 325 330 335			
45	Arg Pro Thr Gly Arg Phe Arg Phe Gly Arg Ala Gly Leu Tyr Ser Ile 340 345 350			
50	Asn Glu Arg Asp Thr Asp Leu Cys Pro Val Gly Lys Arg Gly Arg Arg 355 360 365			
55	Ile Asn Arg Arg Val Glu Phe Asn Asn Arg Leu Ile His Tyr Asn Ala 370 375 380			
60	Phe Leu Asp Glu Ser Arg Ser Ala Ala Leu Ser Thr Tyr Tyr Ile Arg 385 390 395 400			
65	Gln Val Ala Lys Ala Ala Ala Ile Lys Ser Arg Asp Asp Leu Tyr 405 410 415			
70	Gln Tyr Leu Leu Ile Asp Asn Gln Val Ser Ala Ala Ile Lys Thr Thr 420 425 430			
75	Arg Ile Ala Glu Ala Ile Ala Ser Ile Gln Leu Tyr Val Asn Arg Ala 435 440 445			
80	Leu Glu Asn Val Glu Glu Asn Ala Asn Ser Gly Val Ile Ser Arg Gln 450 455 460			
85	Phe Phe Ile Asp Trp Asp Lys Tyr Asn Lys Arg Tyr Ser Thr Trp Ala 465 470 475 480			
90	Gly Val Ser Gln Leu Val Tyr Tyr Pro Glu Asn Tyr Ile Asp Pro Thr 485 490 495			
95	Met Arg Ile Gly Gln Thr Lys Met Met Asp Ala Leu Leu Gln Ser Val 500 505 510			
100	Ser Gln Ser Gln Leu Asn Ala Asp Thr Val Glu Asp Ala Phe Met Ser 515 520 525			
105	Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys Val Ile Ser Ala 530 535 540			
110	Tyr His Asp Asn Ile Asn Asn Asp Gln Gly Leu Thr Tyr Phe Ile Gly 545 550 555 560			
115	Leu Ser Glu Thr Asp Ala Gly Glu Tyr Tyr Trp Arg Ser Val Asp His 565 570 575			

Ser Lys Phe Asn Asp Gly Lys Phe Ala Ala Asn Ala Trp Ser Glu Trp
 580 585 590
 5 His Lys Ile Asp Cys Pro Ile Asn Pro Tyr Lys Ser Thr Ile Arg Pro
 595 600 605
 Val Ile Tyr Lys Ser Arg Leu Tyr Leu Leu Trp Leu Glu Gln Lys Glu
 610 615 620
 10 Ile Thr Lys Gln Thr Gly Asn Ser Lys Asp Gly Tyr Gln Thr Glu Thr
 625 630 635 640
 Asp Tyr Arg Tyr Glu Leu Lys Leu Ala His Ile Arg Tyr Asp Gly Thr
 645 650 655
 15 Trp Asn Thr Pro Ile Thr Phe Asp Val Asn Lys Lys Ile Ser Glu Leu
 660 665 670
 20 Lys Leu Glu Lys Asn Arg Ala Pro Gly Leu Tyr Cys Ala Gly Tyr Gln
 675 680 685
 Gly Glu Asp Thr Leu Leu Val Met Phe Tyr Asn Gln Gln Asp Thr Leu
 690 695 700
 25 Asp Ser Tyr Lys Asn Ala Ser Met Gln Gly Leu Tyr Ile Phe Ala Asp
 705 710 715 720
 Met Ala Ser Lys Asp Met Thr Pro Glu Gln Ser Asn Val Tyr Arg Asp
 725 730 735
 30 Asn Ser Tyr Gln Gln Phe Asp Thr Asn Asn Val Arg Arg Val Asn Asn
 740 745 750
 Arg Tyr Ala Glu Asp Tyr Glu Ile Pro Ser Ser Val Ser Ser Arg Lys
 755 760 765
 Asp Tyr Gly Trp Gly Asp Tyr Tyr Leu Ser Met Val Tyr Asn Gly Asp
 770 775 780
 40 Ile Pro Thr Ile Asn Tyr Lys Ala Ala Ser Ser Asp Leu Lys Ile Tyr
 785 790 795 800
 Ile Ser Pro Lys Leu Arg Ile Ile His Asn Gly Tyr Glu Gly Gln Lys
 805 810 815
 45 Arg Asn Gln Cys Asn Leu Met Asn Lys Tyr Gly Lys Leu Gly Asp Lys
 820 825 830
 Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn
 835 840 845

(2) INFORMATION FOR SEQ ID NO:38:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

60 (ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38 (TcdA₁₁- pk71 internal peptide):

65

Arg Tyr Tyr Asn Leu Ser Asp Glu Glu Leu Ser Gln Phe Ile Gly
 1 5 10 15

Lys

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39 (TcdA_{ii}- pK44 internal peptide):

Gly Thr Ala Thr Asp Val Ser Gly Pro Val Glu Ile Asn Thr Ala
 1 5 10 15
 Ile Ser Pro Ala Lys
 20

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40 (TcbA_{iii} N-terminus):

Ala Asn Ser Leu Thr Ala Leu Phe Leu Pro Gln
 1 5 10

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41 (TcdA_{iii} N-terminus):

Leu Arg Ser Ala Asn Thr Leu Thr Asp Leu Phe Leu Pro Gln
 1 5 10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42 (TcdA-pk57 internal peptide):

Arg Ala Leu Glu Val Glu Arg Thr Val Ser Leu Ala Glu Val Tyr
1 5 10 15

Ala Gly Leu Glu

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43 (TcdA_{iii}-pK20 internal peptide):Ile Arg Glu Asp Tyr Pro Ala Ser Leu Gly Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Asp Asp Ser Gly Asp Asp Asp Lys Val Thr Asn Thr Asp Ile His Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Asp Val Xaa Gly Ser Lys Ala Asn Glu Lys Leu Lys
1 5 10

5 (2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7551 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46 (*tcdA*):

15 ATG AAC GAG TCT GTA AAA GAG ATA CCT GAT GTA TTA AAA AGC CAG TGT 48
Met Asn Glu Ser Val Lys Glu Ile Pro Asp Val Leu Lys Ser Gln Cys
1 5 10 15

20 GGT TTT AAT TGT CTG ACA GAT ATT AGC CAC AGC TCT TTT AAT GAA TTT 96
Gly Phe Asn Cys Leu Thr Asp Ile Ser His Ser Ser Phe Asn Glu Phe
20 25 30

25 CGC CAG CAA GTA TCT GAG CAC CTC TCC TGG TCC GAA ACA CAC GAC TTA 144
Arg Gln Gln Val Ser Glu His Leu Ser Trp Ser Glu Thr His Asp Leu
35 40 45

30 TAT CAT GAT GCA CAA CAG GCA CAA AAG GAT AAT CGC CTG TAT GAA GCG 192
Tyr His Asp Ala Gln Gln Ala Gln Lys Asp Asn Arg Leu Tyr Glu Ala
50 55 60

35 CGT ATT CTC AAA CGC GCC AAT CCC CAA TTA CAA AAT GCG GTG CAT CTT 240
Arg Ile Leu Lys Arg Ala Asn Pro Gln Leu Gln Asn Ala Val His Leu
65 70 75 80

40 GCC ATT CTC GCT CCC AAT GCT GAA CTG ATA GGC TAT AAC AAT CAA TTT 288
Ala Ile Leu Ala Pro Asn Ala Glu Leu Ile Gly Tyr Asn Asn Gln Phe
85 90 95

45 AGC GGT AGA GCC AGT CAA TAT GTT GCG CCG GGT ACC GTT TCT TCC ATG 336
Ser Gly Arg Ala Ser Gln Tyr Val Ala Pro Gly Thr Val Ser Ser Met
100 105 110

50 TTC TCC CCC GCC GCT TAT TTG ACT GAA CTT TAT CGT GAA GCA CGC AAT 384
Phe Ser Pro Ala Ala Tyr Leu Thr Glu Leu Tyr Arg Glu Ala Arg Asn
115 120 125

55 TTA CAC GCA AGT GAC TCC GTT TAT TAT CTG GAT ACC CGC CGC CCA GAT 432
Leu His Ala Ser Asp Ser Val Tyr Tyr Leu Asp Thr Arg Arg Pro Asp
130 135 140

60 CTC AAA TCA ATG GCG CTC AGT CAG CAA AAT ATG GAT ATA GAA TTA TCC 480
Leu Lys Ser Met Ala Leu Ser Gln Gln Asn Met Asp Ile Glu Leu Ser
145 150 155 160

55 ACA CTC TCT TTG TCC AAT GAG CTG TTA TTG GAA AGC ATT AAA ACT GAA 528
Thr Leu Ser Leu Ser Asn Glu Leu Leu Glu Ser Ile Lys Thr Glu
165 170 175

60 TCT AAA CTG GAA AAC TAT ACT AAA GTG ATG GAA ATG CTC TCC ACT TTC 576
Ser Lys Leu Glu Asn Tyr Thr Lys Val Met Glu Met Leu Thr Phe
180 185 190

65 CGT CCT TCC GGC GCA ACG CCT TAT CAT GAT GCT TAT GAA AAT GTG CGT 624
Arg Pro Ser Gly Ala Thr Pro Tyr His Asp Ala Tyr Glu Asn Val Arg
195 200 205

GAA GTT ATC CAG CTA CAA GAT CCT GGA CTT GAG CAA CTC AAT GCA TCA 672
Glu Val Ile Gln Leu Gln Asp Pro Gly Leu Glu Gln Leu Asn Ala Ser

	210	215	220	
5	CCG GCA ATT GCC GGG TTG ATG CAT CAA GCC TCC CTA TTG GGT ATT AAC 720 Pro Ala Ile Ala Gly Leu Met His Gln Ala Ser Leu Leu Gly Ile Asn 240 225 230 235 240			
10	GCT TCA ATC TCG CCT GAG CTA TTT AAT ATT CTG ACG GAG GAG ATT ACC 768 Ala Ser Ile Ser Pro Glu Leu Phe Asn Ile Leu Thr Glu Glu Ile Thr 255 245 250 255			
15	GAA GGT AAT GCT GAG GAA CTT TAT AAG AAA AAT TTT GGT AAT ATC GAA 816 Glu Gly Asn Ala Glu Glu Leu Tyr Lys Lys Asn Phe Gly Asn Ile Glu 270 260 265 270			
20	CCG GCC TCA TTG GCT ATG CCG GAA TAC CTT AAA CGT TAT TAT AAT TTA 864 Pro Ala Ser Leu Ala Met Pro Glu Tyr Leu Lys Arg Tyr Tyr Asn Leu 285 275 280 285			
25	AGC GAT GAA GAA CTT AGT CAG TTT ATT GGT AAA GCC AGC AAT TTT GGT 912 Ser Asp Glu Glu Leu Ser Gln Phe Ile Gly Lys Ala Ser Asn Phe Gly 300 290 295 300			
30	CAA CAG GAA TAT AGT AAT AAC CAA CTT ATT ACT CCG GTA GTC AAC AGC 960 Gln Gln Glu Tyr Ser Asn Asn Gln Leu Ile Thr Pro Val Val Asn Ser 320 305 310 315			
35	AGT GAT GGC ACG GTT AAG GTA TAT CGG ATC ACC CGC GAA TAT ACA ACC 1008 Ser Asp Gly Thr Val Lys Val Tyr Arg Ile Thr Arg Glu Tyr Thr Thr 335 325 330 335			
40	AAT GCT TAT CAA ATG GAT GTG GAG CTA TTT CCC TTC GGT GGT GAG AAT 1056 Asn Ala Tyr Gln Met Asp Val Glu Leu Phe Pro Phe Gly Gly Glu Asn 350 340 345 350			
45	TAT CGG TTA GAT TAT AAA TTC AAA AAT TTT TAT AAT GCC TCT TAT TTA 1104 Tyr Arg Leu Asp Tyr Lys Phe Lys Asn Phe Tyr Asn Ala Ser Tyr Leu 365 355 360 365			
50	TCC ATC AAG TTA AAT GAT AAA AGA GAA CTT GTT CGA ACT GAA GGC GCT 1152 Ser Ile Lys Leu Asn Asp Lys Arg Glu Leu Val Arg Thr Glu Gly Ala 380 370 375 380			
55	CCT CAA GTC AAT ATA GAA TAC TCC GCA AAT ATC ACA TTA AAT ACC GCT 1200 Pro Gln Val Asn Ile Glu Tyr Ser Ala Asn Ile Thr Leu Asn Thr Ala 400 385 390 395			
60	GAT ATC AGT CAA CCT TTT GAA ATT GGC CTG ACA CGA GTA CTT CCT TCC 1248 Asp Ile Ser Gln Pro Phe Glu Ile Gly Leu Thr Arg Val Leu Pro Ser 415 405 410 415			
65	GGT TCT TGG GCA TAT GCC GCC GCA AAA TTT ACC GTT GAA GAG TAT AAC 1296 Gly Ser Trp Ala Tyr Ala Ala Ala Lys Phe Thr Val Glu Glu Tyr Asn 430 420 425 430			
70	CAA TAC TCT TTT CTG CTA AAA CTT AAC AAG GCT ATT CGT CTA TCA CGT 1344 Gln Tyr Ser Phe Leu Leu Lys Leu Asn Lys Ala Ile Arg Leu Ser Arg 445 435 440 445			
75	GCG ACA GAA TTG TCA CCC ACG ATT CTG GAA GGC ATT GTG CGC AGT GTT 1392 Ala Thr Glu Leu Ser Pro Thr Ile Leu Glu Gly Ile Val Arg Ser Val 460 450 455 460			
80	AAT CTA CAA CTG GAT ATC AAC ACA GAC GTA TTA GGT AAA GTT TTT CTG 1440 Asn Leu Gln Leu Asp Ile Asn Thr Asp Val Leu Gly Lys Val Phe Leu 480 465 470 475			
85	ACT AAA TAT TAT ATG CAG CGT TAT GCT ATT CAT GCT GAA ACT GCC CTG 1488 Thr Lys Tyr Tyr Met Gln Arg Tyr Ala Ile His Ala Glu Thr Ala Leu 495 485 490 495			
90	ATA CTA TGC AAC GCG CCT ATT TCA CAA CGT TCA TAT GAT AAT CAA CCT 1536			

	Ile	Leu	Cys	Asn	Ala		Ile	Ser	Gln	Arg	Ser	Tyr	Asp		Gln	Pro	
				500					505						510		
5	AGC	CAA	TTT	GAT	CGC	CTG	TTT	AAT	ACG	CCA	TTA	CTG	AAC	GGA	CAA	TAT	1584
	Ser	Gln	Phe	Asp	Arg	Leu	Phe	Asn	Thr	Pro	Leu	Leu	Asn	Gly	Gln	Tyr	
			515					520					525				
10	TTT	TCT	ACC	GGC	GAT	GAG	GAG	ATT	GAT	TTA	AAT	TCA	GGT	AGC	ACC	GGC	1632
	Phe	Ser	Thr	Gly	Asp	Glu	Glu	Ile	Asp	Leu	Asn	Ser	Gly	Ser	Thr	Gly	
			530				535					540					
15	GAT	TGG	CGA	AAA	ACC	ATA	CTT	AAG	CGT	GCA	TTT	AAT	ATT	GAT	GAT	GTC	1680
	Asp	Trp	Arg	Lys	Thr	Ile	Leu	Lys	Arg	Ala	Phe	Asn	Ile	Asp	Asp	Val	
						550						555				560	
20	TCG	CTC	TTC	CGC	CTG	CTT	AAA	ATT	ACC	GAC	CAT	GAT	AAT	AAA	GAT	GGA	1728
	Ser	Leu	Phe	Arg	Leu	Leu	Lys	Ile	Thr	Asp	His	Asp	Asn	Lys	Asp	Gly	
					565					570				575			
25	AAA	ATT	AAA	AAT	AAC	CTA	AAG	AAT	CTT	TCC	AAT	TTA	TAT	ATT	GGA	AAA	1776
	Lys	Ile	Lys	Asn	Asn	Leu	Lys	Asn	Leu	Ser	Asn	Leu	Tyr	Ile	Gly	Lys	
				580				585						590			
30	TTA	CTG	GCA	GAT	ATT	CAT	CAA	TTA	ACC	ATT	GAT	GAA	CTG	GAT	TTA	TTA	1824
	Leu	Leu	Ala	Asp	Ile	His	Gln	Leu	Thr	Ile	Asp	Glu	Leu	Asp	Leu	Leu	
			595				600						605				
35	CTG	ATT	GCC	GTA	GGT	GAA	GGA	AAA	ACT	AAT	TTA	TCC	GCT	ATC	AGT	GAT	1872
	Leu	Ile	Ala	Val	Gly	Glu	Gly	Lys	Thr	Asn	Leu	Ser	Ala	Ile	Ser	Asp	
			610			615						620					
40	AAG	CAA	TTG	GCT	ACC	CTG	ATC	AGA	AAA	CTC	AAT	ACT	ATT	ACC	AGC	TGG	1920
	Lys	Gln	Leu	Ala	Thr	Leu	Ile	Arg	Lys	Leu	Asn	Thr	Ile	Thr	Ser	Trp	
			625			630				635						640	
45	CTA	CAT	ACA	CAG	AAG	TGG	AGT	GTA	TTC	CAG	CTA	TTT	ATC	ATG	ACC	TCC	1968
	Leu	His	Thr	Gln	Lys	Trp	Ser	Val	Phe	Gln	Leu	Phe	Ile	Met	Thr	Ser	
				645				650						655			
50	ACC	AGC	TAT	AAC	AAA	ACG	CTA	ACG	CCT	GAA	ATT	AAG	AAT	TTG	CTG	GAT	2016
	Thr	Ser	Tyr	Asn	Lys	Thr	Leu	Thr	Pro	Glu	Ile	Lys	Asn	Leu	Leu	Asp	
				660				665						670			
55	ACC	GTC	TAC	CAC	GGT	TTA	CAA	GGT	TTT	GAT	AAA	GAC	AAA	GCA	GAT	TTG	2064
	Thr	Val	Tyr	His	Gly	Leu	Gln	Gly	Phe	Asp	Lys	Asp	Lys	Ala	Asp	Leu	
			675				680					685					
60	CTA	CAT	GTC	ATG	GCG	CCC	TAT	ATT	GCG	GCC	ACC	TTG	CAA	TTA	TCA	TCG	2112
	Leu	His	Val	Met	Ala	Pro	Tyr	Ile	Ala	Ala	Thr	Leu	Gln	Leu	Ser	Ser	
			690				695					700					
65	GAA	AAT	GTC	GCC	CAC	TCG	GTA	CTC	CTT	TGG	GCA	GAT	AAG	TTA	CAG	CCC	2160
	Glu	Asn	Val	Ala	His	Ser	Val	Leu	Leu	Trp	Ala	Asp	Lys	Leu	Gln	Pro	
			705			710				715						720	
70	GGC	GAC	GGC	GCA	ATG	ACA	GCA	GAA	AAA	TTC	TGG	GAC	TGG	TTG	AAT	ACT	2208
	Gly	Asp	Gly	Ala	Met	Thr	Ala	Glu	Lys	Phe	Trp	Asp	Trp	Leu	Asn	Thr	
					725					730				735			
75	AAG	TAT	ACG	CCG	GGT	TCA	TCG	GAA	GCC	GTA	GAA	ACG	CAG	GAA	CAT	ATC	2256
	Lys	Tyr	Thr	Pro	Gly	Ser	Ser	Glu	Ala	Val	Glu	Thr	Gln	Glu	His	Ile	
				740				745						750			
80	GTT	CAG	TAT	TGT	CAG	GCT	CTG	GCA	CAA	TTG	GAA	ATG	GTT	TAC	CAT	TCC	2304
	Val	Gln	Tyr	Cys	Gln	Ala	Leu	Ala	Gln	Leu	Glu	Met	Val	Tyr	His	Ser	
			755				760						765				
85	ACC	GGC	ATC	AAC	GAA	AAC	GCC	TTC	CGT	CTA	TTT	GTG	ACA	AAA	CCA	GAG	2352
	Thr	Gly	Ile	Asn	Glu	Asn	Ala	Phe	Arg	Leu	Phe	Val	Thr	Lys	Pro	Glu	
			770				775					780					

	ATG	TTT	GGC	GCT	ACA	ACT	GGA	GCA	GCG	CCC	GCG	CAT	GAT	GCC	CTT	TCA	2400
	Met	Phe	Gly	Ala	Ala	Thr	Gly	Ala	Ala	Pro	Ala	His	Asp	Ala	Leu	Ser	
	785					790				795					800		
5	CTG	ATT	ATG	CTG	ACA	CGT	TTT	GCG	GAT	TGG	GTG	AAC	GCA	CTA	GGC	GAA	2448
	Leu	Ile	Met	Leu	Thr	Arg	Phe	Ala	Asp	Trp	Val	Asn	Ala	Leu	Gly	Glu	
					805					810					815		
10	AAA	GCG	TCC	TCG	GTG	CTA	GCG	GCA	TTT	GAA	GCT	AAC	TCG	TTA	ACG	GCA	2496
	Lys	Ala	Ser	Ser	Val	Leu	Ala	Ala	Phe	Glu	Ala	Asn	Ser	Leu	Thr	Ala	
					820				825					830			
15	GAA	CAA	CTG	GCT	GAT	GCC	ATG	AAT	CTT	GAT	GCT	AAT	TTG	CTG	TTG	CAA	2544
	Glu	Gln	Leu	Ala	Asp	Ala	Met	Asn	Leu	Asp	Ala	Asn	Leu	Leu	Leu	Gln	
			835					840					845				
20	GCC	AGT	ATT	CAA	GCA	CAA	AAT	CAT	CAA	CAT	CTT	CCC	CCA	GTA	ACT	CCA	2592
	Ala	Ser	Ile	Gln	Ala	Gln	Asn	His	Gln	His	Leu	Pro	Pro	Val	Thr	Pro	
		850					855					860					
	GAA	AAT	GCG	TTC	TCC	TGT	TGG	ACA	TCT	ATC	AAT	ACT	ATC	CTG	CAA	TGG	2640
	Glu	Asn	Ala	Phe	Ser	Cys	Trp	Thr	Ser	Ile	Asn	Thr	Ile	Leu	Gln	Trp	
		865				870					875				880		
25	GTT	AAT	GTC	GCA	CAA	CAA	TTG	AAT	GTC	GCC	CCA	CAG	GGC	GTT	TCC	GCT	2688
	Val	Asn	Val	Ala	Gln	Gln	Leu	Asn	Val	Ala	Pro	Gln	Gly	Val	Ser	Ala	
					885					890					895		
30	TTG	GTC	GGG	CTG	GAT	TAT	ATT	CAA	TCA	ATG	AAA	GAG	ACA	CCG	ACC	TAT	2736
	Leu	Val	Gly	Leu	Asp	Tyr	Ile	Gln	Ser	Met	Lys	Glu	Thr	Pro	Thr	Tyr	
				900					905					910			
35	GCC	CAG	TGG	GAA	AAC	GCG	GCA	GGC	GTA	TTA	ACC	GCC	GGG	TTG	AAT	TCA	2784
	Ala	Gln	Trp	Glu	Asn	Ala	Ala	Gly	Val	Leu	Thr	Ala	Gly	Leu	Asn	Ser	
			915					920					925				
40	CAA	CAG	GCT	AAT	ACA	TTA	CAC	GCT	TTT	CTG	GAT	GAA	TCT	CGC	AGT	GCC	2832
	Gln	Gln	Ala	Asn	Thr	Leu	His	Ala	Phe	Leu	Asp	Glu	Ser	Arg	Ser	Ala	
		930					935					940					
	GCA	TTA	AGC	ACC	TAC	TAT	ATC	CGT	CAA	GTC	GCC	AAG	GCA	GCG	GCG	GCT	2880
	Ala	Leu	Ser	Thr	Tyr	Tyr	Ile	Arg	Gln	Val	Ala	Lys	Ala	Ala	Ala	Ala	
		945				950					955				960		
45	ATT	AAA	AGC	CGT	GAT	GAC	TTG	TAT	CAA	TAC	TTA	CTG	ATT	GAT	AAT	CAG	2928
	Ile	Lys	Ser	Arg	Asp	Asp	Leu	Tyr	Gln	Tyr	Leu	Leu	Ile	Asp	Asn	Gln	
				965					970					975			
50	GTT	TCT	GCG	GCA	ATA	AAA	ACC	ACC	CGG	ATC	GCC	GAA	GCC	ATT	GCC	AGT	2976
	Val	Ser	Ala	Ala	Ile	Lys	Thr	Thr	Arg	Ile	Ala	Glu	Ala	Ile	Ala	Ser	
				980					985					990			
55	ATT	CAA	CTG	TAC	GTC	AAC	CGG	GCA	TTG	GAA	AAT	GTG	GAA	GAA	AAT	GCC	3024
	Ile	Gln	Leu	Tyr	Val	Asn	Arg	Ala	Leu	Glu	Asn	Val	Glu	Glu	Asn	Ala	
			995				1000					1005					
60	AAT	TCG	GGG	GTT	ATC	AGC	CGC	CAA	TTC	TTT	ATC	GAC	TGG	GAC	AAA	TAC	3072
	Asn	Ser	Gly	Val	Ile	Ser	Arg	Gln	Phe	Phe	Ile	Asp	Trp	Asp	Lys	Tyr	
		1010					1015					1020					
	AAT	AAA	CGC	TAC	AGC	ACT	TGG	GCG	GGT	GTT	TCT	CAA	TTA	GTT	TAC	TAC	3120
	Asn	Lys	Arg	Tyr	Ser	Thr	Trp	Ala	Gly	Val	Ser	Gln	Leu	Val	Tyr	Tyr	
		1025				1030				1035					1040		
65	CCG	GAA	AAC	TAT	ATT	GAT	CCG	ACC	ATG	CGT	ATC	GGA	CAA	ACC	AAA	ATG	3168
	Pro	Glu	Asn	Tyr	Ile	Asp	Pro	Thr	Met	Arg	Ile	Gly	Gln	Thr	Lys	Met	
				1045					1050						1055		
70	ATG	GAC	GCA	TTA	CTG	CAA	TCC	GTC	AGC	CAA	AGC	CAA	TTA	AAC	GCC	GAT	3216
	Met	Asp	Ala	Leu	Leu	Gln	Ser	Val	Ser	Gln	Ser	Gln	Leu	Asn	Ala	Asp	
				1060					1065					1070			

	ACC	GTC	GAA	GAT	GCC	TTT	ATG	TCT	TAT	CTG	ACA	TCG	TTT	GAA	CAA	GTG	3264
	Thr	Val	Glu	Asp	Ala	Phe	Met	Ser	Tyr	Leu	Thr	Ser	Phe	Glu	Gln	Val	
			1075					1080					1085				
5	GCT	AAT	CTT	AAA	GTT	ATT	AGC	GCA	TAT	CAC	GAT	AAT	ATT	AAT	AAC	GAT	3312
	Ala	Asn	Leu	Lys	Val	Ile	Ser	Ala	Tyr	His	Asp	Asn	Ile	Asn	Asn	Asp	
		1090					1095					1100					
10	CAA	GGG	CTG	ACC	TAT	TTT	ATC	GGA	CTC	AGT	GAA	ACT	GAT	GCC	GGT	GAA	3360
	Gln	Gly	Leu	Thr	Tyr	Phe	Ile	Gly	Leu	Ser	Glu	Thr	Asp	Ala	Gly	Glu	
		1105				1110					1115					1120	
15	TAT	TAT	TGG	CGC	AGT	GTC	GAT	CAC	AGT	AAA	TTC	AAC	GAC	GGT	AAA	TTC	3408
	Tyr	Tyr	Trp	Arg	Ser	Val	Asp	His	Ser	Lys	Phe	Asn	Asp	Gly	Lys	Phe	
					1125					1130					1135		
20	GCG	GCT	AAT	GCC	TGG	AGT	GAA	TGG	CAT	AAA	ATT	GAT	TGT	CCA	ATT	AAC	3456
	Ala	Ala	Asn	Ala	Trp	Ser	Glu	Trp	His	Lys	Ile	Asp	Cys	Pro	Ile	Asn	
				1140					1145					1150			
25	CCT	TAT	AAA	AGC	ACT	ATC	CGT	CCA	GTG	ATA	TAT	AAA	TCC	CGC	CTG	TAT	3504
	Pro	Tyr	Lys	Ser	Thr	Ile	Arg	Pro	Val	Ile	Tyr	Lys	Ser	Arg	Leu	Tyr	
			1155					1160					1165				
30	CTG	CTC	TGG	TTG	GAA	CAA	AAG	GAG	ATC	ACC	AAA	CAG	ACA	GGA	AAT	AGT	3552
	Leu	Leu	Trp	Leu	Glu	Gln	Lys	Glu	Ile	Thr	Lys	Gln	Thr	Gly	Asn	Ser	
		1170					1175					1180					
35	AAA	GAT	GGC	TAT	CAA	ACT	GAA	ACG	GAT	TAT	CGT	TAT	GAA	CTA	AAA	TTG	3600
	Lys	Asp	Gly	Tyr	Gln	Thr	Glu	Thr	Asp	Tyr	Arg	Tyr	Glu	Leu	Lys	Leu	
		1185				1190					1195					1200	
40	GCG	CAT	ATC	CGC	TAT	GAT	GGC	ACT	TGG	AAT	ACG	CCA	ATC	ACC	TTT	GAT	3648
	Ala	His	Ile	Arg	Tyr	Asp	Gly	Thr	Trp	Asn	Thr	Pro	Ile	Thr	Phe	Asp	
					1205					1210					1215		
45	GTC	AAT	AAA	AAA	ATA	TCC	GAG	CTA	AAA	CTG	GAA	AAA	AAT	AGA	GCG	CCC	3696
	Val	Asn	Lys	Lys	Ile	Ser	Glu	Leu	Lys	Leu	Glu	Lys	Asn	Arg	Ala	Pro	
				1220					1225					1230			
50	GGA	CTC	TAT	TGT	GCC	GGT	TAT	CAA	GGT	GAA	GAT	ACG	TTG	CTG	GTG	ATG	3744
	Gly	Leu	Tyr	Cys	Ala	Gly	Tyr	Gln	Gly	Glu	Asp	Thr	Leu	Leu	Val	Met	
			1235					1240					1245				
55	TTT	TAT	AAC	CAA	CAA	GAC	ACA	CTA	GAT	AGT	TAT	AAA	AAC	GCT	TCA	ATG	3792
	Phe	Tyr	Asn	Gln	Gln	Asp	Thr	Leu	Asp	Ser	Tyr	Lys	Asn	Ala	Ser	Met	
		1250				1255						1260					
60	CAA	GGA	CTA	TAT	ATC	TTT	GCT	GAT	ATG	GCA	TCC	AAA	GAT	ATG	ACC	CCA	3840
	Gln	Gly	Leu	Tyr	Ile	Phe	Ala	Asp	Met	Ala	Ser	Lys	Asp	Met	Thr	Pro	
		1265				1270					1275					1280	
65	GAA	CAG	AGC	AAT	GTT	TAT	CGG	GAT	AAT	AGC	TAT	CAA	CAA	TTT	GAT	ACC	3888
	Glu	Gln	Ser	Asn	Val	Tyr	Arg	Asp	Asn	Ser	Tyr	Gln	Gln	Phe	Asp	Thr	
					1285					1290					1295		
70	AAT	AAT	GTC	AGA	AGA	GTG	AAT	AAC	CGC	TAT	GCA	GAG	GAT	TAT	GAG	ATT	3936
	Asn	Asn	Val	Arg	Arg	Val	Asn	Asn	Arg	Tyr	Ala	Glu	Asp	Tyr	Glu	Ile	
				1300					1305					1310			
75	CCT	TCC	TCG	GTA	AGT	AGC	CGT	AAA	GAC	TAT	GGT	TGG	GGA	GAT	TAT	TAC	3984
	Pro	Ser	Ser	Val	Ser	Ser	Arg	Lys	Asp	Tyr	Gly	Trp	Gly	Asp	Tyr	Tyr	
			1315					1320					1325				
80	CTC	AGC	ATG	GTA	TAT	AAC	GGA	GAT	ATT	CCA	ACT	ATC	AAT	TAC	AAA	GCC	4032
	Leu	Ser	Met	Val	Tyr	Asn	Gly	Asp	Ile	Pro	Thr	Ile	Asn	Tyr	Lys	Ala	
		1330					1335					1340					
85	GCA	TCA	AGT	GAT	TTA	AAA	ATC	TAT	ATC	TCA	CCA	AAA	TTA	AGA	ATT	ATT	4080
	Ala	Ser	Ser	Asp	Leu	Lys	Ile	Tyr	Ile	Ser	Pro	Lys	Leu	Arg	Ile	Ile	

	1345		1350		1355		1360	
5	CAT AAT GGA TAT GAA GGA CAG AAG CGC AAT CAA TGC AAT CTG ATG AAT 4128 His Asn Gly Tyr Glu Gly Gln Lys Arg Asn Gln Cys Asn Leu Met Asn 1365 1370 1375							
10	AAA TAT GGC AAA CTA GGT GAT AAA TTT ATT GTT TAT ACT AGC TTG GGG 4176 Lys Tyr Gly Lys Leu Gly Asp Lys Phe Ile Val Tyr Thr Ser Leu Gly 1380 1385 1390							
15	GTC AAT CCA AAT AAC TCG TCA AAT AAG CTC ATG TTT TAC CCC GTC TAT 4224 Val Asn Pro Asn Asn Ser Ser Asn Lys Leu Met Phe Tyr Pro Val Tyr 1395 1400 1405							
20	CAA TAT AGC GGA AAC ACC AGT GGA CTC AAT CAA GGG AGA CTA CTA TTC 4272 Gln Tyr Ser Gly Asn Thr Ser Gly Leu Asn Gln Gly Arg Leu Leu Phe 1410 1415 1420							
25	CAC CGT GAC ACC ACT TAT CCA TCT AAA GTA GAA GCT TGG ATT CCT GGA 4320 His Arg Asp Thr Thr Tyr Pro Ser Lys Val Glu Ala Trp Ile Pro Gly 1425 1430 1435 1440							
30	GCA AAA CGT TCT CTA ACC AAC CAA AAT GCC GCC ATT GGT GAT GAT TAT 4368 Ala Lys Arg Ser Leu Thr Asn Gln Asn Ala Ala Ile Gly Asp Asp Tyr 1445 1450 1455							
35	GCT ACA GAC TCT CTG AAT AAA CCG GAT GAT CTT AAG CAA TAT ATC TTT 4416 Ala Thr Asp Ser Leu Asn Lys Pro Asp Asp Leu Lys Gln Tyr Ile Phe 1460 1465 1470							
40	ATG ACT GAC AGT AAA GGG ACT GCT ACT GAT GTC TCA GGC CCA GTA GAG 4464 Met Thr Asp Ser Lys Gly Thr Ala Thr Asp Val Ser Gly Pro Val Glu 1475 1480 1485							
45	ATT AAT ACT GCA ATT TCT CCA GCA AAA GTT CAG ATA ATA GTC AAA GCG 4512 Ile Asn Thr Ala Ile Ser Pro Ala Lys Val Gln Ile Ile Val Lys Ala 1490 1495 1500							
50	GGT GGC AAG GAG CAA ACT TTT ACC GCA GAT AAA GAT GTC TCC ATT CAG 4560 Gly Gly Lys Glu Gln Thr Phe Thr Ala Asp Lys Asp Val Ser Ile Gln 1505 1510 1515 1520							
55	CCA TCA CCT AGC TTT GAT GAA ATG AAT TAT CAA TTT AAT GCC CTT GAA 4608 Pro Ser Pro Ser Phe Asp Glu Met Asn Tyr Gln Phe Asn Ala Leu Glu 1525 1530 1535							
60	ATA GAC GGT TCT GGT CTG AAT TTT ATT AAC AAC TCA GCC AGT ATT GAT 4656 Ile Asp Gly Ser Gly Leu Asn Phe Ile Asn Asn Ser Ala Ser Ile Asp 1540 1545 1550							
65	GTT ACT TTT ACC GCA TTT GCG GAG GAT GGC CGC AAA CTG GGT TAT GAA 4704 Val Thr Phe Thr Ala Phe Ala Glu Asp Gly Arg Lys Leu Gly Tyr Glu 1555 1560 1565							
70	AGT TTC AGT ATT CCT GTT ACC CTC AAG GTA AGT ACC GAT AAT GCC CTG 4752 Ser Phe Ser Ile Pro Val Thr Leu Lys Val Ser Thr Asp Asn Ala Leu 1570 1575 1580							
	ACC CTG CAC CAT AAT GAA AAT GGT GCG CAA TAT ATG CAA TGG CAA TCC 4800 Thr Leu His His Asn Glu Asn Gly Ala Gln Tyr Met Gln Trp Gln Ser 1585 1590 1595 1600							
	TAT CGT ACC CGC CTG AAT ACT CTA TTT GCC CGC CAG TTG GTT GCA CGC 4848 Tyr Arg Thr Arg Leu Asn Thr Leu Phe Ala Arg Gln Leu Val Ala Arg 1605 1610 1615							
	GCC ACC ACC GGA ATC GAT ACA ATT CTG AGT ATG GAA ACT CAG AAT ATT 4896 Ala Thr Thr Gly Ile Asp Thr Ile Leu Ser Met Glu Thr Gln Asn Ile 1620 1625 1630							
	CAG GAA CCG CAG TTA GGC AAA GGT TTC TAT GCT ACG TTC GTG ATA CCT 4944							

	Gln	Glu	Pro	Gln	Leu		Lys	Gly	Phe	Tyr	Ala	Thr	Phe	V	le	Pro	
			1635					1640						1645			
5	CCC	TAT	AAC	CTA	TCA	ACT	CAT	GGT	GAT	GAA	CGT	TGG	TTT	AAG	CTT	TAT	4992
	Pro	Tyr	Asn	Leu	Ser	Thr	His	Gly	Asp	Glu	Arg	Trp	Phe	Lys	Leu	Tyr	
		1650					1655					1660					
10	ATC	AAA	CAT	GTT	GTT	GAT	AAT	AAT	TCA	CAT	ATT	ATC	TAT	TCA	GGC	CAG	5040
	Ile	Lys	His	Val	Val	Asp	Asn	Asn	Ser	His	Ile	Ile	Tyr	Ser	Gly	Gln	
	1665					1670				1675						1680	
15	CTA	ACA	GAT	ACA	AAT	ATA	AAC	ATC	ACA	TTA	TTT	ATT	CCT	CTT	GAT	GAT	5088
	Leu	Thr	Asp	Thr	Asn	Ile	Asn	Ile	Thr	Leu	Phe	Ile	Pro	Leu	Asp	Asp	
					1685					1690					1695		
20	GTC	CCA	TTG	AAT	CAA	GAT	TAT	CAC	GCC	AAG	GTT	TAT	ATG	ACC	TTC	AAG	5136
	Val	Pro	Leu	Asn	Gln	Asp	Tyr	His	Ala	Lys	Val	Tyr	Met	Thr	Phe	Lys	
				1700					1705					1710			
25	AAA	TCA	CCA	TCA	GAT	GGT	ACC	TGG	TGG	GGC	CCT	CAC	TTT	GTT	AGA	GAT	5184
	Lys	Ser	Pro	Ser	Asp	Gly	Thr	Trp	Trp	Gly	Pro	His	Phe	Val	Arg	Asp	
			1715					1720					1725				
30	GAT	AAA	GGA	ATA	GTA	ACA	ATA	AAC	CCT	AAA	TCC	ATT	TTG	ACC	CAT	TTT	5232
	Asp	Lys	Gly	Ile	Val	Thr	Ile	Asn	Pro	Lys	Ser	Ile	Leu	Thr	His	Phe	
		1730					1735						1740				
35	GAG	AGC	GTC	AAT	GTC	CTG	AAT	AAT	ATT	AGT	AGC	GAA	CCA	ATG	GAT	TTC	5280
	Glu	Ser	Val	Asn	Val	Leu	Asn	Asn	Ile	Ser	Ser	Glu	Pro	Met	Asp	Phe	
	1745					1750					1755					1760	
40	AGC	GGC	GCT	AAC	AGC	CTC	TAT	TTC	TGG	GAA	CTG	TTC	TAC	TAT	ACC	CCG	5328
	Ser	Gly	Ala	Asn	Ser	Leu	Tyr	Phe	Trp	Glu	Leu	Phe	Tyr	Tyr	Thr	Pro	
				1765						1770					1775		
45	ATG	CTG	GTT	GCT	CAA	CGT	TTG	CTG	CAT	GAA	CAG	AAC	TTC	GAT	GAA	GCC	5376
	Met	Leu	Val	Ala	Gln	Arg	Leu	Leu	His	Glu	Gln	Asn	Phe	Asp	Glu	Ala	
				1780					1785					1790			
50	AAC	CGT	TGG	CTG	AAA	TAT	GTC	TGG	AGT	CCA	TCC	GGT	TAT	ATT	GTC	CAC	5424
	Asn	Arg	Trp	Leu	Lys	Tyr	Val	Trp	Ser	Pro	Ser	Gly	Tyr	Ile	Val	His	
			1795					1800					1805				
55	GGC	CAG	ATT	CAG	AAC	TAC	CAG	TGG	AAC	CTC	CGC	CCG	TTA	CTG	GAA	GAC	5472
	Gly	Gln	Ile	Gln	Asn	Tyr	Gln	Trp	Asn	Val	Arg	Pro	Leu	Leu	Glu	Asp	
		1810					1815					1820					
60	ACC	AGT	TGG	AAC	AGT	GAT	CCT	TTG	GAT	TCC	GTC	GAT	CCT	GAC	GCG	GTA	5520
	Thr	Ser	Trp	Asn	Ser	Asp	Pro	Leu	Asp	Ser	Val	Asp	Pro	Asp	Ala	Val	
	1825					1830					1835					1840	
65	GCA	CAG	CAC	GAT	CCA	ATG	CAC	TAC	AAA	GTT	TCA	ACT	TTT	ATG	CGT	ACC	5568
	Ala	Gln	His	Asp	Pro	Met	His	Tyr	Lys	Val	Ser	Thr	Phe	Met	Arg	Thr	
				1845						1850					1855		
70	TTG	GAT	CTA	TTG	ATA	GCA	CGC	GGC	GAC	CAT	GCT	TAT	CGC	CAA	CTG	GAA	5616
	Leu	Asp	Leu	Leu	Ile	Ala	Arg	Gly	Asp	His	Ala	Tyr	Arg	Gln	Leu	Glu	
				1860				1865						1870			
75	CGA	GAT	ACA	CTC	AAC	GAA	GCG	AAG	ATG	TGG	TAT	ATG	CAA	GCG	CTG	CAT	5664
	Arg	Asp	Thr	Leu	Asn	Glu	Ala	Lys	Met	Trp	Tyr	Met	Gln	Ala	Leu	His	
			1875					1880					1885				
80	CTA	TTA	GGT	GAC	AAA	CCT	TAT	CTA	CCG	CTG	AGT	ACG	ACA	TGG	AGT	GAT	5712
	Leu	Leu	Gly	Asp	Lys	Pro	Tyr	Leu	Pro	Leu	Ser	Thr	Thr	Trp	Ser	Asp	
		1890					1895					1900					
85	CCA	CGA	CTA	GAC	AGA	GCC	GCG	GAT	ATC	ACT	ACC	CAA	AAT	GCT	CAC	GAC	5760
	Pro	Arg	Leu	Asp	Arg	Ala	Ala	Asp	Ile	Thr		Gln	Asn	Ala	His	Asp	
	1905					1910					1915					1920	

	AGC	GCA	ATA	GTG	CTG	CGG	CAG	AAT	ATA	CCT	ACA	CCG	GCA	CCT	TTA	5808
	Ser	Ala	Ile	Val	Ala	Leu	Arg	Gln	Asn	Ile	Pro	Thr	Pro	Ala	Pro	Leu
				1925						1930					1935	
5	TCA	TTG	CGC	AGC	GCT	AAT	ACC	CTG	ACT	GAT	CTC	TTC	CTG	CCG	CAA	ATC
	Ser	Leu	Arg	Ser	Ala	Asn	Thr	Leu	Thr	Asp	Leu	Phe	Leu	Pro	Gln	Ile
				1940					1945					1950		
10	AAT	GAA	GTG	ATG	ATG	AAT	TAC	TGG	CAG	ACA	TTA	GCT	CAG	AGA	GTA	TAC
	Asn	Glu	Val	Met	Met	Asn	Tyr	Trp	Gln	Thr	Leu	Ala	Gln	Arg	Val	Tyr
			1955					1960					1965			
15	AAT	CTG	CGT	CAT	AAC	CTC	TCT	ATC	GAC	GGC	CAG	CCG	TTA	TAT	CTG	CCA
	Asn	Leu	Arg	His	Asn	Leu	Ser	Ile	Asp	Gly	Gln	Pro	Leu	Tyr	Leu	Pro
		1970					1975					1980				
20	ATC	TAT	GCC	ACA	CCG	GCC	GAT	CCG	AAA	GCG	TTA	CTC	AGC	GCC	GCC	GTT
	Ile	Tyr	Ala	Thr	Pro	Ala	Asp	Pro	Lys	Ala	Leu	Leu	Ser	Ala	Ala	Val
	1985					1990					1995					2000
25	GCC	ACT	TCT	CAA	GGT	GGA	GGC	AAG	CTA	CCG	GAA	TCA	TTT	ATG	TCC	CTG
	Ala	Thr	Ser	Gln	Gly	Gly	Gly	Lys	Leu	Pro	Glu	Ser	Phe	Met	Ser	Leu
				2005						2010					2015	
30	TGG	CGT	TTC	CCG	CAC	ATG	CTG	GAA	AAT	GCG	CGC	GGC	ATG	GTT	AGC	CAG
	Trp	Arg	Phe	Pro	His	Met	Leu	Glu	Asn	Ala	Arg	Gly	Met	Val	Ser	Gln
				2020					2025					2030		
35	CTC	ACC	CAG	TTC	GGC	TCC	ACG	TTA	CAA	AAT	ATT	ATC	GAA	CGT	CAG	GAC
	Leu	Thr	Gln	Phe	Gly	Ser	Thr	Leu	Gln	Asn	Ile	Ile	Glu	Arg	Gln	Asp
			2035					2040					2045			
40	GCG	GAA	GCG	CTC	AAT	GCG	TTA	TTA	CAA	AAT	CAG	GCC	GCC	GAG	CTG	ATA
	Ala	Glu	Ala	Leu	Asn	Ala	Leu	Leu	Gln	Asn	Gln	Ala	Ala	Glu	Leu	Ile
		2050				2055					2060					
45	TTG	ACT	AAC	CTG	AGC	ATT	CAG	GAC	AAA	ACC	ATT	GAA	GAA	TTG	GAT	GCC
	Leu	Thr	Asn	Leu	Ser	Ile	Gln	Asp	Lys	Thr	Ile	Glu	Glu	Leu	Asp	Ala
	2065					2070					2075					2080
50	GAG	AAA	ACG	GTG	TTG	GAA	AAA	TCC	AAA	GCG	GGA	GCA	CAA	TCG	CGC	TTT
	Glu	Lys	Thr	Val	Leu	Glu	Lys	Ser	Lys	Ala	Gly	Ala	Gln	Ser	Arg	Phe
				2085						2090					2095	
55	GAT	AGC	TAC	GGC	AAA	CTG	TAC	GAT	GAG	AAT	ATC	AAC	GCC	GGT	GAA	AAC
	Asp	Ser	Tyr	Gly	Lys	Leu	Tyr	Asp	Glu	Asn	Ile	Asn	Ala	Gly	Glu	Asn
				2100					2105					2110		
60	CAA	GCC	ATG	ACG	CTA	CGA	GCG	TCC	GCC	GCC	GGG	CTT	ACC	ACG	GCA	GTT
	Gln	Ala	Met	Thr	Leu	Arg	Ala	Ser	Ala	Ala	Gly	Leu	Thr	Thr	Ala	Val
			2115					2120					2125			
65	CAG	GCA	TCC	CGT	CTG	GCC	GGT	GCG	GCG	GCT	GAT	CTG	GTG	CCT	AAC	ATC
	Gln	Ala	Ser	Arg	Leu	Ala	Gly	Ala	Ala	Ala	Asp	Leu	Val	Pro	Asn	Ile
		2130				2135						2140				
70	TTC	GGC	TTT	GCC	GGT	GGC	GGC	AGC	CGT	TGG	GGG	GCT	ATC	GCT	GAG	GCG
	Phe	Gly	Phe	Ala	Gly	Gly	Gly	Ser	Arg	Trp	Gly	Ala	Ile	Ala	Glu	Ala
	2145				2150						2155					2160
75	ACA	GGT	TAT	GTG	ATG	GAA	TTC	TCC	GCG	AAT	GTT	ATG	AAC	ACC	GAA	GCG
	Thr	Gly	Tyr	Val	Met	Glu	Phe	Ser	Ala	Asn	Val	Met	Asn	Thr	Glu	Ala
				2165						2170					2175	
80	GAT	AAA	ATT	AGC	CAA	TCT	GAA	ACC	TAC	CGT	CGT	CGC	CGT	CAG	GAG	TGG
	Asp	Lys	Ile	Ser	Gln	Ser	Glu	Thr	Tyr	Arg	Arg	Arg	Arg	Gln	Glu	Trp
				2180					2185					2190		
85	GAG	ATC	CAG	CGG	AAT	AAT	GCC	GAA	GCG	GAA	TTG	AAG	CAA	ATC	GAT	GCT
	Glu	Ile	Gln	Arg	Asn	Asn	Ala	Glu	Ala	Glu	Leu	Lys	Gln	Ile	Asp	Ala
			2195				2200						2205			

5	CAG Gln 2210	CTC Leu	AAA Lys 2210	TCA Ser	CTC Leu	GCT Ala 2215	GTA Val 2215	CGC Arg	CGC Arg	GAA Glu 2220	GCC Ala 2220	GCC Ala 2220	GTA Val	TTG Leu	CAG Gln	AAA Lys	6672
10	ACC Thr 2225	AGT Ser	CTG Leu	AAA Lys	ACC Thr	CAA Gln 2230	CAA Gln 2230	GAA Glu	CAG Gln	ACC Thr	CAA Gln 2235	TCT Ser	CAA Gln	TTG Leu	GCC Ala	TTC Phe 2240	6720
15	CTG Leu	CAA Gln	CGT Arg	AAG Lys	TTC Phe 2245	AGC Ser	AAT Asn	CAG Gln	GCG Ala	TTA Leu 2250	TAC Tyr	AAC Asn	TGG Trp	CTG Leu	CGT Arg	GGT Gly 2255	6768
20	CGA Arg	CTG Leu	GCG Ala	GCG Ala 2260	ATT Ile	TAC Tyr	TTC Phe	CAG Gln	TTC Phe 2265	TAC Tyr	GAT Asp	TTG Leu	GCC Ala	GTC Val	GCG Ala	CGT Arg	6816
25	TGC Cys	CTG Leu	ATG Met 2275	GCA Ala	GAA Glu	CAA Gln	GCT Ala	TAC Tyr 2280	CGT Arg	TGG Trp	GAA Glu	CTC Leu	AAT Asn 2285	GAT Asp	GAC Asp	TCT Ser	6864
30	GCC Ala 2290	CGC Arg	TTC Phe	ATT Ile	AAA Lys	CCG Pro	GGC Gly 2295	GCC Ala	TGG Trp	CAG Gln	GGA Gly 2300	ACC Thr	TAT Tyr	GCC Ala	GGT Gly	CTG Leu	6912
35	CTT Leu 2305	GCA Ala	GGT Gly	GAA Glu	ACC Thr	TTG Leu 2310	ATG Met	CTG Leu	AGT Ser	CTG Leu	GCA Ala 2315	CAA Gln	ATG Met	GAA Glu	GAC Asp	GCT Ala 2320	6960
40	CAT His	CTG Leu	AAA Lys	CGC Arg	GAT Asp 2325	AAA Lys	CGC Arg	GCA Ala	TTA Leu	GAG Glu 2330	GTT Val	GAA Glu	CGC Arg	ACA Thr	GTA Val	TCG Ser 2335	7008
45	CTG Leu	GCC Ala	GAA Glu	GTT Val 2340	TAT Tyr	GCA Ala	GGA Gly	TTA Leu	CCA Pro	AAA Lys 2345	GAT Asp	AAC Asn	GGT Gly	CCA Pro	TTT Phe	TCC Ser 2350	7056
50	CTG Leu	GCT Ala	CAG Gln	GAA Glu	ATT Ile 2355	GAC Asp	AAG Lys	CTG Leu	GTG Val	AGT Ser	CAA Gln	GGT Gly	TCA Ser	GGC Gly	AGT Ser	GCC Ala	7104
55	GGC Gly 2370	AGT Ser	GGT Gly	AAT Asn	AAT Asn	AAT Asn	TTG Leu 2375	GCG Ala	TTC Phe	GGC Gly	GCC Ala	GGC Gly 2380	ACG Thr	GAC Asp	ACT Thr	AAA Lys	7152
60	ACC Thr 2385	TCT Ser	TTG Leu	CAG Gln	GCA Ala	TCA Ser 2390	GTT Val	TCA Ser	TTC Phe	GCT Ala	GAT Asp 2395	TTG Leu	AAA Lys	ATT Ile	CGT Arg	GAA Glu 2400	7200
65	GAT Asp	TAC Tyr	CCG Pro	GCA Ala	TCG Ser 2405	CTT Leu	GGC Gly	AAA Lys	ATT Ile	CGA Arg 2410	CGT Arg	ATC Ile	AAA Lys	CAG Gln	ATC Ile	AGC Ser 2415	7248
70	GTC Val	ACT Thr	TTG Leu	CCC Pro	GCG Ala	CTA Leu	CTG Leu	GGA Gly	CCG Pro	TAT Tyr	CAG Gln	GAT Asp	GTA Val	CAG Gln	GCA Ala	ATA Ile	7296
75	TTG Leu	TCT Ser	TAC Tyr	GGC Gly	GAT Asp	AAA Lys	GCC Ala	GGA Gly	TTA Leu	GCT Ala	AAC Asn	GGC Gly	TGT Cys	GAA Glu	GCG Ala	CTG Leu	7344
80	GCA Ala 2450	GTT Val	TCT Ser	CAC His	GGT Gly	ATG Met	AAT Asn 2455	GAC Asp	AGC Ser	GGC Gly	CAA Gln	TTC Phe 2460	CAG Gln	CTC Leu	GAT Asp	TTC Phe	7392
85	AAC Asn 2465	GAT Asp	GGC Gly	AAA Lys	TTC Phe	CTG Leu 2470	CCA Pro	TTC Phe	GAA Glu	GGC Gly	ATC Ile 2475	GCC Ala	ATT Ile	GAT Asp	CAA Gln	GGC Gly 2480	7440
90	ACG Thr	CTG Leu	ACA Thr	CTG Leu	AGC Ser	TTC Phe	CCA Pro	AAT Asn	GCA Ala	TCT Ser	ATG Met	CCG Pro	GAG Glu	AAA Lys	GGT Gly	AAA Lys	7488

[illegible]

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2516 amino acids
(B) TYPE: amino acids
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47 (TcdA):

	Features	From	To	Description
	Peptide	1	2516	TcdA proteins
	Peptide	89	1937	TcdA _{ii} peptide
25	Fragment	89	100	TcdA _{ii} N-terminus (SEQ ID NO:13)
	Fragment	284	299	(SEQ ID NO:38)
	Fragment	554	563	(SEQ ID NO:17)
	Fragment	1080	1092	(SEQ ID NO:23; 12/13)
	Fragment	1385	1400	(SEQ ID NO:18)
30	Fragment	1478	1497	(SEQ ID NO:39)
	Fragment	1620	1642	(SEQ ID NO:21; 19/23)
	Fragment	1938	1948	(SEQ ID NO:41)
	Peptide	1938	2516	TcdA _{iii} peptide
	Fragment	2327	2345	(SEQ ID NO:42)
35	Fragment	2398	2408	(SEQ ID NO:43)

	Met 1	Asn	Glu	Ser	Val 5	Lys	Glu	Ile	Pro	Asp 10	Val	Leu	Lys	Ser	Gln 15	Cys
40	Gly	Phe	Asn 20	Cys	Leu	Thr	Asp	Ile	Ser 25	His	Ser	Ser	Phe	Asn 30	Glu	Phe
	Arg	Gln	Gln 35	Val	Ser	Glu	His	Leu 40	Ser	Trp	Ser	Glu	Thr 45	His	Asp	Leu
45	Tyr 50	His	Asp	Ala	Gln	Gln	Ala 55	Gln	Lys	Asp	Asn	Arg 60	Leu	Tyr	Glu	Ala
	Arg 65	Ile	Leu	Lys	Arg	Ala 70	Asn	Pro	Gln	Leu	Gln 75	Asn	Ala	Val	His	Leu 80
50	Ala	Ile	Leu	Ala	Pro 85	Asn	Ala	Glu	Leu	Ile 90	Gly	Tyr	Asn	Asn	Gln 95	Phe
55	Ser	Gly	Arg	Ala 100	Ser	Gln	Tyr	Val	Ala 105	Pro	Gly	Thr	Val	Ser 110	Ser	Met
	Phe	Ser	Pro 115	Ala	Ala	Tyr	Leu	Thr 120	Glu	Leu	Tyr	Arg	Glu 125	Ala	Arg	Asn
60	Leu 130	His	Ala	Ser	Asp	Ser	Val 135	Tyr	Tyr	Leu	Asp	Thr 140	Arg	Arg	Pro	Asp
	Leu 145	Lys	Ser	Met	Ala	Leu 150	Ser	Gln	Gln	Asn	Met 155	Asp	Ile	Glu	Leu	Ser 160
65	Thr	Leu	Ser	Leu	Ser	Asn	Glu	Leu	Leu	Leu	Glu	Ser	Ile	Lys	Thr	Glu

	165								170								175															
	Ser	Lys	Leu	Glu	Asn	Tyr	Thr	Lys	Val	Met	Glu	Met	Leu	Ser	Thr	Phe																
				180					185					190																		
5	Arg	Pro	Ser	Gly	Ala	Thr	Pro	Tyr	His	Asp	Ala	Tyr	Glu	Asn	Val	Arg																
			195					200					205																			
10	Glu	Val	Ile	Gln	Leu	Gln	Asp	Pro	Gly	Leu	Glu	Gln	Leu	Asn	Ala	Ser																
			210				215						220																			
	Pro	Ala	Ile	Ala	Gly	Leu	Met	His	Gln	Ala	Ser	Leu	Leu	Gly	Ile	Asn																
			225			230					235				240																	
15	Ala	Ser	Ile	Ser	Pro	Glu	Leu	Phe	Asn	Ile	Leu	Thr	Glu	Glu	Ile	Thr																
					245					250					255																	
	Glu	Gly	Asn	Ala	Glu	Glu	Leu	Tyr	Lys	Lys	Asn	Phe	Gly	Asn	Ile	Glu																
				260					265					270																		
20	Pro	Ala	Ser	Leu	Ala	Met	Pro	Glu	Tyr	Leu	Lys	Arg	Tyr	Tyr	Asn	Leu																
			275					280					285																			
25	Ser	Asp	Glu	Glu	Leu	Ser	Gln	Phe	Ile	Gly	Lys	Ala	Ser	Asn	Phe	Gly																
		290					295					300																				
	Gln	Gln	Glu	Tyr	Ser	Asn	Asn	Gln	Leu	Ile	Thr	Pro	Val	Val	Asn	Ser																
		305				310					315				320																	
30	Ser	Asp	Gly	Thr	Val	Lys	Val	Tyr	Arg	Ile	Thr	Arg	Glu	Tyr	Thr	Thr																
					325					330					335																	
	Asn	Ala	Tyr	Gln	Met	Asp	Val	Glu	Leu	Phe	Pro	Phe	Gly	Gly	Glu	Asn																
				340				345					350																			
35	Tyr	Arg	Leu	Asp	Tyr	Lys	Phe	Lys	Asn	Phe	Tyr	Asn	Ala	Ser	Tyr	Leu																
			355					360					365																			
40	Ser	Ile	Lys	Leu	Asn	Asp	Lys	Arg	Glu	Leu	Val	Arg	Thr	Glu	Gly	Ala																
		370					375					380																				
	Pro	Gln	Val	Asn	Ile	Glu	Tyr	Ser	Ala	Asn	Ile	Thr	Leu	Asn	Thr	Ala																
		385				390					395				400																	
45	Asp	Ile	Ser	Gln	Pro	Phe	Glu	Ile	Gly	Leu	Thr	Arg	Val	Leu	Pro	Ser																
					405					410					415																	
	Gly	Ser	Trp	Ala	Tyr	Ala	Ala	Ala	Lys	Phe	Thr	Val	Glu	Glu	Tyr	Asn																
				420					425				430																			
50	Gln	Tyr	Ser	Phe	Leu	Leu	Lys	Leu	Asn	Lys	Ala	Ile	Arg	Leu	Ser	Arg																
			435					440					445																			
55	Ala	Thr	Glu	Leu	Ser	Pro	Thr	Ile	Leu	Glu	Gly	Ile	Val	Arg	Ser	Val																
		450					455					460																				
	Asn	Leu	Gln	Leu	Asp	Ile	Asn	Thr	Asp	Val	Leu	Gly	Lys	Val	Phe	Leu																
		465				470					475				480																	
60	Thr	Lys	Tyr	Tyr	Met	Gln	Arg	Tyr	Ala	Ile	His	Ala	Glu	Thr	Ala	Leu																
					485					490					495																	
	Ile	Leu	Cys	Asn	Ala	Pro	Ile	Ser	Gln	Arg	Ser	Tyr	Asp	Asn	Gln	Pro																
				500					505				510																			
65	Ser	Gln	Phe	Asp	Arg	Leu	Phe	Asn	Thr	Pro	Leu	Leu	Asn	Gly	Gln	Tyr																
			515					520					525																			
70	Phe	Ser	Thr	Gly	Asp	Glu	Glu	Ile	Asp	Leu	Asn	Ser	Gly	Ser	Thr	Gly																
		530					535					540																				

	Asp	Trp	Arg	Lys	Thr	Ile	Leu	Lys	Arg	Ala	Phe	Asn	Ile	Asp	Asp	Val
	545					550					555					560
5	Ser	Leu	Phe	Arg	Leu	Leu	Lys	Ile	Thr	Asp	His	Asp	Asn	Lys	Asp	Gly
					565					570					575	
	Lys	Ile	Lys	Asn	Asn	Leu	Lys	Asn	Leu	Ser	Asn	Leu	Tyr	Ile	Gly	Lys
				580					585					590		
10	Leu	Leu	Ala	Asp	Ile	His	Gln	Leu	Thr	Ile	Asp	Glu	Leu	Asp	Leu	Leu
			595					600					605			
	Leu	Ile	Ala	Val	Gly	Glu	Gly	Lys	Thr	Asn	Leu	Ser	Ala	Ile	Ser	Asp
15		610					615					620				
	Lys	Gln	Leu	Ala	Thr	Leu	Ile	Arg	Lys	Leu	Asn	Thr	Ile	Thr	Ser	Trp
	625					630					635					640
20	Leu	His	Thr	Gln	Lys	Trp	Ser	Val	Phe	Gln	Leu	Phe	Ile	Met	Thr	Ser
				645						650				655		
	Thr	Ser	Tyr	Asn	Lys	Thr	Leu	Thr	Pro	Glu	Ile	Lys	Asn	Leu	Leu	Asp
				660					665					670		
25	Thr	Val	Tyr	His	Gly	Leu	Gln	Gly	Phe	Asp	Lys	Asp	Lys	Ala	Asp	Leu
			675					680					685			
	Leu	His	Val	Met	Ala	Pro	Tyr	Ile	Ala	Ala	Thr	Leu	Gln	Leu	Ser	Ser
30		690					695					700				
	Glu	Asn	Val	Ala	His	Ser	Val	Leu	Leu	Trp	Ala	Asp	Lys	Leu	Gln	Pro
	705					710					715					720
35	Gly	Asp	Gly	Ala	Met	Thr	Ala	Glu	Lys	Phe	Trp	Asp	Trp	Leu	Asn	Thr
				725						730					735	
	Lys	Tyr	Thr	Pro	Gly	Ser	Ser	Glu	Ala	Val	Glu	Thr	Gln	Glu	His	Ile
				740					745					750		
40	Val	Gln	Tyr	Cys	Gln	Ala	Leu	Ala	Gln	Leu	Glu	Met	Val	Tyr	His	Ser
			755				760						765			
	Thr	Gly	Ile	Asn	Glu	Asn	Ala	Phe	Arg	Leu	Phe	Val	Thr	Lys	Pro	Glu
45		770					775					780				
	Met	Phe	Gly	Ala	Ala	Thr	Gly	Ala	Ala	Pro	Ala	His	Asp	Ala	Leu	Ser
	785					790					795					800
50	Leu	Ile	Met	Leu	Thr	Arg	Phe	Ala	Asp	Trp	Val	Asn	Ala	Leu	Gly	Glu
				805						810					815	
	Lys	Ala	Ser	Ser	Val	Leu	Ala	Ala	Phe	Glu	Ala	Asn	Ser	Leu	Thr	Ala
				820					825					830		
55	Glu	Gln	Leu	Ala	Asp	Ala	Met	Asn	Leu	Asp	Ala	Asn	Leu	Leu	Leu	Gln
			835					840					845			
	Ala	Ser	Ile	Gln	Ala	Gln	Asn	His	Gln	His	Leu	Pro	Pro	Val	Thr	Pro
60		850					855					860				
	Glu	Asn	Ala	Phe	Ser	Cys	Trp	Thr	Ser	Ile	Asn	Thr	Ile	Leu	Gln	Trp
	865					870					875					880
65	Val	Asn	Val	Ala	Gln	Gln	Leu	Asn	Val	Ala	Pro	Gln	Gly	Val	Ser	Ala
				885						890					895	
	Leu	Val	Gly	Leu	Asp	Tyr	Ile	Gln	Ser	Met	Lys	Glu	Thr	Pro	Thr	Tyr
				900					905					910		
70	Ala	Gln	Trp	Glu	Asn	Ala	Ala	Gly	Val	Leu	Thr	Ala	Gly	Leu	Asn	Ser
			915					920					925			

	Gln	Gln	Ala	Asn	Thr	Leu	His	Ala	Phe	Leu	Asp	Glu	Ser	Arg	Ser	Ala
	930						935					940				
5	Ala	Leu	Ser	Thr	Tyr	Tyr	Ile	Arg	Gln	Val	Ala	Lys	Ala	Ala	Ala	Ala
	945					950					955					960
	Ile	Lys	Ser	Arg	Asp	Asp	Leu	Tyr	Gln	Tyr	Leu	Leu	Ile	Asp	Asn	Gln
10					965					970					975	
	Val	Ser	Ala	Ala	Ile	Lys	Thr	Thr	Arg	Ile	Ala	Glu	Ala	Ile	Ala	Ser
				980					985					990		
	Ile	Gln	Leu	Tyr	Val	Asn	Arg	Ala	Leu	Glu	Asn	Val	Glu	Glu	Asn	Ala
15			995					1000					1005			
	Asn	Ser	Gly	Val	Ile	Ser	Arg	Gln	Phe	Phe	Ile	Asp	Trp	Asp	Lys	Tyr
	1010						1015					1020				
20	Asn	Lys	Arg	Tyr	Ser	Thr	Trp	Ala	Gly	Val	Ser	Gln	Leu	Val	Tyr	Tyr
	1025					1030					1035					1040
	Pro	Glu	Asn	Tyr	Ile	Asp	Pro	Thr	Met	Arg	Ile	Gly	Gln	Thr	Lys	Met
25					1045					1050						
	Met	Asp	Ala	Leu	Leu	Gln	Ser	Val	Ser	Gln	Ser	Gln	Leu	Asn	Ala	Asp
				1060					1065					1070		
30	Thr	Val	Glu	Asp	Ala	Phe	Met	Ser	Tyr	Leu	Thr	Ser	Phe	Glu	Gln	Val
			1075					1080					1085			
	Ala	Asn	Leu	Lys	Val	Ile	Ser	Ala	Tyr	His	Asp	Asn	Ile	Asn	Asn	Asp
							1095					1100				
35	Gln	Gly	Leu	Thr	Tyr	Phe	Ile	Gly	Leu	Ser	Glu	Thr	Asp	Ala	Gly	Glu
	1105					1110					1115					1120
	Tyr	Tyr	Trp	Arg	Ser	Val	Asp	His	Ser	Lys	Phe	Asn	Asp	Gly	Lys	Phe
40					1125					1130					1135	
	Ala	Ala	Asn	Ala	Trp	Ser	Glu	Trp	His	Lys	Ile	Asp	Cys	Pro	Ile	Asn
				1140					1145					1150		
45	Pro	Tyr	Lys	Ser	Thr	Ile	Arg	Pro	Val	Ile	Tyr	Lys	Ser	Arg	Leu	Tyr
			1155					1160					1165			
	Leu	Leu	Trp	Leu	Glu	Gln	Lys	Glu	Ile	Thr	Lys	Gln	Thr	Gly	Asn	Ser
		1170					1175					1180				
50	Lys	Asp	Gly	Tyr	Gln	Thr	Glu	Thr	Asp	Tyr	Arg	Tyr	Glu	Leu	Lys	Leu
	1185					1190					1195					1200
	Ala	His	Ile	Arg	Tyr	Asp	Gly	Thr	Trp	Asn	Thr	Pro	Ile	Thr	Phe	Asp
55					1205					1210					1215	
	Val	Asn	Lys	Lys	Ile	Ser	Glu	Leu	Lys	Leu	Glu	Lys	Asn	Arg	Ala	Pro
				1220					1225					1230		
60	Gly	Leu	Tyr	Cys	Ala	Gly	Tyr	Gln	Gly	Glu	Asp	Thr	Leu	Leu	Val	Met
			1235					1240					1245			
	Phe	Tyr	Asn	Gln	Gln	Asp	Thr	Leu	Asp	Ser	Tyr	Lys	Asn	Ala	Ser	Met
			1250				1255					1260				
65	Gln	Gly	Leu	Tyr	Ile	Phe	Ala	Asp	Met	Ala	Ser	Lys	Asp	Met	Thr	Pro
	1265					1270					1275					1280
	Glu	Gln	Ser	Asn	Val	Tyr	Arg	Asp	Asn	Ser	Tyr	Gln	Gln	Phe	Asp	Thr
70					1285					1290					1295	
	Asn	Asn	Val	Arg	Arg	Val	Asn	Asn	Arg	Tyr	Ala	Glu	Asp	Tyr	Glu	Ile

	1300	1305	1310
	Pro Ser Ser Val Ser Ser Arg Lys Asp Tyr Gly Trp Gly Asp Tyr Tyr 1315 1320 1325		
5	Leu Ser Met Val Tyr Asn Gly Asp Ile Pro Thr Ile Asn Tyr Lys Ala 1330 1335 1340		
10	Ala Ser Ser Asp Leu Lys Ile Tyr Ile Ser Pro Lys Leu Arg Ile Ile 1345 1350 1355 1360		
	His Asn Gly Tyr Glu Gly Gln Lys Arg Asn Gln Cys Asn Leu Met Asn 1365 1370 1375		
15	Lys Tyr Gly Lys Leu Gly Asp Lys Phe Ile Val Tyr Thr Ser Leu Gly 1380 1385 1390		
	Val Asn Pro Asn Asn Ser Ser Asn Lys Leu Met Phe Tyr Pro Val Tyr 1395 1400 1405		
20	Gln Tyr Ser Gly Asn Thr Ser Gly Leu Asn Gln Gly Arg Leu Leu Phe 1410 1415 1420		
25	His Arg Asp Thr Thr Tyr Pro Ser Lys Val Glu Ala Trp Ile Pro Gly 1425 1430 1435 1440		
	Ala Lys Arg Ser Leu Thr Asn Gln Asn Ala Ala Ile Gly Asp Asp Tyr 1445 1450 1455		
30	Ala Thr Asp Ser Leu Asn Lys Pro Asp Asp Leu Lys Gln Tyr Ile Phe 1460 1465 1470		
	Met Thr Asp Ser Lys Gly Thr Ala Thr Asp Val Ser Gly Pro Val Glu 1475 1480 1485		
35	Ile Asn Thr Ala Ile Ser Pro Ala Lys Val Gln Ile Ile Val Lys Ala 1490 1495 1500		
40	Gly Gly Lys Glu Gln Thr Phe Thr Ala Asp Lys Asp Val Ser Ile Gln 1505 1510 1515 1520		
	Pro Ser Pro Ser Phe Asp Glu Met Asn Tyr Gln Phe Asn Ala Leu Glu 1525 1530 1535		
45	Ile Asp Gly Ser Gly Leu Asn Phe Ile Asn Asn Ser Ala Ser Ile Asp 1540 1545 1550		
	Val Thr Phe Thr Ala Phe Ala Glu Asp Gly Arg Lys Leu Gly Tyr Glu 1555 1560 1565		
50	Ser Phe Ser Ile Pro Val Thr Leu Lys Val Ser Thr Asp Asn Ala Leu 1570 1575 1580		
55	Thr Leu His His Asn Glu Asn Gly Ala Gln Tyr Met Gln Trp Gln Ser 1585 1590 1595 1600		
	Tyr Arg Thr Arg Leu Asn Thr Leu Phe Ala Arg Gln Leu Val Ala Arg 1605 1610 1615		
60	Ala Thr Thr Gly Ile Asp Thr Ile Leu Ser Met Glu Thr Gln Asn Ile 1620 1625 1630		
	Gln Glu Pro Gln Leu Gly Lys Gly Phe Tyr Ala Thr Phe Val Ile Pro 1635 1640 1645		
65	Pro Tyr Asn Leu Ser Thr His Gly Asp Glu Arg Trp Phe Lys Leu Tyr 1650 1655 1660		
70	Ile Lys His Val Val Asp Asn Asn Ser His Ile Ile Tyr Ser Gly Gln 1665 1670 1675 1680		

Leu Thr Asp Thr Asn Ile Thr Leu Phe Ile Pro Asp Asp
 1685 1690 1695
 5 Val Pro Leu Asn Gln Asp Tyr His Ala Lys Val Tyr Met Thr Phe Lys
 1700 1705 1710
 Lys Ser Pro Ser Asp Gly Thr Trp Trp Gly Pro His Phe Val Arg Asp
 1715 1720 1725
 10 Asp Lys Gly Ile Val Thr Ile Asn Pro Lys Ser Ile Leu Thr His Phe
 1730 1735 1740
 Glu Ser Val Asn Val Leu Asn Asn Ile Ser Ser Glu Pro Met Asp Phe
 1745 1750 1755 1760
 15 Ser Gly Ala Asn Ser Leu Tyr Phe Trp Glu Leu Phe Tyr Tyr Thr Pro
 1765 1770 1775
 Met Leu Val Ala Gln Arg Leu Leu His Glu Gln Asn Phe Asp Glu Ala
 1780 1785 1790
 20 Asn Arg Trp Leu Lys Tyr Val Trp Ser Pro Ser Gly Tyr Ile Val His
 1795 1800 1805
 25 Gly Gln Ile Gln Asn Tyr Gln Trp Asn Val Arg Pro Leu Leu Glu Asp
 1810 1815 1820
 Thr Ser Trp Asn Ser Asp Pro Leu Asp Ser Val Asp Pro Asp Ala Val
 1825 1830 1835 1840
 30 Ala Gln His Asp Pro Met His Tyr Lys Val Ser Thr Phe Met Arg Thr
 1845 1850 1855
 Leu Asp Leu Leu Ile Ala Arg Gly Asp His Ala Tyr Arg Gln Leu Glu
 1860 1865 1870
 35 Arg Asp Thr Leu Asn Glu Ala Lys Met Trp Tyr Met Gln Ala Leu His
 1875 1880 1885
 40 Leu Leu Gly Asp Lys Pro Tyr Leu Pro Leu Ser Thr Thr Trp Ser Asp
 1890 1895 1900
 Pro Arg Leu Asp Arg Ala Ala Asp Ile Thr Thr Gln Asn Ala His Asp
 1905 1910 1915 1920
 45 Ser Ala Ile Val Ala Leu Arg Gln Asn Ile Pro Thr Pro Ala Pro Leu
 1925 1930 1935
 Ser Leu Arg Ser Ala Asn Thr Leu Thr Asp Leu Phe Leu Pro Gln Ile
 1940 1945 1950
 Asn Glu Val Met Met Asn Tyr Trp Gln Thr Leu Ala Gln Arg Val Tyr
 1955 1960 1965
 55 Asn Leu Arg His Asn Leu Ser Ile Asp Gly Gln Pro Leu Tyr Leu Pro
 1970 1975 1980
 Ile Tyr Ala Thr Pro Ala Asp Pro Lys Ala Leu Leu Ser Ala Ala Val
 1985 1990 1995 2000
 60 Ala Thr Ser Gln Gly Gly Gly Lys Leu Pro Glu Ser Phe Met Ser Leu
 2005 2010 2015
 Trp Arg Phe Pro His Met Leu Glu Asn Ala Arg Gly Met Val Ser Gln
 2020 2025 2030
 65 Leu Thr Gln Phe Gly Ser Thr Leu Gln Asn Ile Ile Glu Arg Gln Asp
 2035 2040 2045
 70 Ala Glu Ala Leu Asn Ala Leu Leu Gln Asn Gln Ala Ala Glu Leu Ile
 2050 2055 2060

Leu Thr Asn Leu Ser Ile Gln Asp Lys Thr Ile Glu Glu Leu Asp Ala
 2065 2070 2075 2080
 5 Glu Lys Thr Val Leu Glu Lys Ser Lys Ala Gly Ala Gln Ser Arg Phe
 2085 2090 2095
 Asp Ser Tyr Gly Lys Leu Tyr Asp Glu Asn Ile Asn Ala Gly Glu Asn
 2100 2105 2110
 10 Gln Ala Met Thr Leu Arg Ala Ser Ala Ala Gly Leu Thr Thr Ala Val
 2115 2120 2125
 Gln Ala Ser Arg Leu Ala Gly Ala Ala Ala Asp Leu Val Pro Asn Ile
 2130 2135 2140
 15 Phe Gly Phe Ala Gly Gly Gly Ser Arg Trp Gly Ala Ile Ala Glu Ala
 2145 2150 2155 2160
 Thr Gly Tyr Val Met Glu Phe Ser Ala Asn Val Met Asn Thr Glu Ala
 2165 2170 2175
 Asp Lys Ile Ser Gln Ser Glu Thr Tyr Arg Arg Arg Arg Gln Glu Trp
 2180 2185 2190
 25 Glu Ile Gln Arg Asn Asn Ala Glu Ala Glu Leu Lys Gln Ile Asp Ala
 2195 2200 2205
 Gln Leu Lys Ser Leu Ala Val Arg Arg Glu Ala Ala Val Leu Gln Lys
 2210 2215 2220
 Thr Ser Leu Lys Thr Gln Gln Glu Gln Thr Gln Ser Gln Leu Ala Phe
 2225 2230 2235 2240
 35 Leu Gln Arg Lys Phe Ser Asn Gln Ala Leu Tyr Asn Trp Leu Arg Gly
 2245 2250 2255
 Arg Leu Ala Ala Ile Tyr Phe Gln Phe Tyr Asp Leu Ala Val Ala Arg
 2260 2265 2270
 40 Cys Leu Met Ala Glu Gln Ala Tyr Arg Trp Glu Leu Asn Asp Asp Ser
 2275 2280 2285
 Ala Arg Phe Ile Lys Pro Gly Ala Trp Gln Gly Thr Tyr Ala Gly Leu
 2290 2295 2300
 Leu Ala Gly Glu Thr Leu Met Leu Ser Leu Ala Gln Met Glu Asp Ala
 2305 2310 2315 2320
 50 His Leu Lys Arg Asp Lys Arg Ala Leu Glu Val Glu Arg Thr Val Ser
 2325 2330 2335
 Leu Ala Glu Val Tyr Ala Gly Leu Pro Lys Asp Asn Gly Pro Phe Ser
 2340 2345 2350
 55 Leu Ala Gln Glu Ile Asp Lys Leu Val Ser Gln Gly Ser Gly Ser Ala
 2355 2360 2365
 Gly Ser Gly Asn Asn Asn Leu Ala Phe Gly Ala Gly Thr Asp Thr Lys
 2370 2375 2380
 Thr Ser Leu Gln Ala Ser Val Ser Phe Ala Asp Leu Lys Ile Arg Glu
 2385 2390 2395 2400
 65 Asp Tyr Pro Ala Ser Leu Gly Lys Ile Arg Arg Ile Lys Gln Ile Ser
 2405 2410 2415
 Val Thr Leu Pro Ala Leu Leu Gly Pro Tyr Gln Asp Val Gln Ala Ile
 2420 2425 2430
 70 Leu Ser Tyr Gly Asp Lys Ala Gly Leu Ala Asn Gly Cys Glu Ala Leu

2435 2440 2445

Ala Val Ser His Gly Met Asn Asp Ser Gly Gln Phe Gln Leu Asp Phe
 2450 2455 2460

5 Asn Asp Gly Lys Phe Leu Pro Phe Glu Gly Ile Ala Ile Asp Gln Gly
 2465 2470 2475 2480

Thr Leu Thr Leu Ser Phe Pro Asn Ala Ser Met Pro Glu Lys Gly Lys
 10 2485 2490 2495

Gln Ala Thr Met Leu Lys Thr Leu Asn Asp Ile Ile Leu His Ile Arg
 2500 2505 2510

15 Tyr Thr Ile Lys
 2516

(2) INFORMATION FOR SEQ ID NO:48:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5547 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48 (tcdA_{ii} coding region):

30

CTG ATA GGC TAT AAC AAT CAA TTT AGC GGT AGA GCC AGT CAA TAT GTT 48
 Leu Ile Gly Tyr Asn Asn Gln Phe Ser Gly Arg Ala Ser Gln Tyr Val
 1 5 10 15

35

GCG CCG GGT ACC GTT TCT TCC ATG TTC TCC CCC GCC GCT TAT TTG ACT 96
 Ala Pro Gly Thr Val Ser Ser Met Phe Ser Pro Ala Ala Tyr Leu Thr
 20 25 30

40

GAA CTT TAT CGT GAA GCA CGC AAT TTA CAC GCA AGT GAC TCC GTT TAT 144
 Glu Leu Tyr Arg Glu Ala Arg Asn Leu His Ala Ser Asp Ser Val Tyr
 35 40 45

45

TAT CTG GAT ACC CGC CGC CCA GAT CTC AAA TCA ATG GCG CTC AGT CAG 192
 Tyr Leu Asp Thr Arg Arg Pro Asp Leu Lys Ser Met Ala Leu Ser Gln
 50 55 60

50

CAA AAT ATG GAT ATA GAA TTA TCC ACA CTC TCT TTG TCC AAT GAG CTG 240
 Gln Asn Met Asp Ile Glu Leu Ser Thr Leu Ser Leu Ser Asn Glu Leu
 65 70 75 80

TTA TTG GAA AGC ATT AAA ACT GAA TCT AAA CTG GAA AAC TAT ACT AAA 288
 Leu Leu Glu Ser Ile Lys Thr Glu Ser Lys Leu Glu Asn Tyr Thr Lys
 85 90 95

55

GTG ATG GAA ATG CTC TCC ACT TTC CGT CCT TCC GGC GCA ACG CCT TAT 336
 Val Met Glu Met Leu Ser Thr Phe Arg Pro Ser Gly Ala Thr Pro Tyr
 100 105 110

60

CAT GAT GCT TAT GAA AAT GTG CGT GAA GTT ATC CAG CTA CAA GAT CCT 384
 His Asp Ala Tyr Glu Asn Val Arg Glu Val Ile Gln Leu Gln Asp Pro
 115 120 125

65

GGA CTT GAG CAA CTC AAT GCA TCA CCG GCA ATT GCC GGG TTG ATG CAT 432
 Gly Leu Glu Gln Leu Asn Ala Ser Pro Ala Ile Ala Gly Leu Met His
 130 135 140

CAA GCC TCC CTA TTG GGT ATT AAC GCT TCA ATC TCG CCT GAG CTA TTT 480
 Gln Ala Ser Leu Leu Gly Ile Asn Ala Ser Ile Ser Pro Glu Leu Phe
 145 150 155 160

5	AAT	ATT	CTG	ACG	GAG	GAG	ATT	ACC	GAA	GGT	AAT	GCT	GAG	GAA	CTT	TAT	528
	Asn	Ile	Leu	Thr	Glu	Glu	Ile	Thr	Glu	Gly	Asn	Ala	Glu	Glu	Leu	Tyr	175
10	AAG	AAA	AAT	TTT	GGT	AAT	ATC	GAA	CCG	GCC	TCA	TTG	GCT	ATG	CCG	GAA	576
	Lys	Lys	Asn	Phe	Gly	Asn	Ile	Glu	Pro	Ala	Ser	Leu	Ala	Met	Pro	Glu	190
15	TAC	CTT	AAA	CGT	TAT	TAT	AAT	TTA	AGC	GAT	GAA	GAA	CTT	AGT	CAG	TTT	624
	Tyr	Leu	Lys	Arg	Tyr	Tyr	Asn	Leu	Ser	Asp	Glu	Glu	Leu	Ser	Gln	Phe	200
20	ATT	GGT	AAA	GCC	AGC	AAT	TTT	GGT	CAA	CAG	GAA	TAT	AGT	AAT	AAC	CAA	672
	Ile	Gly	Lys	Ala	Ser	Asn	Phe	Gly	Gln	Gln	Glu	Tyr	Ser	Asn	Asn	Gln	210
25	CTT	ATT	ACT	CCG	GTA	GTC	AAC	AGC	AGT	GAT	GGC	ACG	GTT	AAG	GTA	TAT	720
	Leu	Ile	Thr	Pro	Val	Val	Asn	Ser	Ser	Asp	Gly	Thr	Val	Lys	Val	Tyr	225
30	CGG	ATC	ACC	CGC	GAA	TAT	ACA	ACC	AAT	GCT	TAT	CAA	ATG	GAT	GTG	GAG	768
	Arg	Ile	Thr	Arg	Glu	Tyr	Thr	Thr	Asn	Ala	Tyr	Gln	Met	Asp	Val	Glu	245
35	CTA	TTT	CCC	TTC	GGT	GGT	GAG	AAT	TAT	CGG	TTA	GAT	TAT	AAA	TTC	AAA	816
	Leu	Phe	Pro	Phe	Gly	Gly	Glu	Asn	Tyr	Arg	Leu	Asp	Tyr	Lys	Phe	Lys	260
40	AAT	TTT	TAT	AAT	GCC	TCT	TAT	TTA	TCC	ATC	AAG	TTA	AAT	GAT	AAA	AGA	864
	Asn	Phe	Tyr	Asn	Ala	Ser	Tyr	Leu	Ser	Ile	Lys	Leu	Asn	Asp	Lys	Arg	275
45	GAA	CTT	GTT	CGA	ACT	GAA	GGC	GCT	CCT	CAA	GTC	AAT	ATA	GAA	TAC	TCC	912
	Glu	Leu	Val	Arg	Thr	Glu	Gly	Ala	Pro	Gln	Val	Asn	Ile	Glu	Tyr	Ser	290
50	GCA	AAT	ATC	ACA	TTA	AAT	ACC	GCT	GAT	ATC	AGT	CAA	CCT	TTT	GAA	ATT	960
	Ala	Asn	Ile	Thr	Leu	Asn	Thr	Ala	Asp	Ile	Ser	Gln	Pro	Phe	Glu	Ile	305
55	GGC	CTG	ACA	CGA	GTA	CTT	CCT	TCC	GGT	TCT	TGG	GCA	TAT	GCC	GCC	GCA	1008
	Gly	Leu	Thr	Arg	Val	Leu	Pro	Ser	Gly	Ser	Trp	Ala	Tyr	Ala	Ala	Ala	325
60	AAA	TTT	ACC	GTT	GAA	GAG	TAT	AAC	CAA	TAC	TCT	TTT	CTG	CTA	AAA	CTT	1056
	Lys	Phe	Thr	Val	Glu	Glu	Tyr	Asn	Gln	Tyr	Ser	Phe	Leu	Leu	Lys	Leu	340
65	AAC	AAG	GCT	ATT	CGT	CTA	TCA	CGT	GCG	ACA	GAA	TTG	TCA	CCC	ACG	ATT	1104
	Asn	Lys	Ala	Ile	Arg	Leu	Ser	Arg	Ala	Thr	Glu	Leu	Ser	Pro	Thr	Ile	355
70	CTG	GAA	GGC	ATT	GTG	CGC	AGT	GTT	AAT	CTA	CAA	CTG	GAT	ATC	AAC	ACA	1152
	Leu	Glu	Gly	Ile	Val	Arg	Ser	Val	Asn	Leu	Gln	Leu	Asp	Ile	Asn	Thr	370
75	GAC	GTA	TTA	GGT	AAA	GTT	TTT	CTG	ACT	AAA	TAT	TAT	ATG	CAG	CGT	TAT	1200
	Asp	Val	Leu	Gly	Lys	Val	Phe	Leu	Thr	Lys	Tyr	Tyr	Met	Gln	Arg	Tyr	385
80	GCT	ATT	CAT	GCT	GAA	ACT	GCC	CTG	ATA	CTA	TGC	AAC	GCG	CCT	ATT	TCA	1248
	Ala	Ile	His	Ala	Glu	Thr	Ala	Leu	Ile	Leu	Cys	Asn	Ala	Pro	Ile	Ser	405
85	CAA	CGT	TCA	TAT	GAT	AAT	CAA	CCT	AGC	CAA	TTT	GAT	CGC	CTG	TTT	AAT	1296
	Gln	Arg	Ser	Tyr	Asp	Asn	Gln	Pro	Ser	Gln	Phe	Asp	Arg	Leu	Phe	Asn	420
90	ACG	CCA	TTA	CTG	AAC	GGA	CAA	TAT	TTT	TCT	ACC	GCG	GAT	GAG	GAG	ATT	1344
	Thr	Pro	Leu	Leu	Asn	Gly	Gln	Tyr	Phe	Ser	Thr	Gly	Asp	Glu	Glu	Ile	

	435							440					445					
5	GAT Asp	TTA Leu	AAT Asn	TCA Ser	GGT Gly	AGC Ser	ACC Thr	GGC Gly	GAT Asp	TGG Trp	CGA Arg	AAA Lys	ACC Thr	ATA Ile	CTT Leu	AAG Lys	1392	
	450						455					460						
10	CGT Arg	GCA Ala	TTT Phe	AAT Asn	ATT Ile	GAT Asp	GAT Asp	GTC Val	TCG Ser	CTC Leu	TTC Phe	CGC Arg	CTG Leu	CTT Leu	AAA Lys	ATT Ile	1440	
	465					470					475					480		
	ACC Thr	GAC Asp	CAT His	GAT Asp	AAT Asn	AAA Lys	GAT Asp	GGA Gly	AAA Lys	ATT Ile	AAA Lys	AAT Asn	AAC Asn	CTA Leu	AAG Lys	AAT Asn	1488	
					485					490					495			
15	CTT Leu	TCC Ser	AAT Asn	TTA Leu	TAT Tyr	ATT Ile	GGA Gly	AAA Lys	TTA Leu	CTG Leu	GCA Ala	GAT Asp	ATT Ile	CAT His	CAA Gln	TTA Leu	1536	
				500					505					510				
20	ACC Thr	ATT Ile	GAT Asp	GAA Glu	CTG Leu	GAT Asp	TTA Leu	TTA Leu	CTG Leu	ATT Ile	GCC Ala	GTA Val	GGT Gly	GAA Glu	GGA Gly	AAA Lys	1584	
			515						520				525					
25	ACT Thr	AAT Asn	TTA Leu	TCC Ser	GCT Ala	ATC Ile	AGT Ser	GAT Asp	AAG Lys	CAA Gln	TTG Leu	GCT Ala	ACC Thr	CTG Leu	ATC Ile	AGA Arg	1632	
		530					535					540						
30	AAA Lys	CTC Leu	AAT Asn	ACT Thr	ATT Ile	ACC Thr	AGC Ser	TGG Trp	CTA Leu	CAT His	ACA Thr	CAG Gln	AAG Lys	TGG Trp	AGT Ser	GTA Val	1680	
	545					550					555					560		
	TTC Phe	CAG Gln	CTA Leu	TTT Phe	ATC Ile	ATG Met	ACC Thr	TCC Ser	ACC Thr	AGC Ser	TAT Tyr	AAC Asn	AAA Lys	ACG Thr	CTA Leu	ACG Thr	1728	
					565					570					575			
35	CCT Pro	GAA Glu	ATT Ile	AAG Lys	AAT Asn	TTG Leu	CTG Leu	GAT Asp	ACC Thr	GTC Val	TAC Tyr	CAC His	GGT Gly	TTA Leu	CAA Gln	GGT Gly	1776	
				580					585					590				
40	TTT Phe	GAT Asp	AAA Lys	GAC Asp	AAA Lys	GCA Ala	GAT Asp	TTG Leu	CTA Leu	CAT His	GTC Val	ATG Met	GCG Ala	CCC Pro	TAT Tyr	ATT Ile	1824	
			595					600					605					
45	GCG Ala	GCC Ala	ACC Thr	TTG Leu	CAA Gln	TTA Leu	TCA Ser	TCG Ser	GAA Glu	AAT Asn	GTC Val	GCC Ala	CAC His	TCG Ser	GTA Val	CTC Leu	1872	
		610					615					620						
50	CTT Leu	TGG Trp	GCA Ala	GAT Asp	AAG Lys	TTA Leu	CAG Gln	CCC Pro	GGC Gly	GAC Asp	GGC Gly	GCA Ala	ATG Met	ACA Thr	GCA Ala	GAA Glu	1920	
	625					630					635					640		
	AAA Lys	TTC Phe	TGG Trp	GAC Asp	TGG Trp	TTG Leu	AAT Asn	ACT Thr	AAG Lys	TAT Tyr	ACG Thr	CCG Pro	GGT Gly	TCA Ser	TCC Ser	GAA Glu	1968	
					645					650					655			
55	GCC Ala	GTA Val	GAA Glu	ACG Thr	CAG Gln	GAA Glu	CAT His	ATC Ile	GTT Val	CAG Gln	TAT Tyr	TGT Cys	CAG Gln	GCT Ala	CTG Leu	GCA Ala	2016	
				660					665					670				
60	CAA Gln	TTG Leu	GAA Glu	ATG Met	GTT Val	TAC Tyr	CAT His	TCC Ser	ACC Thr	GGC Gly	ATC Ile	AAC Asn	GAA Glu	AAC Asn	GCC Ala	TTC Phe	2064	
			675					680					685					
65	CGT Arg	CTA Leu	TTT Phe	GTG Val	ACA Thr	AAA Lys	CCA Pro	GAG Glu	ATG Met	TTT Phe	GGC Gly	GCT Ala	GCA Ala	ACT Thr	GGA Gly	GCA Ala	2112	
		690					695					700						
70	GCG Ala	CCC Pro	GCG Ala	CAT His	GAT Asp	GCC Ala	CTT Leu	TCA Ser	CTG Leu	ATT Ile	ATG Met	CTG Leu	ACA Thr	CGT Arg	TTT Phe	GCG Ala	2160	
	705					710					715					720		
	GAT Asp	TGG Leu	GTG Val	AAC Asn	GCA Ala	CTA Leu	GGC Pro	GAA Glu	AAA Met	GCG Phe	TCC Ser	TCG Val	GTG Val	CTA Leu	GCG Phe	GCA Ala	2208	

	Asp	Trp	Val	Asn	Ala	Leu	Gly	Glu	Lys	Ala	Ser	Ser	Val	Leu	Ala	Ala	
				725						730					735		
5	TTT	GAA	GCT	AAC	TCG	TTA	ACG	GCA	GAA	CAA	CTG	GCT	GAT	GCC	ATG	AAT	2256
	Phe	Glu	Ala	Asn	Ser	Leu	Thr	Ala	Glu	Gln	Leu	Ala	Asp	Ala	Met	Asn	
				740					745					750			
10	CTT	GAT	GCT	AAT	TTG	CTG	TTG	CAA	GCC	AGT	ATT	CAA	GCA	CAA	AAT	CAT	2304
	Leu	Asp	Ala	Asn	Leu	Leu	Leu	Gln	Ala	Ser	Ile	Gln	Ala	Gln	Asn	His	
				755				760					765				
15	CAA	CAT	CTT	CCC	CCA	GTA	ACT	CCA	GAA	AAT	GCG	TTC	TCC	TGT	TGG	ACA	2352
	Gln	His	Leu	Pro	Pro	Val	Thr	Pro	Glu	Asn	Ala	Phe	Ser	Cys	Trp	Thr	
				770			775					780					
20	TCT	ATC	AAT	ACT	ATC	CTG	CAA	TGG	GTT	AAT	GTC	GCA	CAA	CAA	TTG	AAT	2400
	Ser	Ile	Asn	Thr	Ile	Leu	Gln	Trp	Val	Asn	Val	Ala	Gln	Gln	Leu	Asn	800
						790				795							
25	GTC	GCC	CCA	CAG	GGC	GTT	TCC	GCT	TTG	GTC	GGG	CTG	GAT	TAT	ATT	CAA	2448
	Val	Ala	Pro	Gln	Gly	Val	Ser	Ala	Leu	Val	Gly	Leu	Asp	Tyr	Ile	Gln	
					805					810					815		
30	TCA	ATG	AAA	GAG	ACA	CCG	ACC	TAT	GCC	CAG	TGG	GAA	AAC	GCG	GCA	GGC	2496
	Ser	Met	Lys	Glu	Thr	Pro	Thr	Tyr	Ala	Gln	Trp	Glu	Asn	Ala	Ala	Gly	
				820					825					830			
35	GTA	TTA	ACC	GCC	GGG	TTG	AAT	TCA	CAA	CAG	GCT	AAT	ACA	TTA	CAC	GCT	2544
	Val	Leu	Thr	Ala	Gly	Leu	Asn	Ser	Gln	Gln	Ala	Asn	Thr	Leu	His	Ala	
				835				840					845				
40	TTT	CTG	GAT	GAA	TCT	CGC	AGT	GCC	GCA	TTA	AGC	ACC	TAC	TAT	ATC	CGT	2592
	Phe	Leu	Asp	Glu	Ser	Arg	Ser	Ala	Ala	Leu	Ser	Thr	Tyr	Tyr	Ile	Arg	
				850			855					860					
45	CAA	GTC	GCC	AAG	GCA	GCG	GCG	GCT	ATT	AAA	AGC	CGT	GAT	GAC	TTG	TAT	2640
	Gln	Val	Ala	Lys	Ala	Ala	Ala	Ile	Lys	Ser	Arg	Asp	Asp	Leu	Tyr		880
						870				875							
50	CAA	TAC	TTA	CTG	ATT	GAT	AAT	CAG	GTT	TCT	GCG	GCA	ATA	AAA	ACC	ACC	2688
	Gln	Tyr	Leu	Leu	Ile	Asp	Asn	Gln	Val	Ser	Ala	Ala	Ile	Lys	Thr	Thr	
						885				890					895		
55	CGG	ATC	GCC	GAA	GCC	ATT	GCC	AGT	ATT	CAA	CTG	TAC	GTC	AAC	CGG	GCA	2736
	Arg	Ile	Ala	Glu	Ala	Ile	Ala	Ser	Ile	Gln	Leu	Tyr	Val	Asn	Arg	Ala	
				900					905					910			
60	TTG	GAA	AAT	GTG	GAA	GAA	AAT	GCC	AAT	TCG	GGG	GTT	ATC	AGC	CGC	CAA	2784
	Leu	Glu	Asn	Val	Glu	Glu	Asn	Ala	Asn	Ser	Gly	Val	Ile	Ser	Arg	Gln	
				915				920					925				
65	TTC	TTT	ATC	GAC	TGG	GAC	AAA	TAC	AAT	AAA	CGC	TAC	AGC	ACT	TGG	GCG	2832
	Phe	Phe	Ile	Asp	Trp	Asp	Lys	Tyr	Asn	Lys	Arg	Tyr	Ser	Thr	Trp	Ala	
				930			935					940					
70	GGT	GTT	TCT	CAA	TTA	GTT	TAC	TAC	CCG	GAA	AAC	TAT	ATT	GAT	CCG	ACC	2880
	Gly	Val	Ser	Gln	Leu	Val	Tyr	Tyr	Pro	Glu	Asn	Tyr	Ile	Asp	Pro	Thr	
						945		950			955				960		
75	ATG	CGT	ATC	GGA	CAA	ACC	AAA	ATG	ATG	GAC	GCA	TTA	CTG	CAA	TCC	GTC	2928
	Met	Arg	Ile	Gly	Gln	Thr	Lys	Met	Met	Asp	Ala	Leu	Leu	Gln	Ser	Val	
						965				970					975		
80	AGC	CAA	AGC	CAA	TTA	AAC	GCC	GAT	ACC	GTC	GAA	GAT	GCC	TTT	ATG	TCT	2976
	Ser	Gln	Ser	Gln	Leu	Asn	Ala	Asp	Thr	Val	Glu	Asp	Ala	Phe	Met	Ser	
				980					985					990			
85	TAT	CTG	ACA	TCG	TTT	GAA	CAA	GTG	GCT	AAT	CTT	AAA	GTT	ATT	AGC	GCA	3024
	Tyr	Leu	Thr	Ser	Phe	Glu	Gln	Val	Ala	Asn	Leu	Lys	Val	Ile	Ser	Ala	
				995				1000					1005				

	TAT	CAC	GAT	AAT	ATT		AAC	GAT	CAA	GGG	CTG	ACC	TAT	TAT	ATC	GGA	3072
	Tyr	His	Asp	Asn	Ile	Asn	Asn	Asp	Gln	Gly	Leu	Thr	Tyr	Phe	Ile	Gly	
		1010					1015					1020					
5	CTC	AGT	GAA	ACT	GAT	GCC	GGT	GAA	TAT	TAT	TGG	CGC	AGT	GTC	GAT	CAC	3120
	Leu	Ser	Glu	Thr	Asp	Ala	Gly	Glu	Tyr	Tyr	Trp	Arg	Ser	Val	Asp	His	
	1025					1030					1035					1040	
10	AGT	AAA	TTC	AAC	GAC	GGT	AAA	TTC	GCG	GCT	AAT	GCC	TGG	AGT	GAA	TGG	3168
	Ser	Lys	Phe	Asn	Asp	Gly	Lys	Phe	Ala	Ala	Asn	Ala	Trp	Ser	Glu	Trp	
					1045					1050					1055		
15	CAT	AAA	ATT	GAT	TGT	CCA	ATT	AAC	CCT	TAT	AAA	AGC	ACT	ATC	CGT	CCA	3216
	His	Lys	Ile	Asp	Cys	Pro	Ile	Asn	Pro	Tyr	Lys	Ser	Thr	Ile	Arg	Pro	
				1060					1065					1070			
20	GTG	ATA	TAT	AAA	TCC	CGC	CTG	TAT	CTG	CTC	TGG	TTG	GAA	CAA	AAG	GAG	3264
	Val	Ile	Tyr	Lys	Ser	Arg	Leu	Tyr	Leu	Leu	Trp	Leu	Glu	Gln	Lys	Glu	
			1075					1080					1085				
25	ATC	ACC	AAA	CAG	ACA	GGA	AAT	AGT	AAA	GAT	GGC	TAT	CAA	ACT	GAA	ACG	3312
	Ile	Thr	Lys	Gln	Thr	Gly	Asn	Ser	Lys	Asp	Gly	Tyr	Gln	Thr	Glu	Thr	
		1090					1095					1100					
30	GAT	TAT	CGT	TAT	GAA	CTA	AAA	TTG	GCG	CAT	ATC	CGC	TAT	GAT	GGC	ACT	3360
	Asp	Tyr	Arg	Tyr	Glu	Leu	Lys	Leu	Ala	His	Ile	Arg	Tyr	Asp	Gly	Thr	
	1105					1110					1115					1120	
35	TGG	AAT	ACG	CCA	ATC	ACC	TTT	GAT	GTC	AAT	AAA	AAA	ATA	TCC	GAG	CTA	3408
	Trp	Asn	Thr	Pro	Ile	Thr	Phe	Asp	Val	Asn	Lys	Lys	Ile	Ser	Glu	Leu	
					1125					1130					1135		
40	AAA	CTG	GAA	AAA	AAT	AGA	GCG	CCC	GGA	CTC	TAT	TGT	GCC	GGT	TAT	CAA	3456
	Lys	Leu	Glu	Lys	Asn	Arg	Ala	Pro	Gly	Leu	Tyr	Cys	Ala	Gly	Tyr	Gln	
				1140					1145					1150			
45	GGT	GAA	GAT	ACG	TTG	CTG	GTG	ATG	TTT	TAT	AAC	CAA	CAA	GAC	ACA	CTA	3504
	Gly	Glu	Asp	Thr	Leu	Leu	Val	Met	Phe	Tyr	Asn	Gln	Gln	Asp	Thr	Leu	
			1155					1160					1165				
50	GAT	AGT	TAT	AAA	AAC	GCT	TCA	ATG	CAA	GGA	CTA	TAT	ATC	TTT	GCT	GAT	3552
	Asp	Ser	Tyr	Lys	Asn	Ala	Ser	Met	Gln	Gly	Leu	Tyr	Ile	Phe	Ala	Asp	
		1170					1175					1180					
55	ATG	GCA	TCC	AAA	GAT	ATG	ACC	CCA	GAA	CAG	AGC	AAT	GTT	TAT	CGG	GAT	3600
	Met	Ala	Ser	Lys	Asp	Met	Thr	Pro	Glu	Gln	Ser	Asn	Val	Tyr	Arg	Asp	
	1185					1190					1195					1200	
60	AAT	AGC	TAT	CAA	CAA	TTT	GAT	ACC	AAT	AAT	GTC	AGA	AGA	GTG	AAT	AAC	3648
	Asn	Ser	Tyr	Gln	Gln	Phe	Asp	Thr	Asn	Asn	Val	Arg	Arg	Val	Asn	Asn	
					1205					1210					1215		
65	CGC	TAT	GCA	GAG	GAT	TAT	GAG	ATT	CCT	TCC	TCG	GTA	AGT	AGC	CGT	AAA	3696
	Arg	Tyr	Ala	Glu	Asp	Tyr	Glu	Ile	Pro	Ser	Ser	Val	Ser	Ser	Arg	Lys	
				1220					1225					1230			
70	GAC	TAT	GGT	TGG	GGA	GAT	TAT	TAC	CTC	AGC	ATG	GTA	TAT	AAC	GGA	GAT	3744
	Asp	Tyr	Gly	Trp	Gly	Asp	Tyr	Tyr	Leu	Ser	Met	Val	Tyr	Asn	Gly	Asp	
			1235					1240					1245				
75	ATT	CCA	ACT	ATC	AAT	TAC	AAA	GCC	GCA	TCA	AGT	GAT	TTA	AAA	ATC	TAT	3792
	Ile	Pro	Thr	Ile	Asn	Tyr	Lys	Ala	Ala	Ser	Ser	Asp	Leu	Lys	Ile	Tyr	
		1250					1255					1260					
80	ATC	TCA	CCA	AAA	TTA	AGA	ATT	ATT	CAT	AAT	GGA	TAT	GAA	GGA	CAG	AAG	3840
	Ile	Ser	Pro	Lys	Leu	Arg	Ile	Ile	His	Asn	Gly	Tyr	Glu	Gly	Gln	Lys	
	1265					1270					1275					1280	
85	CGC	AAT	CAA	TGC	AAT	CTG	ATG	AAT	AAA	TAT	GGC	AAA	CTA	GGT	GAT	AAA	3888
	Arg	Asn	Gln	Cys	Asn	Leu	Met	Asn	Lys	Tyr	Gly	Lys	Leu	Gly	Asp	Lys	
					1285					1290					1295		

5	TTT ATT GTT TAT ACT AGC TTG GGG GTC AAT CCA AAT AAC TCG TCA AAT 3936 Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn Ser Ser Asn 1300 1305 1310
10	AAG CTC ATG TTT TAC CCC GTC TAT CAA TAT AGC GGA AAC ACC AGT GGA 3984 Lys Leu Met Phe Tyr Pro Val Tyr Gln Tyr Ser Gly Asn Thr Ser Gly 1315 1320 1325
15	CTC AAT CAA GGG AGA CTA CTA TTC CAC CGT GAC ACC ACT TAT CCA TCT 4032 Leu Asn Gln Gly Arg Leu Leu Phe His Arg Asp Thr Thr Tyr Pro Ser 1330 1335 1340
20	AAA GTA GAA GCT TGG ATT CCT GGA GCA AAA CGT TCT CTA ACC AAC CAA 4080 Lys Val Glu Ala Trp Ile Pro Gly Ala Lys Arg Ser Leu Thr Asn Gln 1345 1350 1355 1360
25	AAT GCC GCC ATT GGT GAT GAT TAT GCT ACA GAC TCT CTG AAT AAA CCG 4128 Asn Ala Ala Ile Gly Asp Asp Tyr Ala Thr Asp Ser Leu Asn Lys Pro 1365 1370 1375
30	GAT GAT CTT AAG CAA TAT ATC TTT ATG ACT GAC AGT AAA GGG ACT GCT 4176 Asp Asp Leu Lys Gln Tyr Ile Phe Met Thr Asp Ser Lys Gly Thr Ala 1380 1385 1390
35	ACT GAT GTC TCA GGC CCA GTA GAG ATT AAT ACT GCA ATT TCT CCA GCA 4224 Thr Asp Val Ser Gly Pro Val Glu Ile Asn Thr Ala Ile Ser Pro Ala 1395 1400 1405
40	AAA GTT CAG ATA ATA GTC AAA GCG GGT GGC AAG GAG CAA ACT TTT ACC 4272 Lys Val Gln Ile Ile Val Lys Ala Gly Gly Lys Glu Gln Thr Phe Thr 1410 1415 1420
45	GCA GAT AAA GAT GTC TCC ATT CAG CCA TCA CCT AGC TTT GAT GAA ATG 4320 Ala Asp Lys Asp Val Ser Ile Gln Pro Ser Pro Ser Phe Asp Glu Met 1425 1430 1435 1440
50	AAT TAT CAA TTT AAT GCC CTT GAA ATA GAC GGT TCT GGT CTG AAT TTT 4368 Asn Tyr Gln Phe Asn Ala Leu Glu Ile Asp Gly Ser Gly Leu Asn Phe 1445 1450 1455
55	ATT AAC AAC TCA GCC AGT ATT GAT GTT ACT TTT ACC GCA TTT GCG GAG 4416 Ile Asn Asn Ser Ala Ser Ile Asp Val Thr Phe Thr Ala Phe Ala Glu 1460 1465 1470
60	GAT GGC CGC AAA CTG GGT TAT GAA AGT TTC AGT ATT CCT GTT ACC CTC 4464 Asp Gly Arg Lys Leu Gly Tyr Glu Ser Phe Ser Ile Pro Val Thr Leu 1475 1480 1485
65	AAG GTA AGT ACC GAT AAT GCC CTG ACC CTG CAC CAT AAT GAA AAT GGT 4512 Lys Val Ser Thr Asp Asn Ala Leu Thr Leu His His Asn Glu Asn Gly 1490 1495 1500
70	GCG CAA TAT ATG CAA TGG CAA TCC TAT CGT ACC CGC CTG AAT ACT CTA 4560 Ala Gln Tyr Met Gln Trp Gln Ser Tyr Arg Thr Arg Leu Asn Thr Leu 1505 1510 1515 1520
75	TTT GCC CGC CAG TTG GTT GCA CGC GCC ACC ACC GGA ATC GAT ACA ATT 4608 Phe Ala Arg Gln Leu Val Ala Arg Ala Thr Thr Gly Ile Asp Thr Ile 1525 1530 1535
80	CTG AGT ATG GAA ACT CAG AAT ATT CAG GAA CCG CAG TTA GGC AAA GGT 4656 Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro Gln Leu Gly Lys Gly 1540 1545 1550
85	TTC TAT GCT ACG TTC GTG ATA CCT CCC TAT AAC CTA TCA ACT CAT GGT 4704 Phe Tyr Ala Thr Phe Val Ile Pro Pro Tyr Asn Leu Ser Thr His Gly 1555 1560 1565
90	GAT GAA CGT TGG TTT AAG CTT TAT ATC AAA CAT GTT GTT GAT AAT AAT 4752 Asp Glu Arg Trp Phe Lys Leu Tyr Ile Lys His Val Val Asp Asn Asn

	1570	1575	1580	
5	TCA CAT ATT ATC TAT TCA GGC CAG CTA ACA GAT ACA AAT ATA AAC ATC 4800 Ser His Ile Ile Tyr Ser Gly Gln Leu Thr Asp Thr Asn Ile Asn Ile 1585 1590 1595 1600			
10	ACA TTA TTT ATT CCT CTT GAT GAT GTC CCA TTG AAT CAA GAT TAT CAC 4848 Thr Leu Phe Ile Pro Leu Asp Asp Val Pro Leu Asn Gln Asp Tyr His 1605 1610 1615			
15	GCC AAG GTT TAT ATG ACC TTC AAG AAA TCA CCA TCA GAT GGT ACC TGG 4896 Ala Lys Val Tyr Met Thr Phe Lys Lys Ser Pro Ser Asp Gly Thr Trp 1620 1625 1630			
20	TGG GGC CCT CAC TTT GTT AGA GAT GAT AAA GGA ATA GTA ACA ATA AAC 4944 Trp Gly Pro His Phe Val Arg Asp Asp Lys Gly Ile Val Thr Ile Asn 1635 1640 1645			
25	CCT AAA TCC ATT TTG ACC CAT TTT GAG AGC GTC AAT GTC CTG AAT AAT 4992 Pro Lys Ser Ile Leu Thr His Phe Glu Ser Val Asn Val Leu Asn Asn 1650 1655 1660			
30	ATT AGT AGC GAA CCA ATG GAT TTC AGC GGC GCT AAC AGC CTC TAT TTC 5040 Ile Ser Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ser Leu Tyr Phe 1665 1670 1675 1680			
35	TGG GAA CTG TTC TAC TAT ACC CCG ATG CTG GTT GCT CAA CGT TTG CTG 5088 Trp Glu Leu Phe Tyr Tyr Thr Pro Met Leu Val Ala Gln Arg Leu Leu 1685 1690 1695			
40	CAT GAA CAG AAC TTC GAT GAA GCC AAC CGT TGG CTG AAA TAT GTC TGG 5136 His Glu Gln Asn Phe Asp Glu Ala Asn Arg Trp Leu Lys Tyr Val Trp 1700 1705 1710			
45	AGT CCA TCC GGT TAT ATT GTC CAC GGC CAG ATT CAG AAC TAC CAG TGG 5184 Ser Pro Ser Gly Tyr Ile Val His Gly Gln Ile Gln Asn Tyr Gln Trp 1715 1720 1725			
50	AAC GTC CGC CCG TTA CTG GAA GAC ACC AGT TGG AAC AGT GAT CCT TTG 5232 Asn Val Arg Pro Leu Leu Glu Asp Thr Ser Trp Asn Ser Asp Pro Leu 1730 1735 1740			
55	GAT TCC GTC GAT CCT GAC GCG GTA GCA CAG CAC GAT CCA ATG CAC TAC 5280 Asp Ser Val Asp Pro Asp Ala Val Ala Gln His Asp Pro Met His Tyr 1745 1750 1755 1760			
60	AAA GTT TCA ACT TTT ATG CGT ACC TTG GAT CTA TTG ATA GCA CGC GGC 5328 Lys Val Ser Thr Phe Met Arg Thr Leu Asp Leu Leu Ile Ala Arg Gly 1765 1770 1775			
65	GAC CAT GCT TAT CGC CAA CTG GAA CGA GAT ACA CTC AAC GAA GCG AAG 5376 Asp His Ala Tyr Arg Gln Leu Glu Arg Asp Thr Leu Asn Glu Ala Lys 1780 1785 1790			
70	ATG TGG TAT ATG CAA GCG CTG CAT CTA TTA GGT GAC AAA CCT TAT CTA 5424 Met Trp Tyr Met Gln Ala Leu His Leu Leu Gly Asp Lys Pro Tyr Leu 1795 1800 1805			
	CCG CTG AGT ACG ACA TGG AGT GAT CCA CGA CTA GAC AGA GCC GCG GAT 5472 Pro Leu Ser Thr Thr Trp Ser Asp Pro Arg Leu Asp Arg Ala Ala Asp 1810 1815 1820			
	ATC ACT ACC CAA AAT GCT CAC GAC AGC GCA ATA GTC GCT CTG CGG CAG 5520 Ile Thr Thr Gln Asn Ala His Asp Ser Ala Ile Val Ala Leu Arg Gln 1825 1830 1835 1840			
	AAT ATA CCT ACA CCG GCA CCT TTA TCA 5547 Asn Ile Pro Thr Pro Ala Pro Leu Ser 1845 1849			

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1849 amino acids
 (B) TYPE: amino acids
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49 (TcdA_{ii}):

Features	From	To	Description
Peptide	1	1849	TcdA _{ii} peptide
Fragment	1	12	TcdA _{ii} N-terminus (SEQ ID NO:13)
Fragment	196	211	(SEQ ID NO:38)
Fragment	466	475	(SEQ ID NO:17)
Fragment	993	1004	(SEQ ID NO:23; 12/13)
Fragment	1297	1312	(SEQ ID NO:18)
Fragment	1390	1409	(SEQ ID NO:39)
Fragment	1532	1554	(SEQ ID NO:21; 19/23)

20 Leu Ile Gly Tyr Asn Asn Gln Phe Ser Gly Arg Ala Ser Gln Tyr Val
 1 5 10 15

25 Ala Pro Gly Thr Val Ser Ser Met Phe Ser Pro Ala Ala Tyr Leu Thr
 20 25 30

Glu Leu Tyr Arg Glu Ala Arg Asn Leu His Ala Ser Asp Ser Val Tyr
 35 40 45

30 Tyr Leu Asp Thr Arg Arg Pro Asp Leu Lys Ser Met Ala Leu Ser Gln
 50 55 60

Gln Asn Met Asp Ile Glu Leu Ser Thr Leu Ser Leu Ser Asn Glu Leu
 65 70 75 80

35 Leu Leu Glu Ser Ile Lys Thr Glu Ser Lys Leu Glu Asn Tyr Thr Lys
 85 90 95

40 Val Met Glu Met Leu Ser Thr Phe Arg Pro Ser Gly Ala Thr Pro Tyr
 100 105 110

His Asp Ala Tyr Glu Asn Val Arg Glu Val Ile Gln Leu Gln Asp Pro
 115 120 125

45 Gly Leu Glu Gln Leu Asn Ala Ser Pro Ala Ile Ala Gly Leu Met His
 130 135 140

Gln Ala Ser Leu Leu Gly Ile Asn Ala Ser Ile Ser Pro Glu Leu Phe
 145 150 155 160

50 Asn Ile Leu Thr Glu Glu Ile Thr Glu Gly Asn Ala Glu Glu Leu Tyr
 165 170 175



55 Lys Lys Asn Phe Gly Asn Ile Glu Pro Ala Ser Leu Ala Met Pro Glu
 180 185 190

Tyr Leu Lys Arg Tyr Tyr Asn Leu Ser Asp Glu Glu Leu Ser Gln Phe
 195 200 205

60 Ile Gly Lys Ala Ser Asn Phe Gly Gln Gln Glu Tyr Ser Asn Asn Gln
 210 215 220

Leu Ile Thr Pro Val Val Asn Ser Ser Asp Gly Thr Val Lys Val Tyr
 225 230 235 240

65 Arg Ile Thr Arg Glu Tyr Thr Thr Asn Ala Tyr Gln Met Asp Val Glu
 245 250 255

Leu Phe Pro Phe Gly  Glu Asn Tyr Arg. Leu Asp Tyr  Phe Lys
 260 265 270
 5 Asn Phe Tyr Asn Ala Ser Tyr Leu Ser Ile Lys Leu Asn Asp Lys Arg
 275 280 285
 Glu Leu Val Arg Thr Glu Gly Ala Pro Gln Val Asn Ile Glu Tyr Ser
 290 295 300
 10 Ala Asn Ile Thr Leu Asn Thr Ala Asp Ile Ser Gln Pro Phe Glu Ile
 305 310 315
 Gly Leu Thr Arg Val Leu Pro Ser Gly Ser Trp Ala Tyr Ala Ala Ala
 325 330 335
 15 Lys Phe Thr Val Glu Glu Tyr Asn Gln Tyr Ser Phe Leu Leu Lys Leu
 340 345 350
 20 Asn Lys Ala Ile Arg Leu Ser Arg Ala Thr Glu Leu Ser Pro Thr Ile
 355 360 365
 Leu Glu Gly Ile Val Arg Ser Val Asn Leu Gln Leu Asp Ile Asn Thr
 370 375 380
 25 Asp Val Leu Gly Lys Val Phe Leu Thr Lys Tyr Tyr Met Gln Arg Tyr
 385 390 395 400
 Ala Ile His Ala Glu Thr Ala Leu Ile Leu Cys Asn Ala Pro Ile Ser
 405 410 415
 30 Gln Arg Ser Tyr Asp Asn Gln Pro Ser Gln Phe Asp Arg Leu Phe Asn
 420 425 430
 Thr Pro Leu Leu Asn Gly Gln Tyr Phe Ser Thr Gly Asp Glu Glu Ile
 435 440 445
 Asp Leu Asn Ser Gly Ser Thr Gly Asp Trp Arg Lys Thr Ile Leu Lys
 450 455 460
 40 Arg Ala Phe Asn Ile Asp Asp Val Ser Leu Phe Arg Leu Leu Lys Ile
 465 470 475 480
 Thr Asp His Asp Asn Lys Asp Gly Lys Ile Lys Asn Asn Leu Lys Asn
 485 490 495
 45 Leu Ser Asn Leu Tyr Ile Gly Lys Leu Leu Ala Asp Ile His Gln Leu
 500 505 510
 Thr Ile Asp Glu Leu Asp Leu Leu Leu Ile Ala Val Gly Glu Gly Lys
 515 520 525
 Thr Asn Leu Ser Ala Ile Ser Asp Lys Gln Leu Ala Thr Leu Ile Arg
 530 535 540
 55 Lys Leu Asn Thr Ile Thr Ser Trp Leu His Thr Gln Lys Trp Ser Val
 545 550 555 560
 Phe Gln Leu Phe Ile Met Thr Ser Thr Ser Tyr Asn Lys Thr Leu Thr
 565 570 575
 60 Pro Glu Ile Lys Asn Leu Leu Asp Thr Val Tyr His Gly Leu Gln Gly
 580 585 590
 Phe Asp Lys Asp Lys Ala Asp Leu Leu His Val Met Ala Pro Tyr Ile
 595 600 605
 65 Ala Ala Thr Leu Gln Leu Ser Ser Glu Asn Val Ala His Ser Val Leu
 610 615 620
 70 Leu Trp Ala Asp Lys Leu Gln Pro Gly Asp Gly Ala Met Thr Ala Glu
 625 630 635 640

Lys Phe Trp Asp Trp Leu Asn Thr Lys Tyr Thr Pro Gly Ser Ser Glu
 645 650 655
 5 Ala Val Glu Thr Gln Glu His Ile Val Gln Tyr Cys Gln Ala Leu Ala
 660 665 670
 Gln Leu Glu Met Val Tyr His Ser Thr Gly Ile Asn Glu Asn Ala Phe
 675 680 685
 10 Arg Leu Phe Val Thr Lys Pro Glu Met Phe Gly Ala Ala Thr Gly Ala
 690 695 700
 Ala Pro Ala His Asp Ala Leu Ser Leu Ile Met Leu Thr Arg Phe Ala
 705 710 715 720
 15 Asp Trp Val Asn Ala Leu Gly Glu Lys Ala Ser Ser Val Leu Ala Ala
 725 730 735
 Phe Glu Ala Asn Ser Leu Thr Ala Glu Gln Leu Ala Asp Ala Met Asn
 740 745 750
 20 Leu Asp Ala Asn Leu Leu Leu Gln Ala Ser Ile Gln Ala Gln Asn His
 755 760 765
 Gln His Leu Pro Pro Val Thr Pro Glu Asn Ala Phe Ser Cys Trp Thr
 770 775 780
 25 Ser Ile Asn Thr Ile Leu Gln Trp Val Asn Val Ala Gln Gln Leu Asn
 785 790 795 800
 30 Val Ala Pro Gln Gly Val Ser Ala Leu Val Gly Leu Asp Tyr Ile Gln
 805 810 815
 Ser Met Lys Glu Thr Pro Thr Tyr Ala Gln Trp Glu Asn Ala Ala Gly
 820 825 830
 35 Val Leu Thr Ala Gly Leu Asn Ser Gln Gln Ala Asn Thr Leu His Ala
 835 840 845
 Phe Leu Asp Glu Ser Arg Ser Ala Ala Leu Ser Thr Tyr Tyr Ile Arg
 850 855 860
 40 Gln Val Ala Lys Ala Ala Ala Ala Ile Lys Ser Arg Asp Asp Leu Tyr
 865 870 875 880
 45 Gln Tyr Leu Leu Ile Asp Asn Gln Val Ser Ala Ala Ile Lys Thr Thr
 885 890 895
 Arg Ile Ala Glu Ala Ile Ala Ser Ile Gln Leu Tyr Val Asn Arg Ala
 900 905 910
 50 Leu Glu Asn Val Glu Glu Asn Ala Asn Ser Gly Val Ile Ser Arg Gln
 915 920 925
 Phe Phe Ile Asp Trp Asp Lys Tyr Asn Lys Arg Tyr Ser Thr Trp Ala
 930 935 940
 55 Gly Val Ser Gln Leu Val Tyr Tyr Pro Glu Asn Tyr Ile Asp Pro Thr
 945 950 955 960
 60 Met Arg Ile Gly Gln Thr Lys Met Met Asp Ala Leu Leu Gln Ser Val
 965 970 975
 Ser Gln Ser Gln Leu Asn Ala Asp Thr Val Glu Asp Ala Phe Met Ser
 980 985 990
 65 Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys Val Ile Ser Ala
 995 1000 1005
 70 Tyr His Asp Asn Ile Asn Asn Asp Gln Gly Leu Thr Tyr Phe Ile Gly
 1010 1015 1020

Leu Ser Glu Thr Asp Ala Gly Glu Tyr Tyr Trp Arg Ser Val Asp His
 1025 1030 1035 1040
 5 Ser Lys Phe Asn Asp Gly Lys Phe Ala Ala Asn Ala Trp Ser Glu Trp
 1045 1050 1055
 His Lys Ile Asp Cys Pro Ile Asn Pro Tyr Lys Ser Thr Ile Arg Pro
 1060 1065 1070
 10 Val Ile Tyr Lys Ser Arg Leu Tyr Leu Leu Trp Leu Glu Gln Lys Glu
 1075 1080 1085
 Ile Thr Lys Gln Thr Gly Asn Ser Lys Asp Gly Tyr Gln Thr Glu Thr
 1090 1095 1100
 15 Asp Tyr Arg Tyr Glu Leu Lys Leu Ala His Ile Arg Tyr Asp Gly Thr
 1105 1110 1115 1120
 20 Trp Asn Thr Pro Ile Thr Phe Asp Val Asn Lys Lys Ile Ser Glu Leu
 1125 1130 1135
 Lys Leu Glu Lys Asn Arg Ala Pro Gly Leu Tyr Cys Ala Gly Tyr Gln
 1140 1145 1150
 25 Gly Glu Asp Thr Leu Leu Val Met Phe Tyr Asn Gln Gln Asp Thr Leu
 1155 1160 1165
 Asp Ser Tyr Lys Asn Ala Ser Met Gln Gly Leu Tyr Ile Phe Ala Asp
 1170 1175 1180
 30 Met Ala Ser Lys Asp Met Thr Pro Glu Gln Ser Asn Val Tyr Arg Asp
 1185 1190 1195 1200
 35 Asn Ser Tyr Gln Gln Phe Asp Thr Asn Asn Val Arg Arg Val Asn Asn
 1205 1210 1215
 Arg Tyr Ala Glu Asp Tyr Glu Ile Pro Ser Ser Val Ser Ser Arg Lys
 1220 1225 1230
 40 Asp Tyr Gly Trp Gly Asp Tyr Tyr Leu Ser Met Val Tyr Asn Gly Asp
 1235 1240 1245
 Ile Pro Thr Ile Asn Tyr Lys Ala Ala Ser Ser Asp Leu Lys Ile Tyr
 1250 1255 1260
 Ile Ser Pro Lys Leu Arg Ile Ile His Asn Gly Tyr Glu Gly Gln Lys
 1265 1270 1275 1280
 50 Arg Asn Gln Cys Asn Leu Met Asn Lys Tyr Gly Lys Leu Gly Asp Lys
 1285 1290 1295
 Phe Ile Val Tyr Thr Ser Leu Gly Val Asn Pro Asn Asn Ser Ser Asn
 1300 1305 1310
 55 Lys Leu Met Phe Tyr Pro Val Tyr Gln Tyr Ser Gly Asn Thr Ser Gly
 1315 1320 1325
 Leu Asn Gln Gly Arg Leu Leu Phe His Arg Asp Thr Thr Tyr Pro Ser
 1330 1335 1340
 Lys Val Glu Ala Trp Ile Pro Gly Ala Lys Arg Ser Leu Thr Asn Gln
 1345 1350 1355 1360
 65 Asn Ala Ala Ile Gly Asp Asp Tyr Ala Thr Asp Ser Leu Asn Lys Pro
 1365 1370 1375
 Asp Asp Leu Lys Gln Tyr Ile Phe Met Thr Asp Ser Lys Gly Thr Ala
 1380 1385 1390
 70 Thr Asp Val Ser Gly Pro Val Glu Ile Asn Thr Ala Ile Ser Pro Ala

	1395	1400	1405
	Lys Val Gln Ile Ile Val	Lys Ala Gly Gly Lys	Glu Gln Thr Phe Thr
	1410	1415	1420
5	Ala Asp Lys Asp Val Ser Ile Gln Pro Ser	Pro Ser Phe Asp Glu Met	
	1425	1430	1435 1440
10	Asn Tyr Gln Phe Asn Ala Leu Glu Ile Asp Gly Ser Gly Leu Asn Phe		
	1445	1450	1455
	Ile Asn Asn Ser Ala Ser Ile Asp Val Thr Phe Thr Ala Phe Ala Glu		
	1460	1465	1470
15	Asp Gly Arg Lys Leu Gly Tyr Glu Ser Phe Ser Ile Pro Val Thr Leu		
	1475	1480	1485
	Lys Val Ser Thr Asp Asn Ala Leu Thr Leu His His Asn Glu Asn Gly		
	1490	1495	1500
20	Ala Gln Tyr Met Gln Trp Gln Ser Tyr Arg Thr Arg Leu Asn Thr Leu		
	1505	1510	1515 1520
25	Phe Ala Arg Gln Leu Val Ala Arg Ala Thr Thr Gly Ile Asp Thr Ile		
	1525	1530	1535
	Leu Ser Met Glu Thr Gln Asn Ile Gln Glu Pro Gln Leu Gly Lys Gly		
	1540	1545	1550
30	Phe Tyr Ala Thr Phe Val Ile Pro Pro Tyr Asn Leu Ser Thr His Gly		
	1555	1560	1565
	Asp Glu Arg Trp Phe Lys Leu Tyr Ile Lys His Val Val Asp Asn Asn		
	1570	1575	1580
35	Ser His Ile Ile Tyr Ser Gly Gln Leu Thr Asp Thr Asn Ile Asn Ile		
	1585	1590	1595 1600
40	Thr Leu Phe Ile Pro Leu Asp Asp Val Pro Leu Asn Gln Asp Tyr His		
	1605	1610	1615
	Ala Lys Val Tyr Met Thr Phe Lys Lys Ser Pro Ser Asp Gly Thr Trp		
	1620	1625	1630
45	Trp Gly Pro His Phe Val Arg Asp Asp Lys Gly Ile Val Thr Ile Asn		
	1635	1640	1645
	Pro Lys Ser Ile Leu Thr His Phe Glu Ser Val Asn Val Leu Asn Asn		
	1650	1655	1660
50	Ile Ser Ser Glu Pro Met Asp Phe Ser Gly Ala Asn Ser Leu Tyr Phe		
	1665	1670	1675 1680
55	Trp Glu Leu Phe Tyr Tyr Thr Pro Met Leu Val Ala Gln Arg Leu Leu		
	1685	1690	1695
	His Glu Gln Asn Phe Asp Glu Ala Asn Arg Trp Leu Lys Tyr Val Trp		
	1700	1705	1710
60	Ser Pro Ser Gly Tyr Ile Val His Gly Gln Ile Gln Asn Tyr Gln Trp		
	1715	1720	1725
	Asn Val Arg Pro Leu Leu Glu Asp Thr Ser Trp Asn Ser Asp Pro Leu		
	1730	1735	1740
65	Asp Ser Val Asp Pro Asp Ala Val Ala Gln His Asp Pro Met His Tyr		
	1745	1750	1755 1760
70	Lys Val Ser Thr Phe Met Arg Thr Leu Asp Leu Leu Ile Ala Arg Gly		
	1765	1770	1775

Asp His Ala Tyr Arg Leu Glu Arg Asp Thr Leu Asn Gln Ala Lys
 1780 1785 1790

5 Met Trp Tyr Met Gln Ala Leu His Leu Leu Gly Asp Lys Pro Tyr Leu
 1795 1800 1805

Pro Leu Ser Thr Thr Trp Ser Asp Pro Arg Leu Asp Arg Ala Ala Asp
 1810 1815 1820

10 Ile Thr Thr Gln Asn Ala His Asp Ser Ala Ile Val Ala Leu Arg Gln
 1825 1830 1835 1840

Asn Ile Pro Thr Pro Ala Pro Leu Ser
 1845 1849

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1740 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50 (*tcdAiii* coding region):

30 TTG CGC AGC GCT AAT ACC CTG ACT GAT CTC TTC CTG CCG CAA ATC AAT 48
 Leu Arg Ser Ala Asn Thr Leu Thr Asp Leu Phe Leu Pro Gln Ile Asn
 1 5 10 15

35 GAA GTG ATG ATG AAT TAC TGG CAG ACA TTA GCT CAG AGA GTA TAC AAT 96
 Glu Val Met Met Asn Tyr Trp Gln Thr Leu Ala Gln Arg Val Tyr Asn
 20 25 30

40 CTG CGT CAT AAC CTC TCT ATC GAC GGC CAG CCG TTA TAT CTG CCA ATC 144
 Leu Arg His Asn Leu Ser Ile Asp Gly Gln Pro Leu Tyr Leu Pro Ile
 35 40 45

45 TAT GCC ACA CCG GCC GAT CCG AAA GCG TTA CTC AGC GCC GCC GTT GCC 192
 Tyr Ala Thr Pro Ala Asp Pro Lys Ala Leu Leu Ser Ala Ala Val Ala
 50 55 60

50 ACT TCT CAA GGT GGA GGC AAG CTA CCG GAA TCA TTT ATG TCC CTG TGG 240
 Thr Ser Gln Gly Gly Gly Lys Leu Pro Glu Ser Phe Met Ser Leu Trp
 65 70 75 80

55 CGT TTC CCG CAC ATG CTG GAA AAT GCG CGC GGC ATG GTT AGC CAG CTC 288
 Arg Phe Pro His Met Leu Glu Asn Ala Arg Gly Met Val Ser Gln Leu
 85 90 95

60 ACC CAG TTC GGC TCC ACG TTA CAA AAT ATT ATC GAA CGT CAG GAC GCG 336
 Thr Gln Phe Gly Ser Thr Leu Gln Asn Ile Ile Glu Arg Gln Asp Ala
 100 105 110

65 GAA GCG CTC AAT GCG TTA TTA CAA AAT CAG GCC GCC GAG CTG ATA TTG 384
 Glu Ala Leu Asn Ala Leu Leu Gln Asn Gln Ala Ala Glu Leu Ile Leu
 115 120 125

ACT AAC CTG AGC ATT CAG GAC AAA ACC ATT GAA GAA TTG GAT GCC GAG 432
 Thr Asn Leu Ser Ile Gln Asp Lys Thr Ile Glu Glu Leu Asp Ala Glu
 130 135 140

AAA ACG GTG TTG GAA AAA TCC AAA GCG GGA GCA CAA TCG CGC TTT GAT 480
 Lys Thr Val Leu Glu Lys Ser Lys Ala Gly Ala Gln Ser Arg Phe Asp
 145 150 155 160

AGC TAC GGC AAA CTG TAC GAT GAG AAT ATC AAC GCC GGT GAA AAC CAA 528

	Ser	Tyr	Gly	Lys	Leu	Tyr	Asp	Glu	Asn	Ile	Asn	Ala	Gly	Glu	Asn	Gln	
					165					170					175		
5	GCC	ATG	ACG	CTA	CGA	GCG	TCC	GCC	GCC	GGG	CTT	ACC	ACG	GCA	GTT	CAG	576
	Ala	Met	Thr	Leu	Arg	Ala	Ser	Ala	Ala	Gly	Leu	Thr	Thr	Ala	Val	Gln	
				180				185					190				
10	GCA	TCC	CGT	CTG	GCC	GGT	GCG	GCG	GCT	GAT	CTG	GTG	CCT	AAC	ATC	TTC	624
	Ala	Ser	Arg	Leu	Ala	Gly	Ala	Ala	Ala	Asp	Leu	Val	Pro	Asn	Ile	Phe	
			195				200					205					
15	GGC	TTT	GCC	GGT	GGC	GGC	AGC	CGT	TGG	GGG	GCT	ATC	GCT	GAG	GCG	ACA	672
	Gly	Phe	Ala	Gly	Gly	Gly	Ser	Arg	Trp	Gly	Ala	Ile	Ala	Glu	Ala	Thr	
		210					215					220					
20	GGT	TAT	GTG	ATG	GAA	TTC	TCC	GCG	AAT	GTT	ATG	AAC	ACC	GAA	GCG	GAT	720
	Gly	Tyr	Val	Met	Glu	Phe	Ser	Ala	Asn	Val	Met	Asn	Thr	Glu	Ala	Asp	
		225				230					235					240	
25	AAA	ATT	AGC	CAA	TCT	GAA	ACC	TAC	CGT	CGT	CGC	CGT	CAG	GAG	TGG	GAG	768
	Lys	Ile	Ser	Gln	Ser	Glu	Thr	Tyr	Arg	Arg	Arg	Arg	Gln	Glu	Trp	Glu	
					245					250					255		
30	ATC	CAG	CGG	AAT	AAT	GCC	GAA	GCG	GAA	TTG	AAG	CAA	ATC	GAT	GCT	CAG	816
	Ile	Gln	Arg	Asn	Asn	Ala	Glu	Ala	Glu	Leu	Lys	Gln	Ile	Asp	Ala	Gln	
				260					265					270			
35	CTC	AAA	TCA	CTC	GCT	GTA	GCG	GCG	GAA	GCC	GCC	GTA	TTG	CAG	AAA	ACC	864
	Leu	Lys	Ser	Leu	Ala	Val	Arg	Arg	Glu	Ala	Ala	Val	Leu	Gln	Lys	Thr	
			275					280					285				
40	AGT	CTG	AAA	ACC	CAA	CAA	GAA	CAG	ACC	CAA	TCT	CAA	TTG	GCC	TTC	CTG	912
	Ser	Leu	Lys	Thr	Gln	Gln	Glu	Gln	Thr	Gln	Ser	Gln	Leu	Ala	Phe	Leu	
			290				295					300					
45	CAA	CGT	AAG	TTC	AGC	AAT	CAG	GCG	TTA	TAC	AAC	TGG	CTG	CGT	GGT	CGA	960
	Gln	Arg	Lys	Phe	Ser	Asn	Gln	Ala	Leu	Tyr	Asn	Trp	Leu	Arg	Gly	Arg	
		305				310					315					320	
50	CTG	GCG	GCG	ATT	TAC	TTC	CAG	TTC	TAC	GAT	TTG	GCC	GTC	GCG	CGT	TGC	1008
	Leu	Ala	Ala	Ile	Tyr	Phe	Gln	Phe	Tyr	Asp	Leu	Ala	Val	Ala	Arg	Cys	
				325					330						335		
55	CTG	ATG	GCA	GAA	CAA	GCT	TAC	CGT	TGG	GAA	CTC	AAT	GAT	GAC	TCT	GCC	1056
	Leu	Met	Ala	Glu	Gln	Ala	Tyr	Arg	Trp	Glu	Leu	Asn	Asp	Asp	Ser	Ala	
			340					345					350				
60	CGC	TTC	ATT	AAA	CCG	GGC	GCC	TGG	CAG	GGA	ACC	TAT	GCC	GGT	CTG	CTT	1104
	Arg	Phe	Ile	Lys	Pro	Gly	Ala	Trp	Gln	Gly	Thr	Tyr	Ala	Gly	Leu	Leu	
			355					360					365				
65	GCA	GGT	GAA	ACC	TTG	ATG	CTG	AGT	CTG	GCA	CAA	ATG	GAA	GAC	GCT	CAT	1152
	Ala	Gly	Glu	Thr	Leu	Met	Leu	Ser	Leu	Ala	Gln	Met	Glu	Asp	Ala	His	
		370				375						380					
70	CTG	AAA	CGC	GAT	AAA	CGC	GCA	TTA	GAG	GTT	GAA	CGC	ACA	GTA	TCG	CTG	1200
	Leu	Lys	Arg	Asp	Lys	Arg	Ala	Leu	Glu	Val	Glu	Arg	Thr	Val	Ser	Leu	
		385				390					395					400	
75	GCC	GAA	GTT	TAT	GCA	GGA	TTA	CCA	AAA	GAT	AAC	GGT	CCA	TTT	TCC	CTG	1248
	Ala	Glu	Val	Tyr	Ala	Gly	Leu	Pro	Lys	Asp	Asn	Gly	Pro	Phe	Ser	Leu	
				405					410					415			
80	GCT	CAG	GAA	ATT	GAC	AAG	CTG	GTG	AGT	CAA	GGT	TCA	GGC	AGT	GCC	GGC	1296
	Ala	Gln	Glu	Ile	Asp	Lys	Leu	Val	Ser	Gln	Gly	Ser	Gly	Ser	Ala	Gly	
			420					425					430				
85	AGT	GGT	AAT	AAT	AAT	TTG	GCG	TTC	GGC	GCC	GGC	ACG	GAC	ACT	AAA	ACC	1344
	Ser	Gly	Asn	Asn	Asn	Leu	Ala	Phe	Gly	Ala	Gly	Thr	Asp	Thr	Lys	Thr	
			435				440						445				

TCT TTG CAG GCA TCA GTC TCA TTC GCT GAT TTG AAA ATT CGT TCA GAT 1392
 Ser Leu Gln Ala Ser Val Ser Phe Ala Asp Leu Lys Ile Arg Glu Asp
 450 455 460

5 TAC CCG GCA TCG CTT GGC AAA ATT CGA CGT ATC AAA CAG ATC AGC GTC 1440
 Tyr Pro Ala Ser Leu Gly Lys Ile Arg Arg Ile Lys Gln Ile Ser Val
 465 470 475 480

10 ACT TTG CCC GCG CTA CTG GGA CCG TAT CAG GAT GTA CAG GCA ATA TTG 1488
 Thr Leu Pro Ala Leu Leu Gly Pro Tyr Gln Asp Val Gln Ala Ile Leu
 485 490 495

15 TCT TAC GGC GAT AAA GCC GGA TTA GCT AAC GGC TGT GAA GCG CTG GCA 1536
 Ser Tyr Gly Asp Lys Ala Gly Leu Ala Asn Gly Cys Glu Ala Leu Ala
 500 505 510

20 GTT TCT CAC GGT ATG AAT GAC AGC GGC CAA TTC CAG CTC GAT TTC AAC 1584
 Val Ser His Gly Met Asn Asp Ser Gly Gln Phe Gln Leu Asp Phe Asn
 515 520 525

GAT GGC AAA TTC CTG CCA TTC GAA GGC ATC GCC ATT GAT CAA GGC ACG 1632
 Asp Gly Lys Phe Leu Pro Phe Glu Gly Ile Ala Ile Asp Gln Gly Thr
 530 535 540

25 CTG ACA CTG AGC TTC CCA AAT GCA TCT ATG CCG GAG AAA GGT AAA CAA 1680
 Leu Thr Leu Ser Phe Pro Asn Ala Ser Met Pro Glu Lys Gly Lys Gln
 545 550 555 560

30 GCC ACT ATG TTA AAA ACC CTG AAC GAT ATC ATT TTG CAT ATT CGC TAC 1728
 Ala Thr Met Leu Lys Thr Leu Asn Asp Ile Ile Leu His Ile Arg Tyr
 565 570 575

35 ACC ATT AAA TAA 1740
 Thr Ile Lys ...
 579

(2) INFORMATION FOR SEQ ID NO:51:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 579 amino acids
 (B) TYPE: amino acids
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51 (TcdA_{iii}):

50 Leu Arg Ser Ala Asn Thr Leu Thr Asp Leu Phe Leu Pro Gln Ile Asn
 1 5 10 15

Glu Val Met Met Asn Tyr Trp Gln Thr Leu Ala Gln Arg Val Tyr Asn
 20 25 30

55 Leu Arg His Asn Leu Ser Ile Asp Gly Gln Pro Leu Tyr Leu Pro Ile
 35 40 45

Tyr Ala Thr Pro Ala Asp Pro Lys Ala Leu Leu Ser Ala Ala Val Ala
 50 55 60

60 Thr Ser Gln Gly Gly Gly Lys Leu Pro Glu Ser Phe Met Ser Leu Trp
 65 70 75 80

65 Arg Phe Pro His Met Leu Glu Asn Ala Arg Gly Met Val Ser Gln Leu
 85 90 95

Thr Gln Phe Gly Ser Thr Leu Gln Asn Ile Ile Glu Arg Gln Asp Ala
 100 105 110

Glu Ala Leu Asn Ala Leu Leu Gln Asn Gln Ala Ala Glu Leu Ile Leu
 115 120 125
 5 Thr Asn Leu Ser Ile Gln Asp Lys Thr Ile Glu Glu Leu Asp Ala Glu
 130 135 140
 Lys Thr Val Leu Glu Lys Ser Lys Ala Gly Ala Gln Ser Arg Phe Asp
 145 150 155 160
 10 Ser Tyr Gly Lys Leu Tyr Asp Glu Asn Ile Asn Ala Gly Glu Asn Gln
 165 170 175
 Ala Met Thr Leu Arg Ala Ser Ala Ala Gly Leu Thr Thr Ala Val Gln
 180 185 190
 15 Ala Ser Arg Leu Ala Gly Ala Ala Ala Asp Leu Val Pro Asn Ile Phe
 195 200 205
 20 Gly Phe Ala Gly Gly Gly Ser Arg Trp Gly Ala Ile Ala Glu Ala Thr
 210 215 220
 Gly Tyr Val Met Glu Phe Ser Ala Asn Val Met Asn Thr Glu Ala Asp
 225 230 235 240
 25 Lys Ile Ser Gln Ser Glu Thr Tyr Arg Arg Arg Gln Glu Trp Glu
 245 250 255
 Ile Gln Arg Asn Asn Ala Glu Ala Glu Leu Lys Gln Ile Asp Ala Gln
 260 265 270
 30 Leu Lys Ser Leu Ala Val Arg Arg Glu Ala Ala Val Leu Gln Lys Thr
 275 280 285
 35 Ser Leu Lys Thr Gln Gln Glu Gln Thr Gln Ser Gln Leu Ala Phe Leu
 290 295 300
 Gln Arg Lys Phe Ser Asn Gln Ala Leu Tyr Asn Trp Leu Arg Gly Arg
 305 310 315 320
 40 Leu Ala Ala Ile Tyr Phe Gln Phe Tyr Asp Leu Ala Val Ala Arg Cys
 325 330 335
 Leu Met Ala Glu Gln Ala Tyr Arg Trp Glu Leu Asn Asp Asp Ser Ala
 340 345 350
 45 Arg Phe Ile Lys Pro Gly Ala Trp Gln Gly Thr Tyr Ala Gly Leu Leu
 355 360 365
 50 Ala Gly Glu Thr Leu Met Leu Ser Leu Ala Gln Met Glu Asp Ala His
 370 375 380
 Leu Lys Arg Asp Lys Arg Ala Leu Glu Val Glu Arg Thr Val Ser Leu
 385 390 395 400
 55 Ala Glu Val Tyr Ala Gly Leu Pro Lys Asp Asn Gly Pro Phe Ser Leu
 405 410 415
 Ala Gln Glu Ile Asp Lys Leu Val Ser Gln Gly Ser Gly Ser Ala Gly
 420 425 430
 60 Ser Gly Asn Asn Asn Leu Ala Phe Gly Ala Gly Thr Asp Thr Lys Thr
 435 440 445
 65 Ser Leu Gln Ala Ser Val Ser Phe Ala Asp Leu Lys Ile Arg Glu Asp
 450 455 460
 Tyr Pro Ala Ser Leu Gly Lys Ile Arg Arg Ile Lys Gln Ile Ser Val
 465 470 475 480
 70 Thr Leu Pro Ala Leu Leu Gly Pro Tyr Gln Asp Val Gln Ala Ile Leu
 485 490 495

Ser Tyr Gly Asp Lys Ala Gly Leu Ala Asn Gly Cys Glu Ala Leu Ala
500 505 510

5 Val Ser His Gly Met Asn Asp Ser Gly Gln Phe Gln Leu Asp Phe Asn
515 520 525

Asp Gly Lys Phe Leu Pro Phe Glu Gly Ile Ala Ile Asp Gln Gly Thr
530 535 540

10 Leu Thr Leu Ser Phe Pro Asn Ala Ser Met Pro Glu Lys Gly Lys Gln
545 550 555 560

Ala Thr Met Leu Lys Thr Leu Asn Asp Ile Ile Leu His Ile Arg Tyr
565 570 575

15 Thr Ile Lys ...
579

20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5532 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52 (*tcbA_{ij}* coding region):

TTT ATA CAA GGT TAT AGT GAT CTG TTT GGT AAT CGT GCT GAT AAC TAT 48
 Phe Ile Gln Gly Tyr Ser Asp Leu Phe Gly Asn Arg Ala Asp Asn Tyr
 1 5 10 15

GCC GCG CCG GGC TCG GTT GCA TCG ATG TTC TCA CCG GCG GCT TAT TTG 96
 Ala Ala Pro Gly Ser Val Ala Ser Met Phe Ser Pro Ala Ala Tyr Leu
 20 25 30

40 ACG GAA TTG TAC CGT GAA GCC AAA AAC TTG CAT GAC AGC AGC TCA ATT 144
 Thr Glu Leu Tyr Arg Glu Ala Lys Asn Leu His Asp Ser Ser Ile
 35 40 45

50 TAT TAC CTA GAT AAA CGT CGC CCG GAT TTA GCA AGC TTA ATG CTC AGC 192
 Tyr Tyr Leu Asp Lys Arg Arg Pro Asp Leu Ala Ser Leu Met Leu Ser
 50 55 60

60 CAG AAA AAT ATG GAT GAG GAA ATT TCA ACG CTG GCT CTC TCT AAT GAA 240
 Gln Lys Asn Met Asp Glu Glu Ile Ser Thr Leu Ala Leu Ser Asn Glu
 65 70 75 80

55 TTG TGC CTT GCC GGG ATC GAA ACA AAA ACA GGA AAA TCA CAA GAT GAA 288
 Leu Cys Leu Ala Gly Ile Glu Thr Lys Thr Gly Lys Ser Gln Asp Glu
 85 90 95

60 GTG ATG GAT ATG TTG TCA ACT TAT CGT TTA AGT GGA GAG ACA CCT TAT 336
 Val Met Asp Met Leu Ser Thr Tyr Arg Leu Ser Gly Glu Thr Pro Tyr
 100 105 110

65 CAT CAC GCT TAT GAA ACT GTT CGT GAA ATC GTT CAT GAA CGT GAT CCA 384
 His His Ala Tyr Glu Thr Val Arg Glu Ile Val His Glu Arg Asp Pro
 115 120 125

GGA TTT CGT CAT TTG TCA CAG GCA CCC ATT GTT GCT GCT AAG CTC GAT 432
 Gly Phe Arg His Leu Ser Gln Ala Pro Ile Val Ala Ala Lys Leu Asp
 130 135 140

CCT GTG ACT TTG TTG GGT ATT AGC TCC CAT ATT TCG CCA GAA CTG TAT 480

	Pro	Val	Thr	Leu	Leu	Gly	Ile	Ser	Ser	His	Ile	Ser	Pro	Glu	Leu	Tyr	
	145					150					155					160	
5	AAC	TTG	CTG	ATT	GAG	GAG	ATC	CCG	GAA	AAA	GAT	GAA	GCC	GCG	CTT	GAT	528
	Asn	Leu	Leu	Ile	Glu	Glu	Ile	Pro	Glu	Lys	Asp	Glu	Ala	Ala	Leu	Asp	175
					165					170							
10	ACG	CTT	TAT	AAA	ACA	AAC	TTT	GGC	GAT	ATT	ACT	ACT	GCT	CAG	TTA	ATG	576
	Thr	Leu	Tyr	Lys	Thr	Asn	Phe	Gly	Asp	Ile	Thr	Thr	Ala	Gln	Leu	Met	
				180					185					190			
15	TCC	CCA	AGT	TAT	CTG	GCC	CGG	TAT	TAT	GGC	GTC	TCA	CCG	GAA	GAT	ATT	624
	Ser	Pro	Ser	Tyr	Leu	Ala	Arg	Tyr	Tyr	Gly	Val	Ser	Pro	Glu	Asp	Ile	
			195					200					205				
20	GCC	TAC	GTG	ACG	ACT	TCA	TTA	TCA	CAT	GTT	GGA	TAT	AGC	AGT	GAT	ATT	672
	Ala	Tyr	Val	Thr	Thr	Ser	Leu	Ser	His	Val	Gly	Tyr	Ser	Ser	Asp	Ile	
		210					215					220					
25	CTG	GTT	ATT	CCG	TTG	GTC	GAT	GGT	GTG	GGT	AAG	ATG	GAA	GTA	GTT	CGT	720
	Leu	Val	Ile	Pro	Leu	Val	Asp	Gly	Val	Gly	Lys	Met	Glu	Val	Val	Arg	240
		225				230					235						
30	GTT	ACC	CGA	ACA	CCA	TCG	GAT	AAT	TAT	ACC	AGT	CAG	ACG	AAT	TAT	ATT	768
	Val	Thr	Arg	Thr	Pro	Ser	Asp	Asn	Tyr	Thr	Ser	Gln	Thr	Asn	Tyr	Ile	
					245				250						255		
35	GAG	CTG	TAT	CCA	CAG	GGT	GGC	GAC	AAT	TAT	TTG	ATC	AAA	TAC	AAT	CTA	816
	Glu	Leu	Tyr	Pro	Gln	Gly	Gly	Asp	Asn	Tyr	Leu	Ile	Lys	Tyr	Asn	Leu	
				260					265					270			
40	AGC	AAT	AGT	TTT	GGT	TTG	GAT	GAT	TTT	TAT	CTG	CAA	TAT	AAA	GAT	GGT	864
	Ser	Asn	Ser	Phe	Gly	Leu	Asp	Asp	Phe	Tyr	Leu	Gln	Tyr	Lys	Asp	Gly	
			275					280					285				
45	TCC	GCT	GAT	TGG	ACT	GAG	ATT	GCC	CAT	AAT	CCC	TAT	CCT	GAT	ATG	GTC	912
	Ser	Ala	Asp	Trp	Thr	Glu	Ile	Ala	His	Asn	Pro	Tyr	Pro	Asp	Met	Val	
		290					295					300					
50	ATA	AAT	CAA	AAG	TAT	GAA	TCA	CAG	GCG	ACA	ATC	AAA	CGT	AGT	GAC	TCT	960
	Ile	Asn	Gln	Lys	Tyr	Glu	Ser	Gln	Ala	Thr	Ile	Lys	Arg	Ser	Asp	Ser	320
		305				310					315						
55	GAC	AAT	ATA	CTC	AGT	ATA	GGG	TTA	CAA	AGA	TGG	CAT	AGC	GGT	AGT	TAT	1008
	Asp	Asn	Ile	Leu	Ser	Ile	Gly	Leu	Gln	Arg	Trp	His	Ser	Gly	Ser	Tyr	
				325					330						335		
60	AAT	TTT	GCC	GCC	GCC	AAT	TTT	AAA	ATT	GAC	CAA	TAC	TCC	CCG	AAA	GCT	1056
	Asn	Phe	Ala	Ala	Ala	Asn	Phe	Lys	Ile	Asp	Gln	Tyr	Ser	Pro	Lys	Ala	
				340				345						350			
65	TTC	CTG	CTT	AAA	ATG	AAT	AAG	GCT	ATT	CGG	TTG	CTC	AAA	GCT	ACC	GGC	1104
	Phe	Leu	Leu	Lys	Met	Asn	Lys	Ala	Ile	Arg	Leu	Leu	Lys	Ala	Thr	Gly	
			355					360					365				
70	CTC	TCT	TTT	GCT	ACG	TTG	GAG	CGT	ATT	GTT	GAT	AGT	GTT	AAT	AGC	ACC	1152
	Leu	Ser	Phe	Ala	Thr	Leu	Glu	Arg	Ile	Val	Asp	Ser	Val	Asn	Ser	Thr	
		370					375					380					
75	AAA	TCC	ATC	ACG	GTT	GAG	GTA	TTA	AAC	AAG	GTT	TAT	CGG	GTA	AAA	TTC	1200
	Lys	Ser	Ile	Thr	Val	Glu	Val	Leu	Asn	Lys	Val	Tyr	Arg	Val	Lys	Phe	400
		385				390					395						
80	TAT	ATT	GAT	CGT	TAT	GGC	ATC	AGT	GAA	GAG	ACA	GCC	GCT	ATT	TTG	GCT	1248
	Tyr	Ile	Asp	Arg	Tyr	Gly	Ile	Ser	Glu	Glu	Thr	Ala	Ala	Ile	Leu	Ala	
				405						410				415			
85	AAT	ATT	AAT	ATC	TCT	CAG	CAA	GCT	GTT	GGC	AAT	CAG	CTT	AGC	CAG	TTT	1296
	Asn	Ile	Asn	Ile	Ser	Gln	Gln	Ala	Val	Gly	Asn	Gln	Leu	Ser	Gln	Phe	
				420					425					430			

	GAG	CAA	CTA	TTT	AAT		CCG	CCG	CTC	AAT	GGT	ATT	CGC	T	AA	ATC	1344
	Glu	Gln	Leu	Phe	Asn	His	Pro	Pro	Leu	Asn	Gly	Ile	Arg	Tyr	Glu	Ile	
			435					440					445				
5	AGT	GAG	GAC	AAC	TCC	AAA	CAT	CTT	CCT	AAT	CCT	GAT	CTG	AAC	CTT	AAA	1392
	Ser	Glu	Asp	Asn	Ser	Lys	His	Leu	Pro	Asn	Pro	Asp	Leu	Asn	Leu	Lys	
		450					455					460					
10	CCA	GAC	AGT	ACC	GGT	GAT	GAT	CAA	CGC	AAG	GCG	GTT	TTA	AAA	CGC	GCG	1440
	Pro	Asp	Ser	Thr	Gly	Asp	Asp	Gln	Arg	Lys	Ala	Val	Leu	Lys	Arg	Ala	
	465				470						475					480	-
15	TTT	CAG	GTT	AAC	GCC	AGT	GAG	TTG	TAT	CAG	ATG	TTA	TTG	ATC	ACT	GAT	1488
	Phe	Gln	Val	Asn	Ala	Ser	Glu	Leu	Tyr	Gln	Met	Leu	Leu	Ile	Thr	Asp	
				485					490						495		
20	CGT	AAA	GAA	GAC	GGT	GTT	ATC	AAA	AAT	AAC	TTA	GAG	AAT	TTG	TCT	GAT	1536
	Arg	Lys	Glu	Asp	Gly	Val	Ile	Lys	Asn	Asn	Leu	Glu	Asn	Leu	Ser	Asp	
				500				505						510			
25	CTG	TAT	TTG	GTT	AGT	TTG	CTG	GCC	CAG	ATT	CAT	AAC	CTG	ACT	ATT	GCT	1584
	Leu	Tyr	Leu	Val	Ser	Leu	Leu	Ala	Gln	Ile	His	Asn	CTG	ACT	Thr	Ile	
			515					520					525			Ala	
30	GAA	TTG	AAC	ATT	TTG	TTG	GTG	ATT	TGT	GGC	TAT	GGC	GAC	ACC	AAC	ATT	1632
	Glu	Leu	Asn	Ile	Leu	Leu	Val	Ile	Cys	Gly	Tyr	Gly	Asp	Thr	Asn	Ile	
		530					535					540					
35	TAT	CAG	ATT	ACC	GAC	GAT	AAT	TTA	GCC	AAA	ATA	GTG	GAA	ACA	TTG	TTG	1680
	Tyr	Gln	Ile	Thr	Asp	Asp	Asn	Leu	Ala	Lys	Ile	Val	Glu	Thr	Leu	Leu	
	545				550						555					560	
40	TGG	ATC	ACT	CAA	TGG	TTG	AAG	ACC	CAA	AAA	TGG	ACA	GTT	ACC	GAC	CTG	1728
	Trp	Ile	Thr	Gln	Trp	Leu	Lys	Thr	Gln	Lys	Trp	Thr	Val	Thr	Asp	Leu	
				565						570					575		
45	TTT	CTG	ATG	ACC	ACG	GCC	ACT	TAC	AGC	ACC	ACT	TTA	ACG	CCA	GAA	ATT	1776
	Phe	Leu	Met	Thr	Thr	Ala	Thr	Tyr	Ser	Thr	Thr	Leu	Thr	Pro	Glu	Ile	
				580				585						590			
50	AGC	AAT	CTG	ACG	GCT	ACG	TTG	TCT	TCA	ACT	TTG	CAT	GGC	AAA	GAG	AGT	1824
	Ser	Asn	Leu	Thr	Ala	Thr	Leu	Ser	Ser	Thr	Leu	His	Gly	Lys	Glu	Ser	
			595				600						605				
55	CTG	ATT	GGG	GAA	GAT	CTG	AAA	AGA	GCA	ATG	GCG	CCT	TGC	TTC	ACT	TCG	1872
	Leu	Ile	Gly	Glu	Asp	Leu	Lys	Arg	Ala	Met	Ala	Pro	Cys	Phe	Thr	Ser	
		610					615					620					
60	GCT	TTG	CAT	TTG	ACT	TCT	CAA	GAA	GTT	GCG	TAT	GAC	CTG	CTG	TTG	TGG	1920
	Ala	Leu	His	Leu	Thr	Ser	Gln	Glu	Val	Ala	Tyr	Asp	Leu	Leu	Leu	Trp	
	625				630						635					640	
65	ATA	GAC	CAG	ATT	CAA	CCG	GCA	CAA	ATA	ACT	GTT	GAT	GGG	TTT	TGG	GAA	1968
	Ile	Asp	Gln	Ile	Gln	Pro	Ala	Gln	Ile	Thr	Val	Asp	Gly	Phe	Trp	Glu	
				645						650					655		
70	GAA	GTG	CAA	ACA	ACA	CCA	ACC	AGC	TTG	AAG	GTG	ATT	ACC	TTT	GCT	CAG	2016
	Glu	Val	Gln	Thr	Thr	Pro	Thr	Ser	Leu	Lys	Val	Ile	Thr	Phe	Ala	Gln	
				660					665					670			
75	GTG	CTG	GCA	CAA	TTG	AGC	CTG	ATC	TAT	CGT	CGT	ATT	GGG	TTA	AGT	GAA	2064
	Val	Leu	Ala	Gln	Leu	Ser	Leu	Ile	Tyr	Arg	Arg	Ile	Gly	Leu	Ser	Glu	
			675					680					685				
80	ACG	GAA	CTG	TCA	CTG	ATC	GTG	ACT	CAA	TCT	TCT	CTG	CTA	GTG	GCA	GGC	2112
	Thr	Glu	Leu	Ser	Leu	Ile	Val	Thr	Gln	Ser	Ser	Leu	Leu	Val	Ala	Gly	
		690					695					700					
85	AAA	AGC	ATA	CTG	GAT	CAC	GGT	CTG	TTA	ACC	CTG	ATG	GCC	TTG	GAA	GGT	2160
	Lys	Ser	Ile	Leu	Asp	His	Gly	Leu	Leu	Thr	Leu	Met	Ala	Leu	Glu	Gly	
	705					710					715					720	

5	TTT CAT ACC TGG GTT AAT GGC TTG GGG CAA CAT GCC TCC TTG ATA TTG 2208 Phe His Thr Trp Val Asn Gly Leu Gly Gln His Ala Ser Leu Ile Leu 725 730 735
10	GCG GCG TTG AAA GAC GGA GCC TTG ACA GTT ACC GAT GTA GCA CAA GCT 2256 Ala Ala Leu Lys Asp Gly Ala Leu Thr Val Thr Asp Val Ala Gln Ala 740 745 750
15	ATG AAT AAG GAG GAA TCT CTC CTA CAA ATG GCA GCT AAT CAG GTG GAG 2304 Met Asn Lys Glu Glu Ser Leu Leu Gln Met Ala Ala Asn Gln Val Glu 755 760 765
20	AAG GAT CTA ACA AAA CTG ACC AGT TGG ACA CAG ATT GAC GCT ATT CTG 2352 Lys Asp Leu Thr Lys Leu Thr Ser Trp Thr Gln Ile Asp Ala Ile Leu 770 775 780
25	CAA TGG TTA CAG ATG TCT TCG GCC TTG GCG GTT TCT CCA CTG GAT CTG 2400 Gln Trp Leu Gln Met Ser Ser Ala Leu Ala Val Ser Pro Leu Asp Leu 785 790 795
30	GCA GGG ATG ATG GCC CTG AAA TAT GGG ATA GAT CAT AAC TAT GCT GCC 2448 Ala Gly Met Met Ala Leu Lys Tyr Gly Ile Asp His Asn Tyr Ala Ala 805 810 815
35	TGG CAA GCT GCG GCG GCT GCG CTG ATG GCT GAT CAT GCT AAT CAG GCA 2496 Trp Gln Ala Ala Ala Ala Leu Met Ala Asp His Ala Asn Gln Ala 820 825 830
40	CAG AAA AAA CTG GAT GAG ACG TTC AGT AAG GCA TTA TGT AAC TAT TAT 2544 Gln Lys Lys Leu Asp Glu Thr Phe Ser Lys Ala Leu Cys Asn Tyr Tyr 835 840 845
45	ATT AAT GCT GTT GTC GAT AGT GCT GCT GGA GTA CGT GAT CGT AAC GGT 2592 Ile Asn Ala Val Val Asp Ser Ala Ala Gly Val Arg Asp Arg Asn Gly 850 855 860
50	TTA TAT ACC TAT TTG CTG ATT GAT AAT CAG GTT TCT GCC GAT GTG ATC 2640 Leu Tyr Thr Tyr Leu Leu Ile Asp Asn Gln Val Ser Ala Asp Val Ile 865 870 875 880
55	ACT TCA CGT ATT GCA GAA GCT ATC GCC GGT ATT CAA CTG TAC GTT AAC 2688 Thr Ser Arg Ile Ala Glu Ala Ile Ala Gly Ile Gln Leu Tyr Val Asn 885 890 895
60	CGG GCT TTA AAC CGA GAT GAA GGT CAG CTT GCA TCG GAC GTT AGT ACC 2736 Arg Ala Leu Asn Arg Asp Glu Gly Gln Leu Ala Ser Asp Val Ser Thr 900 905 910
65	CGT CAG TTC TTC ACT GAC TGG GAA CGT TAC AAT AAA CGT TAC AGT ACT 2784 Arg Gln Phe Phe Thr Asp Trp Glu Arg Tyr Asn Lys Arg Tyr Ser Thr 915 920 925
70	TGG GCT GGT GTC TCT GAA CTG GTC TAT TAT CCA GAA AAC TAT GTT GAT 2832 Trp Ala Gly Val Ser Glu Leu Val Tyr Tyr Pro Glu Asn Tyr Val Asp 930 935 940
75	CCC ACT CAG CGC ATT GGG CAA ACC AAA ATG ATG GAT GCG CTG TTG CAA 2880 Pro Thr Gln Arg Ile Gly Gln Thr Lys Met Met Asp Ala Leu Leu Gln 945 950 955 960
80	TCC ATC AAC CAG AGC CAG CTA AAT GCG GAT ACG GTG GAA GAT GCT TTC 2928 Ser Ile Asn Gln Ser Gln Leu Asn Ala Asp Thr Val Glu Asp Ala Phe 965 970 975
85	AAA ACT TAT TTG ACC AGC TTT GAG CAG GTA GCA AAT CTG AAA GTA ATT 2976 Lys Thr Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys Val Ile 980 985 990
90	AGT GCT TAC CAC GAT AAT GTG AAT GTG GAT CAA GGA TTA ACT TAT TTT 3024 Ser Ala Tyr His Asp Asn Val Asn Val Asp Gln Gly Leu Thr Tyr Phe

	995	1000	1005	
5	ATC GGT ATC GAC CAA GCA GCT CCG GGT ACG TAT TAC TGG CGT AGT GTT 3072 Ile Gly Ile Asp Gln Ala Ala Pro Gly Thr Tyr Tyr Trp Arg Ser Val 1010 1015 1020			
10	GAT CAC AGC AAA TGT GAA AAT GGC AAG TTT GCC GCT AAT GCT TGG GGT 3120 Asp His Ser Lys Cys Glu Asn Gly Lys Phe Ala Ala Asn Ala Trp Gly 1025 1030 1035 1040			
15	GAG TGG AAT AAA ATT ACC TGT GCT GTC AAT CCT TGG AAA AAT ATC ATC 3168 Glu Trp Asn Lys Ile Thr Cys Ala Val Asn Pro Trp Lys Asn Ile Ile 1045 1050 1055			
20	CGT CCG GTT GTT TAT ATG TCC CGC TTA TAT CTG CTA TGG CTG GAG CAG 3216 Arg Pro Val Val Tyr Met Ser Arg Leu Tyr Leu Leu Trp Leu Glu Gln 1060 1065 1070			
25	CAA TCA AAG AAA AGT GAT GAT GGT AAA ACC ACG ATT TAT CAA TAT AAC 3264 Gln Ser Lys Lys Ser Asp Asp Gly Lys Thr Thr Ile Tyr Gln Tyr Asn 1075 1080 1085			
30	TTA AAA CTG GCT CAT ATT CGT TAC GAC GGT AGT TGG AAT ACA CCA TTT 3312 Leu Lys Leu Ala His Ile Arg Tyr Asp Gly Ser Trp Asn Thr Pro Phe 1090 1095 1100			
35	ACT TTT GAT GTG ACA GAA AAG GTA AAA AAT TAC ACG TCG AGT ACT GAT 3360 Thr Phe Asp Val Thr Glu Lys Val Lys Asn Tyr Thr Ser Ser Thr Asp 1105 1110 1115 1120			
40	GCT GCT GAA TCT TTA GGG TTG TAT TGT ACT GGT TAT CAA GGG GAA GAC 3408 Ala Ala Glu Ser Leu Gly Leu Tyr Cys Thr Gly Tyr Gln Gly Glu Asp 1125 1130 1135			
45	ACT CTA TTA GTT ATG TTC TAT TCG ATG CAG AGT AGT TAT AGC TCC TAT 3456 Thr Leu Leu Val Met Phe Tyr Ser Met Gln Ser Ser Tyr Ser Ser Tyr 1140 1145 1150			
50	ACC GAT AAT AAT GCG CCG GTC ACT GGG CTA TAT ATT TTC GCT GAT ATG 3504 Thr Asp Asn Asn Ala Pro Val Thr Gly Leu Tyr Ile Phe Ala Asp Met 1155 1160 1165			
55	TCA TCA GAC AAT ATG ACG AAT GCA CAA GCA ACT AAC TAT TGG AAT AAC 3552 Ser Ser Asp Asn Met Thr Asn Ala Gln Ala Thr Asn Tyr Trp Asn Asn 1170 1175 1180			
60	AGT TAT CCG CAA TTT GAT ACT GTG ATG GCA GAT CCG GAT AGC GAC AAT 3600 Ser Tyr Pro Gln Phe Asp Thr Val Met Ala Asp Pro Asp Ser Asp Asn 1185 1190 1195 1200			
65	AAA AAA GTC ATA ACC AGA AGA GTT AAT AAC CGT TAT GCG GAG GAT TAT 3648 Lys Lys Val Ile Thr Arg Arg Val Asn Asn Arg Tyr Ala Glu Asp Tyr 1205 1210 1215			
70	GAA ATT CCT TCC TCT GTG ACA AGT AAC AGT AAT TAT TCT TGG GGT GAT 3696 Glu Ile Pro Ser Ser Val Thr Ser Asn Ser Asn Tyr Ser Trp Gly Asp 1220 1225 1230			
75	CAC AGT TTA ACC ATG CTT TAT GGT GGT AGT GTT CCT AAT ATT ACT TTT 3744 His Ser Leu Thr Met Leu Tyr Gly Gly Ser Val Pro Asn Ile Thr Phe 1235 1240 1245			
80	GAA TCG GCG GCA GAA GAT TTA AGG CTA TCT ACC AAT ATG GCA TTG AGT 3792 Glu Ser Ala Ala Glu Asp Leu Arg Leu Ser Thr Asn Met Ala Leu Ser 1250 1255 1260			
85	ATT ATT CAT AAT GGA TAT GCG GGA ACC CGC CGT ATA CAA TGT AAT CTT 3840 Ile Ile His Asn Gly Tyr Ala Gly Thr Arg Arg Ile Gln Cys Asn Leu 1265 1270 1275 1280			
90	ATG AAA CAA TAC GCT TCA TTA GGT GAT AAA TTT ATA ATT TAT GAT TCA 3888			

	Met	Lys	Gln	Tyr	Ala	Ser	Leu	Gly	Asp	Lys	Phe	Ile	Ile	Tyr	Asp	Ser	
					1285					1290					1295		
5	TCA	TTT	GAT	GAT	GCA	AAC	CGT	TTT	AAT	CTG	GTG	CCA	TTG	TTT	AAA	TTC	3936
	Ser	Phe	Asp	Asp	Ala	Asn	Arg	Phe	Asn	Leu	Val	Pro	Leu	Phe	Lys	Phe	
					1300					1305					1310		
10	GGA	AAA	GAC	GAG	AAC	TCA	GAT	GAT	AGT	ATT	TGT	ATA	TAT	AAT	GAA	AAC	3984
	Gly	Lys	Asp	Glu	Asn	Ser	Asp	Asp	Ser	Ile	Cys	Ile	Tyr	Asn	Glu	Asn	
					1315					1320					1325		
15	CCT	TCC	TCT	GAA	GAT	AAG	AAG	TGG	TAT	TTT	TCT	TCG	AAA	GAT	GAC	AAT	4032
	Pro	Ser	Ser	Glu	Asp	Lys	Lys	Trp	Tyr	Phe	Ser	Ser	Lys	Asp	Asp	Asn	
					1330										1340		
20	AAA	ACA	GCG	GAT	TAT	AAT	GGT	GGA	ACT	CAA	TGT	ATA	GAT	GCT	GGA	ACC	4080
	Lys	Thr	Ala	Asp	Tyr	Asn	Gly	Gly	Thr	Gln	Cys	Ile	Asp	Ala	Gly	Thr	
						1345					1355				1360		
25	AGT	AAC	AAA	GAT	TTT	TAT	TAT	AAT	CTC	CAG	GAG	ATT	GAA	GTA	ATT	AGT	4128
	Ser	Asn	Lys	Asp	Phe	Tyr	Tyr	Asn	Leu	Gln	Glu	Ile	Glu	Val	Ile	Ser	
						1365					1370				1375		
30	GTT	ACT	GGT	GGG	TAT	TGG	TCG	AGT	TAT	AAA	ATA	TCC	AAC	CCG	ATT	AAT	4176
	Val	Thr	Gly	Gly	Tyr	Trp	Ser	Ser	Tyr	Lys	Ile	Ser	Asn	Pro	Ile	Asn	
						1380					1385				1390		
35	ATC	AAT	ACG	GGC	ATT	GAT	AGT	GCT	AAA	GTA	AAA	GTC	ACC	GTA	AAA	GCG	4224
	Ile	Asn	Thr	Gly	Ile	Asp	Ser	Ala	Lys	Val	Lys	Val	Thr	Val	Lys	Ala	
						1395					1400				1405		
40	GGT	GGT	GAC	GAT	CAA	ATC	TTT	ACT	GCT	GAT	AAT	AGT	ACC	TAT	GTT	CCT	4272
	Gly	Gly	Asp	Asp	Gln	Ile	Phe	Thr	Ala	Asp	Asn	Ser	Thr	Tyr	Val	Pro	
						1410					1415				1420		
45	CAG	CAA	CCG	GCA	CCC	AGT	TTT	GAG	GAG	ATG	ATT	TAT	CAG	TTC	AAT	AAC	4320
	Gln	Gln	Pro	Ala	Pro	Ser	Phe	Glu	Glu	Met	Ile	Tyr	Gln	Phe	Asn	Asn	
						1425					1435				1440		
50	CTG	ACA	ATA	GAT	TGT	AAG	AAT	TTA	AAT	TTC	ATC	GAC	AAT	CAG	GCA	CAT	4368
	Leu	Thr	Ile	Asp	Cys	Lys	Asn	Leu	Asn	Phe	Ile	Asp	Asn	Gln	Ala	His	
						1445					1450				1455		
55	ATT	GAG	ATT	GAT	TTC	ACC	GCT	ACG	GCA	CAA	GAT	GGC	CGA	TTC	TTG	GGT	4416
	Ile	Glu	Ile	Asp	Phe	Thr	Ala	Thr	Ala	Gln	Asp	Gly	Arg	Phe	Leu	Gly	
						1460					1465				1470		
60	GCA	GAA	ACT	TTT	ATT	ATC	CCG	GTA	ACT	AAA	AAA	GTT	CTC	GGT	ACT	GAG	4464
	Ala	Glu	Thr	Phe	Ile	Ile	Pro	Val	Thr	Lys	Lys	Val	Leu	Gly	Thr	Glu	
						1475									1485		
65	AAC	GTG	ATT	GCG	TTA	TAT	AGC	GAA	AAT	AAC	GGT	GTT	CAA	TAT	ATG	CAA	4512
	Asn	Val	Ile	Ala	Leu	Tyr	Ser	Glu	Asn	Asn	Gly	Val	Gln	Tyr	Met	Gln	
						1490					1495				1500		
70	ATT	GGC	GCA	TAT	CGT	ACC	CGT	TTG	AAT	ACG	TTA	TTC	GCT	CAA	CAG	TTG	4560
	Ile	Gly	Ala	Tyr	Arg	Thr	Arg	Leu	Asn	Thr	Leu	Phe	Ala	Gln	Gln	Leu	
						1505						1515			1520		
75	GTT	AGC	CGT	GCT	AAT	CGT	GGC	ATT	GAT	GCA	GTG	CTC	AGT	ATG	GAA	ACT	4608
	Val	Ser	Arg	Ala	Asn	Arg	Gly	Ile	Asp	Ala	Val	Leu	Ser	Met	Glu	Thr	
						1525					1530				1535		
80	CAG	AAT	ATT	CAG	GAA	CCG	CAA	TTA	GGA	GCG	GGC	ACA	TAT	GTG	CAG	CTT	4656
	Gln	Asn	Ile	Gln	Glu	Pro	Gln	Leu	Gly	Ala	Gly	Thr	Tyr	Val	Gln	Leu	
						1540					1545				1550		
85	GTG	TTG	GAT	AAA	TAT	GAT	GAG	TCT	ATT	CAT	GGC	ACT	AAT	AAA	AGC	TTT	4704
	Val	Leu	Asp	Lys	Tyr	Asp	Glu	Ser	Ile	His	Gly	Thr	Asn	Lys	Ser	Phe	
						1555					1560				1565		

GCT ATT GAA TAT GTT ATA TTT AAA GAG AAC GAT AGT GTG ATT 4752
 Ala Ile Glu Tyr Val Asp Ile Phe Lys Glu Asn Asp Ser Phe Val Ile
 1570 1575 1580

5 TAT CAA GGA GAA CTT AGC GAA ACA AGT CAA ACT GTT GTG AAA GTT TTC 4800
 Tyr Gln Gly Glu Leu Ser Glu Thr Ser Gln Thr Val Val Lys Val Phe
 1585 1590 1595 1600

10 TTA TCC TAT TTT ATA GAG GCG ACT GGA AAT AAG AAC CAC TTA TGG GTA 4848
 Leu Ser Tyr Phe Ile Glu Ala Thr Gly Asn Lys Asn His Leu Trp Val
 1605 1610 1615

15 CGT GCT AAA TAC CAA AAG GAA ACG ACT GAT AAG ATC TTG TTC GAC CGT 4896
 Arg Ala Lys Tyr Gln Lys Glu Thr Thr Asp Lys Ile Leu Phe Asp Arg
 1620 1625 1630

ACT GAT GAG AAA GAT CCG CAC GGT TGG TTT CTC AGC GAC GAT CAC AAG 4944
 Thr Asp Glu Lys Asp Pro His Gly Trp Phe Leu Ser Asp Asp His Lys
 1635 1640 1645

20 ACC TTT AGT GGT CTC TCT TCC GCA CAG GCA TTA AAG AAC GAC AGT GAA 4992
 Thr Phe Ser Gly Leu Ser Ser Ala Gln Ala Leu Lys Asn Asp Ser Glu
 1650 1655 1660

25 CCG ATG GAT TTC TCT GGC GCC AAT GCT CTC TAT TTC TGG GAA CTG TTC 5040
 Pro Met Asp Phe Ser Gly Ala Asn Ala Leu Tyr Phe Trp Glu Leu Phe
 1665 1670 1675 1680

30 TAT TAC ACG CCG ATG ATG ATG GCT CAT CGT TTG TTG CAG GAA CAG AAT 5088
 Tyr Tyr Thr Pro Met Met Met Ala His Arg Leu Leu Gln Glu Gln Asn
 1685 1690 1695

35 TTT GAT GCG GCG AAC CAT TGG TTC CGT TAT GTC TGG AGT CCA TCC GGT 5136
 Phe Asp Ala Ala Asn His Trp Phe Arg Tyr Val Trp Ser Pro Ser Gly
 1700 1705 1710

40 TAT ATC GTT GAT GGT AAA ATT GCT ATC TAC CAC TGG AAC GTG CGA CCG 5184
 Tyr Ile Val Asp Gly Lys Ile Ala Ile Tyr His Trp Asn Val Arg Pro
 1715 1720 1725

CTG GAA GAA GAC ACC AGT TGG AAT GCA CAA CAA CTG GAC TCC ACC GAT 5232
 Leu Glu Glu Asp Thr Ser Trp Asn Ala Gln Gln Leu Asp Ser Thr Asp
 1730 1735 1740

45 CCA GAT GCT GTA GCC CAA GAT GAT CCG ATG CAC TAC AAG GTG GCT ACC 5280
 Pro Asp Ala Val Ala Gln Asp Asp Pro Met His Tyr Lys Val Ala Thr
 1745 1750 1755 1760

50 TTT ATG GCG ACG TTG GAT CTG CTA ATG GCC CGT GGT GAT GCT GCT TAC 5328
 Phe Met Ala Thr Leu Asp Leu Leu Met Ala Arg Gly Asp Ala Ala Tyr
 1765 1770 1775

55 CGC CAG TTA GAG CGT GAT ACG TTG GCT GAA GCT AAA ATG TGG TAT ACA 5376
 Arg Gln Leu Glu Arg Asp Thr Leu Ala Glu Ala Lys Met Trp Tyr Thr
 1780 1785 1790

60 CAG GCG CTT AAT CTG TTG GGT GAT GAG CCA CAA GTG ATG CTG AGT ACG 5424
 Gln Ala Leu Asn Leu Leu Gly Asp Glu Pro Gln Val Met Leu Ser Thr
 1795 1800 1805

ACT TGG GCT AAT CCA ACA TTG GGT AAT GCT GCT TCA AAA ACC ACA CAG 5472
 Thr Trp Ala Asn Pro Thr Leu Gly Asn Ala Ala Ser Lys Thr Thr Gln
 1810 1815 1820

65 CAG GTT CGT CAG CAA GTG CTT ACC CAG TTG CGT CTC AAT AGC AGG GTA 5520
 Gln Val Arg Gln Gln Val Leu Thr Gln Leu Arg Leu Asn Ser Arg Val
 1825 1830 1835 1840

70 AAA ACC CCG TTG 5532
 Lys Thr Pro Leu
 1844

(2) INFORMATION FOR SEQ ID NO:53:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1844 amino acids
 (B) TYPE: amino acids
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53 (TcbAii):

	Features	From	To	Description
	Peptide	1	1844	TcbAii peptide
15	Fragment	1	11	(SEQ ID NO:1)
	Fragment	978	990	(SEQ ID NO:23)
	Fragment	1387	1401	(SEQ ID NO:22)
	Fragment	1484	1505	(SEQ ID NO:24)
20	Fragment	1527	1552	(SEQ ID NO:21)

Phe Ile Gln Gly Tyr Ser Asp Leu Phe Gly Asn Arg Ala Asp Asn Tyr
 1 5 10 15
 Ala Ala Pro Gly Ser Val Ala Ser Met Phe Ser Pro Ala Ala Tyr Leu
 20 25 30
 Thr Glu Leu Tyr Arg Glu Ala Lys Asn Leu His Asp Ser Ser Ser Ile
 35 40 45
 Tyr Tyr Leu Asp Lys Arg Arg Pro Asp Leu Ala Ser Leu Met Leu Ser
 50 55 60
 Gln Lys Asn Met Asp Glu Glu Ile Ser Thr Leu Ala Leu Ser Asn Glu
 65 70 75 80
 Leu Cys Leu Ala Gly Ile Glu Thr Lys Thr Gly Lys Ser Gln Asp Glu
 85 90 95
 Val Met Asp Met Leu Ser Thr Tyr Arg Leu Ser Gly Glu Thr Pro Tyr
 100 105 110
 His His Ala Tyr Glu Thr Val Arg Glu Ile Val His Glu Arg Asp Pro
 115 120 125
 Gly Phe Arg His Leu Ser Gln Ala Pro Ile Val Ala Ala Lys Leu Asp
 130 135 140
 Pro Val Thr Leu Leu Gly Ile Ser Ser His Ile Ser Pro Glu Leu Tyr
 145 150 155 160
 Asn Leu Leu Ile Glu Glu Ile Pro Glu Lys Asp Glu Ala Ala Leu Asp
 165 170 175
 Thr Leu Tyr Lys Thr Asn Phe Gly Asp Ile Thr Thr Ala Gln Leu Met
 180 185 190
 Ser Pro Ser Tyr Leu Ala Arg Tyr Tyr Gly Val Ser Pro Glu Asp Ile
 195 200 205
 Ala Tyr Val Thr Thr Ser Leu Ser His Val Gly Tyr Ser Ser Asp Ile
 210 215 220
 Leu Val Ile Pro Leu Val Asp Gly Val Gly Lys Met Glu Val Val Arg
 225 230 235 240
 Val Thr Arg Thr Pro Ser Asp Asn Tyr Thr Ser Gln Thr Asn Tyr Ile
 245 250 255

	Glu	Leu	Tyr	Pro	Gln		Gly	Asp	Asn	Tyr	Leu	Ile	Lys	Tyr	Asn	Leu
				260					265					270		
5	Ser	Asn	Ser	Phe	Gly	Leu	Asp	Asp	Phe	Tyr	Leu	Gln	Tyr	Lys	Asp	Gly
			275					280					285			
	Ser	Ala	Asp	Trp	Thr	Glu	Ile	Ala	His	Asn	Pro	Tyr	Pro	Asp	Met	Val
		290					295					300				
10	Ile	Asn	Gln	Lys	Tyr	Glu	Ser	Gln	Ala	Thr	Ile	Lys	Arg	Ser	Asp	Ser
	305					310					315					320
	Asp	Asn	Ile	Leu	Ser	Ile	Gly	Leu	Gln	Arg	Trp	His	Ser	Gly	Ser	Tyr
					325					330					335	
15	Asn	Phe	Ala	Ala	Ala	Asn	Phe	Lys	Ile	Asp	Gln	Tyr	Ser	Pro	Lys	Ala
				340					345					350		
	Phe	Leu	Leu	Lys	Met	Asn	Lys	Ala	Ile	Arg	Leu	Leu	Lys	Ala	Thr	Gly
20			355					360					365			
	Leu	Ser	Phe	Ala	Thr	Leu	Glu	Arg	Ile	Val	Asp	Ser	Val	Asn	Ser	Thr
		370					375					380				
25	Lys	Ser	Ile	Thr	Val	Glu	Val	Leu	Asn	Lys	Val	Tyr	Arg	Val	Lys	Phe
	385					390					395					400
	Tyr	Ile	Asp	Arg	Tyr	Gly	Ile	Ser	Glu	Glu	Thr	Ala	Ala	Ile	Leu	Ala
					405					410					415	
30	Asn	Ile	Asn	Ile	Ser	Gln	Gln	Ala	Val	Gly	Asn	Gln	Leu	Ser	Gln	Phe
				420					425					430		
	Glu	Gln	Leu	Phe	Asn	His	Pro	Pro	Leu	Asn	Gly	Ile	Arg	Tyr	Glu	Ile
35			435					440					445			
	Ser	Glu	Asp	Asn	Ser	Lys	His	Leu	Pro	Asn	Pro	Asp	Leu	Asn	Leu	Lys
		450					455					460				
40	Pro	Asp	Ser	Thr	Gly	Asp	Asp	Gln	Arg	Lys	Ala	Val	Leu	Lys	Arg	Ala
	465					470					475					480
	Phe	Gln	Val	Asn	Ala	Ser	Glu	Leu	Tyr	Gln	Met	Leu	Leu	Ile	Thr	Asp
					485					490					495	
45	Arg	Lys	Glu	Asp	Gly	Val	Ile	Lys	Asn	Asn	Leu	Glu	Asn	Leu	Ser	Asp
				500					505					510		
	Leu	Tyr	Leu	Val	Ser	Leu	Leu	Ala	Gln	Ile	His	Asn	Leu	Thr	Ile	Ala
50			515					520					525			
	Glu	Leu	Asn	Ile	Leu	Leu	Val	Ile	Cys	Gly	Tyr	Gly	Asp	Thr	Asn	Ile
		530					535					540				
55	Tyr	Gln	Ile	Thr	Asp	Asp	Asn	Leu	Ala	Lys	Ile	Val	Glu	Thr	Leu	Leu
	545				550						555					560
	Trp	Ile	Thr	Gln	Trp	Leu	Lys	Thr	Gln	Lys	Trp	Thr	Val	Thr	Asp	Leu
					565					570					575	
60	Phe	Leu	Met	Thr	Ala	Thr	Tyr	Ser	Thr	Thr	Leu	Thr	Pro	Glu	Ile	
				580				585					590			
	Ser	Asn	Leu	Thr	Ala	Thr	Leu	Ser	Ser	Thr	Leu	His	Gly	Lys	Glu	Ser
65			595					600					605			
	Leu	Ile	Gly	Glu	Asp	Leu	Lys	Arg	Ala	Met	Ala	Pro	Cys	Phe	Thr	Ser
		610					615					620				
70	Ala	Leu	His	Leu	Thr	Ser	Gln	Glu	Val	Ala	Tyr	Asp	Leu	Leu	Leu	Trp
	625					630					635					640

Ile Asp Gln Ile Gln Pro Ala Gln Ile Thr Val Asp Gly Phe Trp Glu
 645 650 655
 5 Glu Val Gln Thr Thr Pro Thr Ser Leu Lys Val Ile Thr Phe Ala Gln
 660 665 670
 Val Leu Ala Gln Leu Ser Leu Ile Tyr Arg Arg Ile Gly Leu Ser Glu
 675 680 685
 10 Thr Glu Leu Ser Leu Ile Val Thr Gln Ser Ser Leu Leu Val Ala Gly
 690 695 700
 15 Lys Ser Ile Leu Asp His Gly Leu Leu Thr Leu Met Ala Leu Glu Gly
 705 710 715 720
 Phe His Thr Trp Val Asn Gly Leu Gly Gln His Ala Ser Leu Ile Leu
 725 730 735
 20 Ala Ala Leu Lys Asp Gly Ala Leu Thr Val Thr Asp Val Ala Gln Ala
 740 745 750
 Met Asn Lys Glu Glu Ser Leu Leu Gln Met Ala Ala Asn Gln Val Glu
 755 760 765
 25 Lys Asp Leu Thr Lys Leu Thr Ser Trp Thr Gln Ile Asp Ala Ile Leu
 770 775 780
 30 Gln Trp Leu Gln Met Ser Ser Ala Leu Ala Val Ser Pro Leu Asp Leu
 785 790 795 800
 Ala Gly Met Met Ala Leu Lys Tyr Gly Ile Asp His Asn Tyr Ala Ala
 805 810 815
 35 Trp Gln Ala Ala Ala Ala Ala Leu Met Ala Asp His Ala Asn Gln Ala
 820 825 830
 Gln Lys Lys Leu Asp Glu Thr Phe Ser Lys Ala Leu Cys Asn Tyr Tyr
 835 840 845
 40 Ile Asn Ala Val Val Asp Ser Ala Ala Gly Val Arg Asp Arg Asn Gly
 850 855 860
 45 Leu Tyr Thr Tyr Leu Leu Ile Asp Asn Gln Val Ser Ala Asp Val Ile
 865 870 875 880
 Thr Ser Arg Ile Ala Glu Ala Ile Ala Gly Ile Gln Leu Tyr Val Asn
 885 890 895
 50 Arg Ala Leu Asn Arg Asp Glu Gly Gln Leu Ala Ser Asp Val Ser Thr
 900 905 910
 Arg Gln Phe Phe Thr Asp Trp Glu Arg Tyr Asn Lys Arg Tyr Ser Thr
 915 920 925
 55 Trp Ala Gly Val Ser Glu Leu Val Tyr Tyr Pro Glu Asn Tyr Val Asp
 930 935 940
 60 Pro Thr Gln Arg Ile Gly Gln Thr Lys Met Met Asp Ala Leu Leu Gln
 945 950 955 960
 Ser Ile Asn Gln Ser Gln Leu Asn Ala Asp Thr Val Glu Asp Ala Phe
 965 970 975
 65 Lys Thr Tyr Leu Thr Ser Phe Glu Gln Val Ala Asn Leu Lys Val Ile
 980 985 990
 Ser Ala Tyr His Asp Asn Val Asn Val Asp Gln Gly Leu Thr Tyr Phe
 995 1000 1005
 70 Ile Gly Ile Asp Gln Ala Ala Pro Gly Thr Tyr Tyr Trp Arg Ser Val

	1010	1015	1020
5	Asp His Ser Lys Cys Glu Asn Gly Lys Phe Ala Ala Asn Ala Trp Gly 1025 1030 1035 1040		
	Glu Trp Asn Lys Ile Thr Cys Ala Val Asn Pro Trp Lys Asn Ile Ile 1045 1050 1055		
10	Arg Pro Val Val Tyr Met Ser Arg Leu Tyr Leu Leu Trp Leu Glu Gln 1060 1065 1070		
	Gln Ser Lys Lys Ser Asp Asp Gly Lys Thr Thr Ile Tyr Gln Tyr Asn 1075 1080 1085		
15	Leu Lys Leu Ala His Ile Arg Tyr Asp Gly Ser Trp Asn Thr Pro Phe 1090 1095 1100		
	Thr Phe Asp Val Thr Glu Lys Val Lys Asn Tyr Thr Ser Ser Thr Asp 1105 1110 1115 1120		
20	Ala Ala Glu Ser Leu Gly Leu Tyr Cys Thr Gly Tyr Gln Gly Glu Asp 1125 1130 1135		
	Thr Leu Leu Val Met Phe Tyr Ser Met Gln Ser Ser Tyr Ser Ser Tyr 1140 1145 1150		
25	Thr Asp Asn Asn Ala Pro Val Thr Gly Leu Tyr Ile Phe Ala Asp Met 1155 1160 1165		
30	Ser Ser Asp Asn Met Thr Asn Ala Gln Ala Thr Asn Tyr Trp Asn Asn 1170 1175 1180		
	Ser Tyr Pro Gln Phe Asp Thr Val Met Ala Asp Pro Asp Ser Asp Asn 1185 1190 1195 1200		
35	Lys Lys Val Ile Thr Arg Arg Val Asn Asn Arg Tyr Ala Glu Asp Tyr 1205 1210 1215		
	Glu Ile Pro Ser Ser Val Thr Ser Asn Ser Asn Tyr Ser Trp Gly Asp 1220 1225 1230		
40	His Ser Leu Thr Met Leu Tyr Gly Gly Ser Val Pro Asn Ile Thr Phe 1235 1240 1245		
45	Glu Ser Ala Ala Glu Asp Leu Arg Leu Ser Thr Asn Met Ala Leu Ser 1250 1255 1260		
	Ile Ile His Asn Gly Tyr Ala Gly Thr Arg Arg Ile Gln Cys Asn Leu 1265 1270 1275 1280		
50	Met Lys Gln Tyr Ala Ser Leu Gly Asp Lys Phe Ile Ile Tyr Asp Ser 1285 1290 1295		
	Ser Phe Asp Asp Ala Asn Arg Phe Asn Leu Val Pro Leu Phe Lys Phe 1300 1305 1310		
55	Gly Lys Asp Glu Asn Ser Asp Asp Ser Ile Cys Ile Tyr Asn Glu Asn 1315 1320 1325		
60	Pro Ser Ser Glu Asp Lys Lys Trp Tyr Phe Ser Ser Lys Asp Asp Asn 1330 1335 1340		
	Lys Thr Ala Asp Tyr Asn Gly Gly Thr Gln Cys Ile Asp Ala Gly Thr 1345 1350 1355 1360		
65	Ser Asn Lys Asp Phe Tyr Tyr Asn Leu Gln Glu Ile Glu Val Ile Ser 1365 1370 1375		
70	Val Thr Gly Gly Tyr Trp Ser Ser Tyr Lys Ile Ser Asn Pro Ile Asn 1380 1385 1390		

Ile Asn Thr Glu Ile Asp Ser Ala Lys Val Lys Val Thr Val Lys Ala
 1395 1400 1405
 5 Gly Gly Asp Asp Gln Ile Phe Thr Ala Asp Asn Ser Thr Tyr Val Pro
 1410 1415 1420
 Gln Gln Pro Ala Pro Ser Phe Glu Glu Met Ile Tyr Gln Phe Asn Asn
 1425 1430 1435 1440
 10 Leu Thr Ile Asp Cys Lys Asn Leu Asn Phe Ile Asp Asn Gln Ala His
 1445 1450 1455
 Ile Glu Ile Asp Phe Thr Ala Thr Ala Gln Asp Gly Arg Phe Leu Gly
 1460 1465 1470
 15 Ala Glu Thr Phe Ile Ile Pro Val Thr Lys Lys Val Leu Gly Thr Glu
 1475 1480 1485
 Asn Val Ile Ala Leu Tyr Ser Glu Asn Asn Gly Val Gln Tyr Met Gln
 1490 1495 1500
 Ile Gly Ala Tyr Arg Thr Arg Leu Asn Thr Leu Phe Ala Gln Gln Leu
 1505 1510 1515 1520
 25 Val Ser Arg Ala Asn Arg Gly Ile Asp Ala Val Leu Ser Met Glu Thr
 1525 1530 1535
 Gln Asn Ile Gln Glu Pro Gln Leu Gly Ala Gly Thr Tyr Val Gln Leu
 1540 1545 1550
 30 Val Leu Asp Lys Tyr Asp Glu Ser Ile His Gly Thr Asn Lys Ser Phe
 1555 1560 1565
 Ala Ile Glu Tyr Val Asp Ile Phe Lys Glu Asn Asp Ser Phe Val Ile
 1570 1575 1580
 Tyr Gln Gly Glu Leu Ser Glu Thr Ser Gln Thr Val Val Lys Val Phe
 1585 1590 1595 1600
 40 Leu Ser Tyr Phe Ile Glu Ala Thr Gly Asn Lys Asn His Leu Trp Val
 1605 1610 1615
 Arg Ala Lys Tyr Gln Lys Glu Thr Thr Asp Lys Ile Leu Phe Asp Arg
 1620 1625 1630
 45 Thr Asp Glu Lys Asp Pro His Gly Trp Phe Leu Ser Asp Asp His Lys
 1635 1640 1645
 Thr Phe Ser Gly Leu Ser Ser Ala Gln Ala Leu Lys Asn Asp Ser Glu
 1650 1655 1660
 Pro Met Asp Phe Ser Gly Ala Asn Ala Leu Tyr Phe Trp Glu Leu Phe
 1665 1670 1675 1680
 55 Tyr Tyr Thr Pro Met Met Met Ala His Arg Leu Leu Gln Glu Gln Asn
 1685 1690 1695
 Phe Asp Ala Ala Asn His Trp Phe Arg Tyr Val Trp Ser Pro Ser Gly
 1700 1705 1710
 60 Tyr Ile Val Asp Gly Lys Ile Ala Ile Tyr His Trp Asn Val Arg Pro
 1715 1720 1725
 Leu Glu Glu Asp Thr Ser Trp Asn Ala Gln Gln Leu Asp Ser Thr Asp
 1730 1735 1740
 Pro Asp Ala Val Ala Gln Asp Asp Pro Met His Tyr Lys Val Ala Thr
 1745 1750 1755 1760
 70 Phe Met Ala Thr Leu Asp Leu Leu Met Ala Arg Gly Asp Ala Ala Tyr
 1765 1770 1775

Arg Gln Leu Glu Arg Asp Thr Leu Ala Glu Ala Lys Met Trp Tyr Thr
 1780 1785 1790

5 Gln Ala Leu Asn Leu Leu Gly Asp Glu Pro Gln Val Met Leu Ser Thr
 1795 1800 1805

Thr Trp Ala Asn Pro Thr Leu Gly Asn Ala Ala Ser Lys Thr Thr Gln
 1810 1815 1820

10 Gln Val Arg Gln Gln Val Leu Thr Gln Leu Arg Leu Asn Ser Arg Val
 1825 1830 1835 1840

Lys Thr Pro Leu
 1844

(2) INFORMATION FOR SEQ ID NO:54:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1722 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54 (*tcbAiii* coding region):

30 CTA GGA ACA GCC AAT TCC CTG ACC GCT TTA TTC CTG CCG CAG GAA AAT 48
 Leu Gly Thr Ala Asn Ser Leu Thr Ala Leu Phe Leu Pro Gln Glu Asn
 1 5 10 15

35 AGC AAG CTC AAA GGC TAC TGG CGG ACA CTG GCG CAG CGT ATG TTT AAT 96
 Ser Lys Leu Lys Gly Tyr Trp Arg Thr Leu Ala Gln Arg Met Phe Asn
 20 25 30

40 TTA CGT CAT AAT CTG TCG ATT GAC GGC CAG CCG CTC TCC TTG CCG CTG 144
 Leu Arg His Asn Leu Ser Ile Asp Gly Gln Pro Leu Ser Leu Pro Leu
 35 40 45

TAT GCT AAA CCG GCT GAT CCA AAA GCT TTA CTG AGT GCG GCG GTT TCA 192
 Tyr Ala Lys Pro Ala Asp Pro Lys Ala Leu Leu Ser Ala Ala Val Ser
 50 55 60

45 GCT TCT CAA GGG GGA GCC GAC TTG CCG AAG GCG CCG CTG ACT ATT CAC 240
 Ala Ser Gln Gly Gly Ala Asp Leu Pro Lys Ala Pro Leu Thr Ile His
 65 70 75 80

50 CGC TTC CCT CAA ATG CTA GAA GGG GCA CGG GGC TTG GTT AAC CAG CTT 288
 Arg Phe Pro Gln Met Leu Glu Gly Ala Arg Gly Leu Val Asn Gln Leu
 85 90 95

55 ATA CAG TTC GGT AGT TCA CTA TTG GGG TAC AGT GAG CGT CAG GAT GCG 336
 Ile Gln Phe Gly Ser Ser Leu Leu Gly Tyr Ser Glu Arg Gln Asp Ala
 100 105 110

60 GAA GCT ATG AGT CAA CTA CTG CAA ACC CAA GCC AGC GAG TTA ATA CTG 384
 Glu Ala Met Ser Gln Leu Leu Gln Thr Gln Ala Ser Glu Leu Ile Leu
 115 120 125

ACC AGT ATT CGT ATG CAG GAT AAC CAA TTG GCA GAG CTG GAT TCG GAA 432
 Thr Ser Ile Arg Met Gln Asp Asn Gln Leu Ala Glu Leu Asp Ser Glu
 130 135 140

65 AAA ACC GCC TTG CAA GTC TCT TTA GCT GGA GTG CAA CAA CGG TTT GAC 480
 Lys Thr Ala Leu Gln Val Ser Leu Ala Gly Val Gln Gln Arg Phe Asp
 145 150 155 160

	AGC	TAT	AGC	CAA	CTG	TAT	GAG	GAG	AAC	ATC	AAC	GCA	GGT	GAG	CAG	CGA	528
	Ser	Tyr	Ser	Gln	Leu	Tyr	Glu	Glu	Asn	Ile	Asn	Ala	Gly	Glu	Gln	Arg	
					165					170					175		
5	GCG	CTG	GCG	TTA	CGC	TCA	GAA	TCT	GCT	ATT	GAG	TCT	CAG	GGA	GCG	CAG	576
	Ala	Leu	Ala	Leu	Arg	Ser	Glu	Ser	Ala	Ile	Glu	Ser	Gln	Gly	Ala	Gln	
				180				185					190				
10	ATT	TCC	CGT	ATG	GCA	GGC	GCG	GGT	GTT	GAT	ATG	GCA	CCA	AAT	ATC	TTC	624
	Ile	Ser	Arg	Met	Ala	Gly	Ala	Gly	Val	Asp	Met	Ala	Pro	Asn	Ile	Phe	
			195					200				205					
15	GGC	CTG	GCT	GAT	GGC	GCG	ATG	CAT	TAT	GGT	GCT	ATT	GCC	TAT	GCC	ATC	672
	Gly	Leu	Ala	Asp	Gly	Gly	Met	His	Tyr	Gly	Ala	Ile	Ala	Tyr	Ala	Ile	
		210					215					220					
20	GCT	GAC	GGT	ATT	GAG	TTG	AGT	GCT	TCT	GCC	AAG	ATG	GTT	GAT	GCG	GAG	720
	Ala	Asp	Gly	Ile	Glu	Leu	Ser	Ala	Ser	Ala	Lys	Met	Val	Asp	Ala	Glu	
	225					230					235					240	
	AAA	GTT	GCT	CAG	TCG	GAA	ATA	TAT	CGC	CGT	CGC	CGT	CAA	GAA	TGG	AAA	768
	Lys	Val	Ala	Gln	Ser	Glu	Ile	Tyr	Arg	Arg	Arg	Arg	Gln	Glu	Trp	Lys	
					245					250					255		
25	ATT	CAG	CGT	GAC	AAC	GCA	CAA	GCG	GAG	ATT	AAC	CAG	TTA	AAC	GCG	CAA	816
	Ile	Gln	Arg	Asp	Asn	Ala	Gln	Ala	Glu	Ile	Asn	Gln	Leu	Asn	Ala	Gln	
				260					265					270			
30	CTG	GAA	TCA	CTG	TCT	ATT	CGC	CGT	GAA	GCC	GCT	GAA	ATG	CAA	AAA	GAG	864
	Leu	Glu	Ser	Leu	Ser	Ile	Arg	Arg	Glu	Ala	Ala	Glu	Met	Gln	Lys	Glu	
			275					280					285				
35	TAC	CTG	AAA	ACC	CAG	CAA	GCT	CAG	GCG	CAG	GCA	CAA	CTT	ACT	TTC	TTA	912
	Tyr	Leu	Lys	Thr	Gln	Gln	Ala	Gln	Ala	Gln	Ala	Gln	Leu	Thr	Phe	Leu	
		290					295					300					
40	AGA	AGC	AAA	TTC	AGT	AAT	CAA	GCG	TTA	TAT	AGT	TGG	TTA	CGA	GGG	CGT	960
	Arg	Ser	Lys	Phe	Ser	Asn	Gln	Ala	Leu	Tyr	Ser	Trp	Leu	Arg	Gly	Arg	
	305					310					315					320	
	TTG	TCA	GGT	ATT	TAT	TTC	CAG	TTC	TAT	GAC	TTG	GCC	GTA	TCA	CGT	TGC	1008
	Leu	Ser	Gly	Ile	Tyr	Phe	Gln	Phe	Tyr	Asp	Leu	Ala	Val	Ser	Arg	Cys	
					325					330					335		
45	CTG	ATG	GCA	GAG	CAA	TCC	TAT	CAA	TGG	GAA	GCT	AAT	GAT	AAT	TCC	ATT	1056
	Leu	Met	Ala	Glu	Gln	Ser	Tyr	Gln	Trp	Glu	Ala	Asn	Asp	Asn	Ser	Ile	
				340					345					350			
50	AGC	TTT	GTC	AAA	CCG	GGT	GCA	TGG	CAA	GGA	ACT	TAC	GCC	GGC	TTA	TTG	1104
	Ser	Phe	Val	Lys	Pro	Gly	Ala	Trp	Gln	Gly	Thr	Tyr	Ala	Gly	Leu	Leu	
			355					360					365				
55	TGT	GGA	GAA	GCT	TTG	ATA	CAA	AAT	CTG	GCA	CAA	ATG	GAA	GAG	GCA	TAT	1152
	Cys	Gly	Glu	Ala	Leu	Ile	Gln	Asn	Leu	Ala	Gln	Met	Glu	Glu	Ala	Tyr	
		370					375					380					
60	CTG	AAA	TGG	GAA	TCT	CGC	GCT	TTG	GAA	GTA	GAA	CGC	ACG	GTT	TCA	TTG	1200
	Leu	Lys	Trp	Glu	Ser	Arg	Ala	Leu	Glu	Val	Glu	Arg	Thr	Val	Ser	Leu	
	385					390					395					400	
	GCA	GTG	GTT	TAT	GAT	TCA	CTG	GAA	GGT	AAT	GAT	CGT	TTT	AAT	TTA	GCG	1248
	Ala	Val	Val	Tyr	Asp	Ser	Leu	Glu	Gly	Asn	Asp	Arg	Phe	Asn	Leu	Ala	
					405					410					415		
65	GAA	CAA	ATA	CCT	GCA	TTA	TTG	GAT	AAG	GGG	GAG	GGA	ACA	GCA	GGA	ACT	1296
	Glu	Gln	Ile	Pro	Ala	Leu	Leu	Asp	Lys	Gly	Glu	Gly	Thr	Ala	Gly	Thr	
				420					425					430			
70	AAA	GAA	AAT	GGG	TTA	TCA	TTG	GCT	AAT	GCT	ATC	CTG	TCA	GCT	TCG	GTC	1344
	Lys	Glu	Asn	Gly	Leu	Ser	Leu	Ala	Asn	Ala	Ile	Leu	Ser	Ala	Ser	Val	
			435					440					445				

AAA TTG TCC GAC TTG AAA CTG GGA ACG GAT TAT CCA GAC AGT ATC GTT 1392
 Lys Leu Ser Asp Leu Lys Leu Gly Thr Asp Tyr Pro Asp Ser Ile Val
 450 455 460
 5 GGT AGC AAC AAG GTT CGT CGT ATT AAG CAA ATC AGT GTT TCG CTA CCT 1440
 Gly Ser Asn Lys Val Arg Arg Ile Lys Gln Ile Ser Val Ser Leu Pro
 465 470 475 480
 10 GCA TTG GTT GGG CCT TAT CAG GAT GTT CAG GCT ATG CTC AGC TAT GGT 1488
 Ala Leu Val Gly Pro Tyr Gln Asp Val Gln Ala Met Leu Ser Tyr Gly -
 485 490 495
 15 GGC AGT ACT CAA TTG CCG AAA GGT TGT TCA GCG TTG GCT GTG TCT CAT 1536
 Gly Ser Thr Gln Leu Pro Lys Gly Cys Ser Ala Leu Ala Val Ser His
 500 505 510
 20 GGT ACC AAT GAT AGT GGT CAG TTC CAG TTG GAT TTC AAT GAC GGC AAA 1584
 Gly Thr Asn Asp Ser Gly Gln Phe Gln Leu Asp Phe Asn Asp Gly Lys
 515 520 525
 TAC CTG CCA TTT GAA GGT ATT GCT CTT GAT GAT CAG GGT ACA CTG AAT 1632
 Tyr Leu Pro Phe Glu Gly Ile Ala Leu Asp Asp Gln Gly Thr Leu Asn
 530 535 540
 25 CTT CAA TTT CCG AAT GCT ACC GAC AAG CAG AAA GCA ATA TTG CAA ACT 1680
 Leu Gln Phe Pro Asn Ala Thr Asp Lys Gln Lys Ala Ile Leu Gln Thr
 545 550 555 560
 30 ATG AGC GAT ATT ATT TTG CAT ATT CGT TAT ACC ATC CGT TAA 1722
 Met Ser Asp Ile Ile Leu His Ile Arg Tyr Thr Ile Arg ***
 565 570 573

35 (2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 amino acids
 (B) TYPE: amino acids
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55 (TcbA_{iii}):

45 Leu Gly Thr Ala Asn Ser Leu Thr Ala Leu Phe Leu Pro Gln Glu Asn
 1 5 10 15
 50 Ser Lys Leu Lys Gly Tyr Trp Arg Thr Leu Ala Gln Arg Met Phe Asn
 20 25 30
 Leu Arg His Asn Leu Ser Ile Asp Gly Gln Pro Leu Ser Leu Pro Leu
 35 40 45
 55 Tyr Ala Lys Pro Ala Asp Pro Lys Ala Leu Leu Ser Ala Ala Val Ser
 50 55 60
 Ala Ser Gln Gly Gly Ala Asp Leu Pro Lys Ala Pro Leu Thr Ile His
 65 70 75 80
 60 Arg Phe Pro Gln Met Leu Glu Gly Ala Arg Gly Leu Val Asn Gln Leu
 85 90 95
 65 Ile Gln Phe Gly Ser Ser Leu Leu Gly Tyr Ser Glu Arg Gln Asp Ala
 100 105 110
 Glu Ala Met Ser Gln Leu Leu Gln Thr Gln Ala Ser Glu Leu Ile Leu
 115 120 125

	Thr	Ser	Ile	Arg	Met	Gln	Asp	Asn	Gln	Leu	Ala	Glu		Asp	Ser	Glu
	130						135					140				
5	Lys	Thr	Ala	Leu	Gln	Val	Ser	Leu	Ala	Gly	Val	Gln	Gln	Arg	Phe	Asp
	145					150					155					160
	Ser	Tyr	Ser	Gln	Leu	Tyr	Glu	Glu	Asn	Ile	Asn	Ala	Gly	Glu	Gln	Arg
					165					170					175	
10	Ala	Leu	Ala	Leu	Arg	Ser	Glu	Ser	Ala	Ile	Glu	Ser	Gln	Gly	Ala	Gln
				180					185					190		
	Ile	Ser	Arg	Met	Ala	Gly	Ala	Gly	Val	Asp	Met	Ala	Pro	Asn	Ile	Phe
15			195					200					205			
	Gly	Leu	Ala	Asp	Gly	Gly	Met	His	Tyr	Gly	Ala	Ile	Ala	Tyr	Ala	Ile
	210						215					220				
20	Ala	Asp	Gly	Ile	Glu	Leu	Ser	Ala	Ser	Ala	Lys	Met	Val	Asp	Ala	Glu
	225					230					235					240
	Lys	Val	Ala	Gln	Ser	Glu	Ile	Tyr	Arg	Arg	Arg	Arg	Gln	Glu	Trp	Lys
					245				250						255	
25	Ile	Gln	Arg	Asp	Asn	Ala	Gln	Ala	Glu	Ile	Asn	Gln	Leu	Asn	Ala	Gln
				260					265					270		
	Leu	Glu	Ser	Leu	Ser	Ile	Arg	Arg	Glu	Ala	Ala	Glu	Met	Gln	Lys	Glu
30			275					280					285			
	Tyr	Leu	Lys	Thr	Gln	Gln	Ala	Gln	Ala	Gln	Ala	Gln	Leu	Thr	Phe	Leu
	290						295					300				
35	Arg	Ser	Lys	Phe	Ser	Asn	Gln	Ala	Leu	Tyr	Ser	Trp	Leu	Arg	Gly	Arg
	305					310					315					320
	Leu	Ser	Gly	Ile	Tyr	Phe	Gln	Phe	Tyr	Asp	Leu	Ala	Val	Ser	Arg	Cys
					325					330					335	
40	Leu	Met	Ala	Glu	Gln	Ser	Tyr	Gln	Trp	Glu	Ala	Asn	Asp	Asn	Ser	Ile
				340					345					350		
	Ser	Phe	Val	Lys	Pro	Gly	Ala	Trp	Gln	Gly	Thr	Tyr	Ala	Gly	Leu	Leu
45			355					360					365			
	Cys	Gly	Glu	Ala	Leu	Ile	Gln	Asn	Leu	Ala	Gln	Met	Glu	Glu	Ala	Tyr
	370						375					380				
50	Leu	Lys	Trp	Glu	Ser	Arg	Ala	Leu	Glu	Val	Glu	Arg	Thr	Val	Ser	Leu
	385					390					395					400
	Ala	Val	Val	Tyr	Asp	Ser	Leu	Glu	Gly	Asn	Asp	Arg	Phe	Asn	Leu	Ala
					405					410					415	
55	Glu	Gln	Ile	Pro	Ala	Leu	Leu	Asp	Lys	Gly	Glu	Gly	Thr	Ala	Gly	Thr
				420					425					430		
	Lys	Glu	Asn	Gly	Leu	Ser	Leu	Ala	Asn	Ala	Ile	Leu	Ser	Ala	Ser	Val
60			435					440					445			
	Lys	Leu	Ser	Asp	Leu	Lys	Leu	Gly	Thr	Asp	Tyr	Pro	Asp	Ser	Ile	Val
	450						455					460				
65	Gly	Ser	Asn	Lys	Val	Arg	Arg	Ile	Lys	Gln	Ile	Ser	Val	Ser	Leu	Pro
	465					470					475					480
	Ala	Leu	Val	Gly	Pro	Tyr	Gln	Asp	Val	Gln	Ala	Met	Leu	Ser	Tyr	Gly
					485					490					495	
70	Gly	Ser	Thr	Gln	Leu	Pro	Lys	Gly	Cys	Ser	Ala	Leu	Ala	Val	Ser	His
				500					505					510		

Gly Thr Asn Asp Ser Gly Gln Phe Gln Leu Asp Phe Asn Asp Gly Lys
 515 520 525

5 Tyr Leu Pro Phe Glu Gly Ile Ala Leu Asp Asp Gln Gly Thr Leu Asn
 530 535 540

Leu Gln Phe Pro Asn Ala Thr Asp Lys Gln Lys Ala Ile Leu Gln Thr
 545 550 555 560

10 Met Ser Asp Ile Ile Leu His Ile Arg Tyr Thr Ile Arg ...
 565 570 573

15 (2) INFORMATION FOR SEQ ID NO:56

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2994 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56 (tcca)

25

1	ATG AAT CAA CTC GCC AGT CCC CTG ATT TCC CGC ACC GAA GAG ATC CAC	48
1	Met Asn Gln Leu Ala Ser Pro Leu Ile Ser Arg Thr Glu Glu Ile His	16
30	49 AAC TTA CCC GGT AAA TTG ACC GAT CTT GGT TAT ACC TCA GTG TTT GAT	96
	17 Asn Leu Pro Gly Lys Leu Thr Asp Leu Gly Tyr Thr Ser Val Phe Asp	32
35	97 GTG GTA CGT ATG CCG CGT GAG CGT TTT ATT CGT GAG CAT CGT GCT GAT	144
	33 Val Val Arg Met Pro Arg Glu Arg Phe Ile Arg Glu His Arg Ala Asp	48
40	145 CTC GGG CGC AGT GCT GAA AAA ATG TAT GAC CTG GCA GTG GGC TAT GCT	192
	49 Leu Gly Arg Ser Ala Glu Lys Met Tyr Asp Leu Ala Val Gly Tyr Ala	64
45	193 CAT CAG GTG TTA CAC CAT TTT CGC CGT AAT TCT CTT AGT GAA GCT GTT	240
	65 His Gln Val Leu His His Phe Arg Arg Asn Ser Leu Ser Glu Ala Val	80
50	241 CAG TTT GGC TTG AGA AGT CCG TTC TCC GTA TCA GGC CCG GAT TAC GCC	288
	81 Gln Phe Gly Leu Arg Ser Pro Phe Ser Val Ser Gly Pro Asp Tyr Ala	96
55	289 AAT CAG TTT CTT GAT GCA AAC ACG GGT TGG AAA GAT AAA GCA CCA AGT	336
	97 Asn Gln Phe Leu Asp Ala Asn Thr Gly Trp Lys Asp Lys Ala Pro Ser	112
60	337 GGA TCA CCG GAA GCC AAT GAT GCG CCG GTA GCC TAT CTG ACT CAT ATT	384
	113 Gly Ser Pro Glu Ala Asn Asp Ala Pro Val Ala Tyr Leu Thr His Ile	128
65	385 TAT CAA TTG GCC CTT GAA CAG GAA AAG AAT GGC GCC ACT ACC ATT ATG	432
	129 Tyr Gln Leu Ala Leu Glu Gln Glu Lys Asn Gly Ala Thr Thr Ile Met	144
	433 AAT ACG CTG GCG GAG CGT CGC CCC GAT CTG GGT GCT TTG TTA ATT AAT	480
	145 Asn Thr Leu Ala Glu Arg Arg Pro Asp Leu Gly Ala Leu Leu Ile Asn	160
	481 GAT AAA GCA ATC AAT GAG GTG ATA CCG CAA TTG CAG TTG GTC AAT GAA	528
	161 Asp Lys Ala Ile Asn Glu Val Ile Pro Gln Leu Gln Leu Val Asn Glu	176

529	ATT CTG	AAA GCT ATT CAG AAG AAA CTG AGT	CTG ACT GAT CTG GAA	576
177	Ile Leu Ser Lys Ala Ile Gln Lys Lys Leu Ser Leu Thr Asp Leu Glu			192
5	577	GCG GTA AAC GCC AGA CTT TCC ACT ACC CGT TAC CCG AAT AAT CTG CCG		624
	193	Ala Val Asn Ala Arg Leu Ser Thr Thr Arg Tyr Pro Asn Asn Leu Pro		208
10	625	TAT CAT TAT GGT CAT CAG CAG ATT CAG ACA GCT CAA TCG GTA TTG GGT		672
	209	Tyr His Tyr Gly His Gln Gln Ile Gln Thr Ala Gln Ser Val Leu Gly		224
15	673	ACT ACG TTG CAA GAT ATC ACT TTG CCA CAG ACG CTG GAT CTG CCG CAA		720
	225	Thr Thr Leu Gln Asp Ile Thr Leu Pro Gln Thr Leu Asp Leu Pro Gln		240
20	721	AAC TTC TGG GCA ACA GCA AAA GGA AAA CTG AGC GAT ACG ACT GCC AGT		768
	241	Asn Phe Trp Ala Thr Ala Lys Gly Lys Leu Ser Asp Thr Thr Ala Ser		256
25	769	GCT TTG ACC CGA CTG CAA ATC ATG GCG AGT CAG TTT TCG CCA GAG CAG		816
	257	Ala Leu Thr Arg Leu Gln Ile Met Ala Ser Gln Phe Ser Pro Glu Gln		272
30	817	CAG AAA ATC ATT ACG GAG ACT GTC GGT CAG GAT TTC TAT CAG CTT AAC		864
	273	Gln Lys Ile Ile Thr Glu Thr Val Gly Gln Asp Phe Tyr Gln Leu Asn		288
35	865	TAT GGT GAC AGT TCG CTT ACT GTG AAT AGT TTC AGC GAC ATG ACC ATA		912
	289	Tyr Gly Asp Ser Ser Leu Thr Val Asn Ser Phe Ser Asp Met Thr Ile		304
40	913	ATG ACT GAT CGA ACA AGT TTG ACT GTA CCC CAG GTA GAA CTG ATG TTG		960
	305	Met Thr Asp Arg Thr Ser Leu Thr Val Pro Gln Val Glu Leu Met Leu		320
45	961	TGT TCA ACT GTC GGA GGT TCT ACG GTT GTT AAG TCT GAT AAT GTG AGT		
	1008			
	321	Cys Ser Thr Val Gly Gly Ser Thr Val Val Lys Ser Asp Asn Val Ser		336
50	1009	TCT GGT GAC ACG ACA GCG ACG CCA TTT GCG TAT GGC GCC CGC TTT ATT		
	1056			
	337	Ser Gly Asp Thr Thr Ala Thr Pro Phe Ala Tyr Gly Ala Arg Phe Ile		352
55	1057	CAT GCC GGT AAG CCG GAG GCG ATT ACC CTG AGT CGC AGT GGT GCG GAG		
	1104			
	353	His Ala Gly Lys Pro Glu Ala Ile Thr Leu Ser Arg Ser Gly Ala Glu		368
60	1105	GCG CAT TTT GCT CTG ACG GTT AAC AAT CTG ACA GAT GAC AAG TTG GAC		
	1152			
	369	Ala His Phe Ala Leu Thr Val Asn Asn Leu Thr Asp Asp Lys Leu Asp		384
65	1153	CGT ATT AAC CGC ACA GTG CGC CTG CAA AAA TGG CTG AAT CTG CCT TAT		
	1200			
	385	Arg Ile Asn Arg Thr Val Arg Leu Gln Lys Trp Leu Asn Leu Pro Tyr		400
70	1201	GAG GAT ATT GAC CTG TTA GTG ACT TCT GCT ATG GAT GCG GAA ACA GGA		
	1248			
	401	Glu Asp Ile Asp Leu Leu Val Thr Ser Ala Met Asp Ala Glu Thr Gly		416
	1249	AAT ACC GCG CTG TCG ATG AAC GAC AAT ACG CTG CGT ATG TTG GGA GTG		
	1296			
	417	Asn Thr Ala Leu Ser Met Asn Asp Asn Thr Leu Arg Met Leu Gly Val		432

1297 TTC AAA CAT TAA AG GCG AAG TAT GGT GTT AGC GCT CAA TTT GCT
 1344
 433 Phe Lys His Tyr Gln Ala Lys Tyr Gly Val Ser Ala Lys Gln Phe Ala 448
 5
 1345 GGC TGG CTG CGC GTA GTG GCC CCG TTT GCC ATT ACA CCG GCA ACG CCG
 1392
 449 Gly Trp Leu Arg Val Val Ala Pro Phe Ala Ile Thr Pro Ala Thr Pro 464
 10
 1393 TTT TTA GAC CAA GTG TTT AAC TCC GTC GGC ACC TTT GAT ACA CCG TTT
 1440
 465 Phe Leu Asp Gln Val Phe Asn Ser Val Gly Thr Phe Asp Thr Pro Phe 480
 15
 1441 GTG ATA GAT AAT CAG GAT TTT GTC TAT ACA TTG ACC ACC GGG GGC GAT
 1488
 481 Val Ile Asp Asn Gln Asp Phe Val Tyr Thr Leu Thr Thr Gly Gly Asp 496
 20
 1489 GGG GCG CGT GTT AAG CAT ATC AGC ACG GCA CTG GGC CTC AAT CAT CGT
 1536
 497 Gly Ala Arg Val Lys His Ile Ser Thr Ala Leu Gly Leu Asn His Arg 512
 25
 1537 CAG TTC CTG TTA TTG GCG GAT AAT ATT GCC CGT CAA CAG GGG AAT GTC
 1584
 513 Gln Phe Leu Leu Leu Ala Asp Asn Ile Ala Arg Gln Gln Gly Asn Val 528
 30
 1585 ACG CAA AGC ACA CTC AAC TGT AAT CTG TTT GTG GTG TCA GCT TTC TAC
 1632
 529 Thr Gln Ser Thr Leu Asn Cys Asn Leu Phe Val Val Ser Ala Phe Tyr 544
 35
 1633 CGT CTG GCT AAT TTG GCG CGC ACA TTG GGG ATA AAT CCA GAG TCT TTC
 1680
 545 Arg Leu Ala Asn Leu Ala Arg Thr Leu Gly Ile Asn Pro Glu Ser Phe 560
 40
 1681 TGT GCC TTG GTT GAT CGA TTA GAT GCA GGT ACA GGC ATC GTC TGG CAG
 1728
 561 Cys Ala Leu Val Asp Arg Leu Asp Ala Gly Thr Gly Ile Val Trp Gln 576
 45
 1729 CAA TTG GCA GGG AAA CCC ACA ATC ACG GTA CCA CAA AAA GAT TCC CCG
 1776
 577 Gln Leu Ala Gly Lys Pro Thr Ile Thr Val Pro Gln Lys Asp Ser Pro 592
 50
 1777 CTG GCG GCG GAT ATT CTG AGT TTG CTG CAA GCG CTA AGT GCG ATT GCT
 1824
 593 Leu Ala Ala Asp Ile Leu Ser Leu Leu Gln Ala Leu Ser Ala Ile Ala 608
 55
 1825 CAA TGG CAA CAA CAG CAC GAT TTA GAA TTT TCA GCA CTG CTT TTG CTG
 1872
 609 Gln Trp Gln Gln Gln His Asp Leu Glu Phe Ser Ala Leu Leu Leu Leu 624
 60
 1873 TTG AGT GAC AAC CCT ATT TCT ACC TCG CAG GGC ACT GAC GAT CAA TTG
 1920
 625 Leu Ser Asp Asn Pro Ile Ser Thr Ser Gln Gly Thr Asp Asp Gln Leu 640
 65
 1921 AAC TTT ATC CGT CAA GTG TGG CAG AAC CTA GGC AGT ACG TTT GTG GGT
 1968
 641 Asn Phe Ile Arg Gln Val Trp Gln Asn Leu Gly Ser Thr Phe Val Gly 656
 70

1969 GCA ACA TTG TCC CGC AGT GGG GCA CCA TTT GTC GAT ACC AAC GGC
 2016
 657 Ala Thr Leu Leu Ser Arg Ser Gly Ala Pro Leu Val Asp Thr Asn Gly 672
 5
 2017 CAC GCT ATT GAC TGG TTT GCT CTG CTC TCA GCA GGT AAT AGT CCG CTT
 2064
 673 His Ala Ile Asp Trp Phe Ala Leu Leu Ser Ala Gly Asn Ser Pro Leu 688
 10
 2065 ATC GAT AAG GTT GGT CTG GTG ACT GAT GCT GGC ATA CAA AGT GTT ATA
 2112
 689 Ile Asp Lys Val Gly Leu Val Thr Asp Ala Gly Ile Gln Ser Val Ile 704
 15
 2113 GCA ACG GTG GTC AAT ACA CAA AGC TTA TCT GAT GAA GAT AAG AAG CTG
 2160
 705 Ala Thr Val Val Asn Thr Gln Ser Leu Ser Asp Glu Asp Lys Lys Leu 720
 20
 2161 GCA ATC ACT ACT CTG ACT AAT ACG TTG AAT CAG GTA CAG AAA ACT CAA
 2208
 721 Ala Ile Thr Thr Leu Thr Asn Thr Leu Asn Gln Val Gln Lys Thr Gln 736
 25
 2209 CAG GGC GTG GCC GTC AGT CTG TTG GCG CAG ACT CTG AAC GTG AGT CAG
 2256
 737 Gln Gly Val Ala Val Ser Leu Leu Ala Gln Thr Leu Asn Val Ser Gln 752
 30
 2257 TCA CTG CCT GCG TTA TTG TTG CGC TGG AGT GGA CAA ACA ACC TAC CAG
 2304
 753 Ser Leu Pro Ala Leu Leu Leu Arg Trp Ser Gly Gln Thr Thr Tyr Gln 768
 35
 2305 TGG TTG AGT GCG ACT TGG GCA TTG AAG GAT GCC GTT AAG ACT GCC GCC
 2352
 769 Trp Leu Ser Ala Thr Trp Ala Leu Lys Asp Ala Val Lys Thr Ala Ala 784
 40
 2353 GAT ATT CCC GCT GAC TAT CTG CGT CAA TTA CGT GAA GTG GTA CGC CGC
 2400
 785 Asp Ile Pro Ala Asp Tyr Leu Arg Gln Leu Arg Glu Val Val Arg Arg 800
 45
 2401 TCC TTG TTG ACC CAA CAA TTC ACG CTG AGT CCT GCA ATG GTG CAA ACC
 2448
 801 Ser Leu Leu Thr Gln Gln Phe Thr Leu Ser Pro Ala Met Val Gln Thr 816
 50
 2449 TTG CTG GAC TAT CCA GCC TAT TTT GGC GCT TCC GCA GAA ACA GTG ACC
 2496
 817 Leu Leu Asp Tyr Pro Ala Tyr Phe Gly Ala Ser Ala Glu Thr Val Thr 832
 55
 2497 GAT ATC AGT TTG TGG ATG CTT TAT ACC CTG AGC TGT TAT AGC GAT TTA
 2544
 833 Asp Ile Ser Leu Trp Met Leu Tyr Thr Leu Ser Cys Tyr Ser Asp Leu 848
 60
 2545 TTG CTC CAA ATG GGT GAA GCT GGT GGT ACC GAA GAT GAT GTA CTG GCC
 2592
 849 Leu Leu Gln Met Gly Glu Ala Gly Gly Thr Glu Asp Asp Val Leu Ala 864
 65
 2593 TAC TTA CGC ACA GCT AAT GCT ACC ACA CCG TTG AGC CAA TCT GAT GCT
 2640
 865 Tyr Leu Arg Thr Ala Asn Ala Thr Thr Pro Leu Ser Gln Ser Asp Ala 880
 70

2641 GCA CAG ACG TCA ACG CTA TTG GGT TGG GAG GTT GAG TTG CAA
 2688
 881 Ala Gln Thr Leu Ala Thr Leu Leu Gly Trp Glu Val Asn Glu Leu Gln 896

5
 2689 GCC GCT TGG TCG GTA TTG GGC GGG ATT GCC AAA ACC ACA CCG CAA CTG
 2736
 897 Ala Ala Trp Ser Val Leu Gly Gly Ile Ala Lys Thr Thr Pro Gln Leu 912

10
 2737 GAT GCG CTT CTG CGT TTG CAA CAG GCA CAG AAC CAA ACT GGT CTT GGC
 2784
 913 Asp Ala Leu Leu Arg Leu Gln Gln Ala Gln Asn Gln Thr Gly Leu Gly 928

15
 2785 GTT ACA CAG CAA CAG CAA GGC TAT CTC CTG AGT CGT GAC AGT GAT TAT
 2832
 929 Val Thr Gln Gln Gln Gln Gly Tyr Leu Leu Ser Arg Asp Ser Asp Tyr 944

20
 2833 ACC CTT TGG CAA AGC ACC GGT CAG GCG CTG GTG GCT GGC GTA TCC CAT
 2880
 945 Thr Leu Trp Gln Ser Thr Gly Gln Ala Leu Val Ala Gly Val Ser His 960

25
 2881 GTC AAG GGC AGT AAC TGA GCATGGCAGA GCTCACTACC TGAGTGGATT TGATTT
 2934
 961 Val Lys Gly Ser Asn End 965

30
 2935 TTCCGTATGG CCTAATGAGG CTATTTCTAA ACCGCCATTT AAGTAAGGCA GATAATTATG
 2994

35 (2) INFORMATION FOR SEQ ID NO:57

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 965 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57 (TccA peptide)

Features	From	To	Description
	1	10	SEQ ID NO:8
1	Met	Asn	Gln Leu Ala Ser Pro Leu Ile Ser Arg Thr Glu Glu Ile His 16
17	Asn	Leu	Pro Gly Lys Leu Thr Asp Leu Gly Tyr Thr Ser Val Phe Asp 32
33	Val	Val	Arg Met Pro Arg Glu Arg Phe Ile Arg Glu His Arg Ala Asp 48
49	Leu	Gly	Arg Ser Ala Glu Lys Met Tyr Asp Leu Ala Val Gly Tyr Ala 64
55	His	Gln	Val Leu His His Phe Arg Arg Asn Ser Leu Ser Glu Ala Val 80
81	Gln	Phe	Gly Leu Arg Ser Pro Phe Ser Val Ser Gly Pro Asp Tyr Ala 96
97	Asn	Gln	Phe Leu Asp Ala Asn Thr Gly Trp Lys Asp Lys Ala Pro Ser 112
113	Gly	Ser	Pro Glu Ala Asn Asp Ala Pro Val Ala Tyr Leu Thr His Ile 128
129	Tyr	Gln	Leu Ala Leu Glu Gln Glu Lys Asn Gly Ala Thr Thr Ile Met 144
145	Asn	Thr	Leu Ala Glu Arg Arg Pro Asp Leu Gly Ala Leu Leu Ile Asn 160
161	Asp	Lys	Ala Ile Asn Glu Val Ile Pro Gln Leu Gln Leu Val Asn Glu 176
177	Ile	Leu	Ser Lys Ala Ile Gln Lys Lys Leu Ser Leu Thr Asp Leu Glu 192

	193	Ala Val Asn Ala Arg Leu Ser Thr Thr Arg Tyr Pro Asn Asn Leu Pro	208
5	209	Tyr His Tyr Gly His Gln Gln Ile Gln Thr Ala Gln Ser Val Leu Gly	224
	225	Thr Thr Leu Gln Asp Ile Thr Leu Pro Gln Thr Leu Asp Leu Pro Gln	240
	241	Asn Phe Trp Ala Thr Ala Lys Gly Lys Leu Ser Asp Thr Thr Ala Ser	256
10	257	Ala Leu Thr Arg Leu Gln Ile Met Ala Ser Gln Phe Ser Pro Glu Gln	272
	273	Gln Lys Ile Ile Thr Glu Thr Val Gly Gln Asp Phe Tyr Gln Leu Asn	288
15	289	Tyr Gly Asp Ser Ser Leu Thr Val Asn Ser Phe Ser Asp Met Thr Ile	304
	305	Met Thr Asp Arg Thr Ser Leu Thr Val Pro Gln Val Glu Leu Met Leu	320
	321	Cys Ser Thr Val Gly Gly Ser Thr Val Val Lys Ser Asp Asn Val Ser	336
20	337	Ser Gly Asp Thr Thr Ala Thr Pro Phe Ala Tyr Gly Ala Arg Phe Ile	352
	353	His Ala Gly Lys Pro Glu Ala Ile Thr Leu Ser Arg Ser Gly Ala Glu	368
25	369	Ala His Phe Ala Leu Thr Val Asn Asn Leu Thr Asp Asp Lys Leu Asp	384
	385	Arg Ile Asn Arg Thr Val Arg Leu Gln Lys Trp Leu Asn Leu Pro Tyr	400
	401	Glu Asp Ile Asp Leu Leu Val Thr Ser Ala Met Asp Ala Glu Thr Gly	416
30	417	Asn Thr Ala Leu Ser Met Asn Asp Asn Thr Leu Arg Met Leu Gly Val	432
	433	Phe Lys His Tyr Gln Ala Lys Tyr Gly Val Ser Ala Lys Gln Phe Ala	448
35	449	Gly Trp Leu Arg Val Val Ala Pro Phe Ala Ile Thr Pro Ala Thr Pro	464
	465	Phe Leu Asp Gln Val Phe Asn Ser Val Gly Thr Phe Asp Thr Pro Phe	480
	481	Val Ile Asp Asn Gln Asp Phe Val Tyr Thr Leu Thr Thr Gly Gly Asp	496
40	497	Gly Ala Arg Val Lys His Ile Ser Thr Ala Leu Gly Leu Asn His Arg	512
	513	Gln Phe Leu Leu Leu Ala Asp Asn Ile Ala Arg Gln Gln Gly Asn Val	528
45	529	Thr Gln Ser Thr Leu Asn Cys Asn Leu Phe Val Val Ser Ala Phe Tyr	544
	545	Arg Leu Ala Asn Leu Ala Arg Thr Leu Gly Ile Asn Pro Glu Ser Phe	560
	561	Cys Ala Leu Val Asp Arg Leu Asp Ala Gly Thr Gly Ile Val Trp Gln	576
50	577	Gln Leu Ala Gly Lys Pro Thr Ile Thr Val Pro Gln Lys Asp Ser Pro	592
	593	Leu Ala Ala Asp Ile Leu Ser Leu Leu Gln Ala Leu Ser Ala Ile Ala	608
55	609	Gln Trp Gln Gln Gln His Asp Leu Glu Phe Ser Ala Leu Leu Leu Leu	624
	625	Leu Ser Asp Asn Pro Ile Ser Thr Ser Gln Gly Thr Asp Asp Gln Leu	640
	641	Asn Phe Ile Arg Gln Val Trp Gln Asn Leu Gly Ser Thr Phe Val Gly	656
60	657	Ala Thr Leu Leu Ser Arg Ser Gly Ala Pro Leu Val Asp Thr Asn Gly	672
	673	His Ala Ile Asp Trp Phe Ala Leu Leu Ser Ala Gly Asn Ser Pro Leu	688
65	689	Ile Asp Lys Val Gly Leu Val Thr Asp Ala Gly Ile Gln Ser Val Ile	704
	705	Ala Thr Val Val Asn Thr Gln Ser Leu Ser Asp Glu Asp Lys Lys Leu	720
	721	Ala Ile Thr Thr Leu Thr Asn Thr Leu Asn Gln Val Gln Lys Thr Gln	736
70	737	Gln Gly Val Ala Val Ser Leu Leu Ala Gln Thr Leu Asn Val Ser Gln	752

753 Ser Leu Pro A au Leu Leu Arg Trp Ser Gly Gln Thr Tyr Gln 768
 769 Trp Leu Ser Ala Thr Trp Ala Leu Lys Asp Ala Val Lys Thr Ala Ala 784
 5 785 Asp Ile Pro Ala Asp Tyr Leu Arg Gln Leu Arg Glu Val Val Arg Arg 800
 801 Ser Leu Leu Thr Gln Gln Phe Thr Leu Ser Pro Ala Met Val Gln Thr 816
 10 817 Leu Leu Asp Tyr Pro Ala Tyr Phe Gly Ala Ser Ala Glu Thr Val Thr 832
 833 Asp Ile Ser Leu Trp Met Leu Tyr Thr Leu Ser Cys Tyr Ser Asp Leu 848
 849 Leu Leu Gln Met Gly Glu Ala Gly Gly Thr Glu Asp Asp Val Leu Ala 864
 15 865 Tyr Leu Arg Thr Ala Asn Ala Thr Thr Pro Leu Ser Gln Ser Asp Ala 880
 881 Ala Gln Thr Leu Ala Thr Leu Leu Gly Trp Glu Val Asn Glu Leu Gln 896
 897 Ala Ala Trp Ser Val Leu Gly Gly Ile Ala Lys Thr Thr Pro Gln Leu 912
 20 913 Asp Ala Leu Leu Arg Leu Gln Gln Ala Gln Asn Gln Thr Gly Leu Gly 928
 929 Val Thr Gln Gln Gln Gln Gly Tyr Leu Leu Ser Arg Asp Ser Asp Tyr 944
 25 945 Thr Leu Trp Gln Ser Thr Gly Gln Ala Leu Val Ala Gly Val Ser His 960
 961 Val Lys Gly Ser Asn 965

30 (2) INFORMATION FOR SEQ ID NO:58

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4932 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58 (tccB)

40 1 ATG TTA TCG ACA ATG GAA AAA CAA CTG AAT GAA TCC CAG CGT GAT GCG 48
 1 Met Leu Ser Thr Met Glu Lys Gln Leu Asn Glu Ser Gln Arg Asp Ala 16
 45 49 TTG GTG ACT GGC TAT ATG AAT TTT GTG GCG CCG ACG TTG AAA GGC GTC 96
 17 Leu Val Thr Gly Tyr Met Asn Phe Val Ala Pro Thr Leu Lys Gly Val 32
 50 97 AGT GGT CAG CCG GTG ACG GTG GAA GAT TTA TAC GAA TAT TTG CTG ATT 144
 33 Ser Gly Gln Pro Val Thr Val Glu Asp Leu Tyr Glu Tyr Leu Leu Ile 48
 55 145 GAC CCG GAA GTG GCT GAT GAG GTT GAG ACG AGT CGG GTA GCA CAA GCG 192
 49 Asp Pro Glu Val Ala Asp Glu Val Glu Thr Ser Arg Val Ala Gln Ala 64
 193 ATT GCC AGC ATA CAG CAA TAT ATG ACT CGT CTG GTC AAC GGC TCT GAA 240
 65 Ile Ala Ser Ile Gln Gln Tyr Met Thr Arg Leu Val Asn Gly Ser Glu 80
 60 241 CCG GGG CGT CAG GCG ATG GAG CCT TCT ACA GCT AAC GAA TGG CGT GAT 288
 81 Pro Gly Arg Gln Ala Met Glu Pro Ser Thr Ala Asn Glu Trp Arg Asp 96
 289 AAT GAT AAC CAA TAT GCT ATC TGG GCT GCG GGG GCT GAG GTT CGA AAT 336
 97 Asn Asp Asn Gln Tyr Ala Ile Trp Ala Ala Gly Ala Glu Val Arg Asn 112
 65 337 TAC GCT GAA AAC TAT ATT TCA CCC ATC ACC CGG CAG GAA AAA AGC CAT 384
 113 Tyr Ala Glu Asn Tyr Ile Ser Pro Ile Thr Arg Gln Glu Lys Ser His 128

	385	TAT	TTC	T	GAG	CTG	GAG	ACG	ACT	TTA	AAT	CAG	CTT	CGA	CTC	GAT	CCG	432
	129	Tyr	Phe	Ser	Glu	Leu	Glu	Thr	Thr	Leu	Asn	Gln	Asn	Arg	Leu	Asp	Pro	144
5	433	GAT	CGT	GTG	CAG	GAT	GCT	GTT	TTG	GCG	TAT	CTC	AAT	GAG	TTT	GAG	GCA	480
	145	Asp	Arg	Val	Gln	Asp	Ala	Val	Leu	Ala	Tyr	Leu	Asn	Glu	Phe	Glu	Ala	160
10	481	GTG	AGT	AAT	CTA	TAT	GTG	CTC	AGT	GGT	TAT	ATT	AAT	CAG	GAT	AAA	TTT	528
	161	Val	Ser	Asn	Leu	Tyr	Val	Leu	Ser	Gly	Tyr	Ile	Asn	Gln	Asp	Lys	Phe	176
15	529	GAC	CAA	GCT	ATC	TAC	TAC	TTT	ATT	GGT	CGC	ACT	ACC	ACT	AAA	CCG	TAT	576
	177	Asp	Gln	Ala	Ile	Tyr	Tyr	Phe	Ile	Gly	Arg	Thr	Thr	Thr	Lys	Pro	Tyr	192
	577	CGC	TAC	TAC	TGG	CGT	CAG	ATG	GAT	TTG	AGT	AAG	AAC	CGT	CAA	GAT	CCG	624
	193	Arg	Tyr	Tyr	Trp	Arg	Gln	Met	Asp	Leu	Ser	Lys	Asn	Arg	Gln	Asp	Pro	208
20	625	GCA	GGG	AAT	CCG	GTG	ACG	CCA	AAT	TGC	TGG	AAT	GAT	TGG	CAG	GAA	ATC	672
	209	Ala	Gly	Asn	Pro	Val	Thr	Pro	Asn	Cys	Trp	Asn	Asp	Trp	Gln	Glu	Ile	224
25	673	ACT	TTG	CCG	CTG	TCT	GGT	GAT	ACG	GTG	CTG	GAG	CAT	ACA	GTT	CGC	CCG	720
	225	Thr	Leu	Pro	Leu	Ser	Gly	Asp	Thr	Val	Leu	Glu	His	Thr	Val	Arg	Pro	240
30	721	GTA	TTT	TAT	AAT	GAT	CGA	CTA	TAT	GTG	GCT	TGG	GTT	GAG	CGT	GAC	CCG	768
	241	Val	Phe	Tyr	Asn	Asp	Arg	Leu	Tyr	Val	Ala	Trp	Val	Glu	Arg	Asp	Pro	256
35	769	GCA	GTA	CAG	AAG	GAT	GCT	GAC	GGT	AAA	AAC	ATC	GGT	AAA	ACC	CAT	GCC	816
	257	Ala	Val	Gln	Lys	Asp	Ala	Asp	Gly	Lys	Asn	Ile	Gly	Lys	Thr	His	Ala	272
	817	TAC	AAC	ATA	AAG	TTT	GGT	TAT	AAA	CGT	TAT	GAT	GAT	ACT	TGG	ACA	GCG	864
	273	Tyr	Asn	Ile	Lys	Phe	Gly	Tyr	Lys	Arg	Tyr	Asp	Asp	Thr	Trp	Thr	Ala	288
40	865	CCG	AAT	ACG	ACC	ACG	TTA	ATG	ACA	CAA	CAA	GCA	GGG	GAA	AGT	TCA	GAA	912
	289	Pro	Asn	Thr	Thr	Thr	Leu	Met	Thr	Gln	Gln	Ala	Gly	Glu	Ser	Ser	Glu	304
45	913	ACA	CAG	CGA	TCC	AGC	CTG	CTG	ATT	GAT	GAA	TCT	AGC	ACC	ACA	TTG	CGC	960
	305	Thr	Gln	Arg	Ser	Ser	Leu	Leu	Ile	Asp	Glu	Ser	Ser	Thr	Thr	Leu	Arg	320
50	961	CAA	GTT	AAT	CTG	TTG	GCT	ACC	ACC	GAT	TTT	AGT	ATC	GAT	CCG	ACG	GAG	
	1008																	
	321	Gln	Val	Asn	Leu	Leu	Ala	Thr	Thr	Asp	Phe	Ser	Ile	Asp	Pro	Thr	Glu	336
55	1009	GAA	ACG	GAC	AGT	AAC	CCG	TAT	GGC	CGC	CTA	ATG	TTG	GGG	GTG	TTT	GTC	
	1056																	
	337	Glu	Thr	Asp	Ser	Asn	Pro	Tyr	Gly	Arg	Leu	Met	Leu	Gly	Val	Phe	Val	352
60	1057	CGT	CAA	TTT	GAA	GGT	GAT	GGG	GCC	AAT	AGA	AAA	AAT	AAA	CCC	GTT	GTT	
	1104																	
	353	Arg	Gln	Phe	Glu	Gly	Asp	Gly	Ala	Asn	Arg	Lys	Asn	Lys	Pro	Val	Val	368
65	1105	TAT	GGT	TAT	CTC	TAT	TGT	GAC	TCA	GCT	TTC	AAT	CGT	CAT	GTT	CTC	AGG	
	1152																	
	369	Tyr	Gly	Tyr	Leu	Tyr	Cys	Asp	Ser	Ala	Phe	Asn	Arg	His	Val	Leu	Arg	384
70	1153	CCG	TTA	AGT	AAG	AAC	TTT	TTG	TTC	AGT	ACT	TAC	CGT	GAT	GAA	ACG	GAT	
	1200																	
	385	Pro	Leu	Ser	Lys	Asn	Phe	Leu	Phe	Ser	Thr	Tyr	Arg	Asp	Glu	Thr	Asp	400

	1201	GGT CAA AAC AGC TTG CAA TTT GCG GTA TAC GAT AAA AAG TAT GTA ATT	
	1248		
5	401	Gly Gln Asn Ser Leu Gln Phe Ala Val Tyr Asp Lys Lys Tyr Val Ile	416
	1249	ACT AAG GTT GTT ACA GGT GCA ACG GAA GAT CCC GAA AAT ACA GGA TGG	
	1296		
10	417	Thr Lys Val Val Thr Gly Ala Thr Glu Asp Pro Glu Asn Thr Gly Trp	432
	1297	GTA AGT AAA GTT GAT GAC TTG AAA CAA GGC ACT ACT GGG GCC TAT GTG	
	1344		
15	433	Val Ser Lys Val Asp Asp Leu Lys Gln Gly Thr Thr Gly Ala Tyr Val	448
	1345	TAT ATC GAT CAA GAT GGC CTG ACG CTT CAT ATA CAA ACC ACA ACT AAT	
	1392		
20	449	Tyr Ile Asp Gln Asp Gly Leu Thr Leu His Ile Gln Thr Thr Thr Asn	464
	1393	GGG GAT TTT ATT AAC CGT CAT ACG TTT GGA TAT AAC GAT CTT GTA TAT	
	1440		
25	465	Gly Asp Phe Ile Asn Arg His Thr Phe Gly Tyr Asn Asp Leu Val Tyr	480
	1441	GAT TCT AAG TCT GGT TAT GGT TTC ACG TGG TCA GGA AAT GAA GGT TTT	
	1488		
30	481	Asp Ser Lys Ser Gly Tyr Gly Phe Thr Trp Ser Gly Asn Glu Gly Phe	496
	1489	TAT CTG GAT TAC CAT GAT GGA AAT TAT TAC ACC TTT CAT AAT GCA ATA	
	1536		
35	497	Tyr Leu Asp Tyr His Asp Gly Asn Tyr Tyr Thr Phe His Asn Ala Ile	512
	1537	ATC AAC TAC TAT CCG TCT GGA TAT GGT GGT GGA TCT GTT CCT AAT GGA	
	1584		
40	513	Ile Asn Tyr Tyr Pro Ser Gly Tyr Gly Gly Gly Ser Val Pro Asn Gly	528
	1585	ACG TGG GCG TTA GAG CAA AGG ATT AAT GAG GGA TGG GCT ATT GCT CCC	
	1632		
45	529	Thr Trp Ala Leu Glu Gln Arg Ile Asn Glu Gly Trp Ala Ile Ala Pro	544
	1633	CTG CTT GAT ACT CTC CAT ACT GTT ACT GTG AAG GGC AGT TAT ATC GCT	
	1680		
50	545	Leu Leu Asp Thr Leu His Thr Val Thr Val Lys Gly Ser Tyr Ile Ala	560
	1681	TGG GAA GGG GAA ACA CCT ACC GGT TAT AAT CTG TAT ATT CCA GAT GGT	
	1728		
55	561	Trp Glu Gly Glu Thr Pro Thr Gly Tyr Asn Leu Tyr Ile Pro Asp Gly	576
	1729	ACC GTG TTG CTA GAT TGG TTT GAT AAA ATA AAT TTT GCT ATT GGT CTT	
	1776		
60	577	Thr Val Leu Leu Asp Trp Phe Asp Lys Ile Asn Phe Ala Ile Gly Leu	592
	1777	AAT AAG CTT GAG TCT GTA TTT ACG TCG CCA GAT TGG CCA ACA CTA ACC	
	1824		
65	593	Asn Lys Leu Glu Ser Val Phe Thr Ser Pro Asp Trp Pro Thr Leu Thr	608
	1825	ACT ATC AAA AAT TTC AGT AAA ATC GCC GAT AAC CGC AAA TTC TAT CAG	
	1872		
70	609	Thr Ile Lys Asn Phe Ser Lys Ile Ala Asp Asn Arg Lys Phe Tyr Gln	624

1873 GAA ATC AAT GCT GAG ACG GCG GAT GGA CGC AAC CTG TTT AAA CGT TAC
 1920
 5 625 Glu Ile Asn Ala Glu Thr Ala Asp Gly Arg Asn Leu Phe Lys Arg Tyr 640

 1921 AGT ACT CAA ACT TTC GGA CTT ACC AGC GGT GCG ACT TAT TCT ACA ACT
 1968
 10 641 Ser Thr Gln Thr Phe Gly Leu Thr Ser Gly Ala Thr Tyr Ser Thr Thr 656

 1969 TAT ACT TTG TCT GAG GCG GAT TTC TCC ACT GAT CCG GAC AAA AAC TAC
 2016
 15 657 Tyr Thr Leu Ser Glu Ala Asp Phe Ser Thr Asp Pro Asp Lys Asn Tyr 672

 2017 CTA CAG GTT TGT TTG AAT GTC GTG TGG GAT CAT TAT GAC CGC CCG TCA
 2064
 20 673 Leu Gln Val Cys Leu Asn Val Val Trp Asp His Tyr Asp Arg Pro Ser 688

 2065 GGG AAA AAA GGG GCT TAT TCT TGG GTC AGT AAG TGG TTT AAC GTC TAT
 2112
 25 689 Gly Lys Lys Gly Ala Tyr Ser Trp Val Ser Lys Trp Phe Asn Val Tyr 704

 2113 GTT GCG TTG CAA GAT AGC AAA GCT CCG GAT GCC ATT CCT CGA TTA GTT
 2160
 30 705 Val Ala Leu Gln Asp Ser Lys Ala Pro Asp Ala Ile Pro Arg Leu Val 720

 2161 TCC CGT TAC GAT AGT AAA CGT GGT CTG GTG CAA TAT CTG GAC TTC TGG
 2208
 35 721 Ser Arg Tyr Asp Ser Lys Arg Gly Leu Val Gln Tyr Leu Asp Phe Trp 736

 2209 ACC TCA TCA TTA CCC GCG AAA ACC CGT CTT AAC ACC ACC TTT GTG CGT
 2256
 40 737 Thr Ser Ser Leu Pro Ala Lys Thr Arg Leu Asn Thr Thr Phe Val Arg 752

 2257 ACT TTG ATT GAG AAG GCT AAT CTG GGG CTG GAT AGT TTG CTG GAT TAC
 2304
 45 753 Thr Leu Ile Glu Lys Ala Asn Leu Gly Leu Asp Ser Leu Leu Asp Tyr 768

 2305 ACC TTG CAG GCA GAT CCT TCT CTG GAA GCA GAT TTA GTG ACT GAC GGC
 2352
 50 769 Thr Leu Gln Ala Asp Pro Ser Leu Glu Ala Asp Leu Val Thr Asp Gly 784



 2353 AAA AGC GAA CCA ATG GAC TTT AAT GGT TCA AAC GGT CTC TAT TTC TGG
 2400
 55 785 Lys Ser Glu Pro Met Asp Phe Asn Gly Ser Asn Gly Leu Tyr Phe Trp 800

 2401 GAA TTG TTC TTT CAC CTG CCG TTT TTG GTT GCT ACA CGC TTT GCC AAC
 2448
 60 801 Glu Leu Phe Phe His Leu Pro Phe Leu Val Ala Thr Arg Phe Ala Asn 816

 2449 GAA CAG CAA TTT TCG CCG GCA CAA AAG AGT TTG CAT TAC ATC TTT GAC
 2496
 65 817 Glu Gln Gln Phe Ser Pro Ala Gln Lys Ser Leu His Tyr Ile Phe Asp 832

 2497 CCG GCG ATG AAA AAC AAG CCA CAC AAT GCC CCG GCT TAT TGG AAT GTA
 2544
 70 833 Pro Ala Met Lys Asn Lys Pro His Asn Ala Pro Ala Tyr Trp Asn Val 848

2545 CGT CCG TTG GAA GGA AAC AGC GAT TTG TCA CCG CAT TTG GAC GAT
 2592
 849 Arg Pro Leu Val Glu Gly Asn Ser Asp Leu Ser Arg His Leu Asp Asp 864
 5
 2593 TCT ATA GAC CCA GAT ACT CAA GCT TAT GCT CAT CCG GTG ATA TAC CAG
 2640
 865 Ser Ile Asp Pro Asp Thr Gln Ala Tyr Ala His Pro Val Ile Tyr Gln 880
 10
 2641 AAA GCG GTG TTT ATT GCC TAT GTC AGT AAC CTG ATT GCT CAG GGA GAT
 2688
 881 Lys Ala Val Phe Ile Ala Tyr Val Ser Asn Leu Ile Ala Gln Gly Asp 896
 15
 2689 ATG TGG TAT CGC CAA TTG ACT CGT GAC GGT CTG ACT CAG GCC CGT GTC
 2736
 897 Met Trp Tyr Arg Gln Leu Thr Arg Asp Gly Leu Thr Gln Ala Arg Val 912
 20
 2737 TAT TAC AAT CTG GCC GCT GAA TTG CTA GGG CCT CGT CCG GAT GTA TCG
 2784
 913 Tyr Tyr Asn Leu Ala Ala Glu Leu Leu Gly Pro Arg Pro Asp Val Ser 928
 25
 2785 CTG AGT AGC ATT TGG ACG CCG CAA ACC CTG GAT ACC TTA GCA GCC GGG
 2832
 929 Leu Ser Ser Ile Trp Thr Pro Gln Thr Leu Asp Thr Leu Ala Ala Gly 944
 30
 2833 CAA AAA GCG GTT TTA CGT GAT TTT GAG CAC CAG TTG GCT AAT AGT GAT
 2880
 945 Gln Lys Ala Val Leu Arg Asp Phe Glu His Gln Leu Ala Asn Ser Asp 960
 35
 2881 ACC GCT TTA CCC GCA TTG CCG GGC CGC AAT GTC AGC TAC TTG AAA CTG
 2928
 961 Thr Ala Leu Pro Ala Leu Pro Gly Arg Asn Val Ser Tyr Leu Lys Leu 976
 40
 2929 GCA GAT AAT GGC TAC TTT AAT GAA CCG CTC AAT GTT CTG ATG TTG TCT
 2976
 977 Ala Asp Asn Gly Tyr Phe Asn Glu Pro Leu Asn Val Leu Met Leu Ser 992
 45
 2977 CAC TGG GAT ACG TTG GAT GCA CGG TTA TAC AAT CTG CGT CAT AAC CTG
 3024
 993 His Trp Asp Thr Leu Asp Ala Arg Leu Tyr Asn Leu Arg His Asn Leu
 1008
 50
 3025 ACC GTT GAT GGC AAG CCG CTT TCG CTG CCG CTG TAT GCT GCG CCT GTT
 3072
 1009 Thr Val Asp Gly Lys Pro Leu Ser Leu Pro Leu Tyr Ala Ala Pro Val
 1024
 55
 3073 GAT CCG GTA GCG TTG TTG GCT CAG CGT GCT CAG TCC GGC ACG TTG ACG
 3120
 1025 Asp Pro Val Ala Leu Leu Ala Gln Arg Ala Gln Ser Gly Thr Leu Thr
 1040
 60
 3121 AAT GGC GTC AGT GGC GCC ATG TTG ACG GTG CCG CCA TAC CGT TTC AGC
 3168
 1041 Asn Gly Val Ser Gly Ala Met Leu Thr Val Pro Pro Tyr Arg Phe Ser
 1056
 65
 3169 GCT ATG TTG CCG CGA GCT TAC AGC GCC GTG GGT ACG TTG ACC AGT TTT
 3216
 70

1057 Ala Met  Pro Arg Ala Tyr Ser Ala Val Gly  Thr Leu Thr Ser Phe
1072

5 3217 GGT CAG AAC CTG CTT AGT TTG TTG GAA CGT AGC GAA CGA GCC TGT CAA
3264
1073 Gly Gln Asn Leu Leu Ser Leu Leu Glu Arg Ser Glu Arg Ala Cys Gln
1088

10 3265 GAA GAG TTG GCG CAA CAG CAA CTG TTG GAT ATG TCC AGC TAT GCC ATC
3312
1089 Glu Glu Leu Ala Gln Gln Gln Leu Leu Asp Met Ser Ser Tyr Ala Ile
1104

15 3313 ACG TTG CAA CAA CAG GCG CTG GAT GGA TTG GCG GCA GAT CGT CTG GCG
3360
1105 Thr Leu Gln Gln Gln Ala Leu Asp Gly Leu Ala Ala Asp Arg Leu Ala
1120

20 3361 CTG CTA GCT AGT CAG GCT ACG GCA CAA CAG CGT CAT GAC CAT TAT TAC
3408
1121 Leu Leu Ala Ser Gln Ala Thr Ala Gln Gln Arg His Asp His Tyr Tyr
1136

25 3409 ACT CTG TAT CAG AAC AAC ATC TCC AGT GCG GAA CAA CTG GTG ATG GAC
3456
1137 Thr Leu Tyr Gln Asn Asn Ile Ser Ser Ala Glu Gln Leu Val Met Asp
1152

30 3457 ACC CAA ACG TCA GCA CAA TCC CTG ATT TCT TCT TCC ACT GGT GTA CAA
3504
1153 Thr Gln Thr Ser Ala Gln Ser Leu Ile Ser Ser Ser Thr Gly Val Gln
1168

35 3505 ACT GCC AGT GGG GCA CTG AAA GTG ATC CCG AAT ATC TTT GGT TTG GCT
3552
1169 Thr Ala Ser Gly Ala Leu Lys Val Ile Pro Asn Ile Phe Gly Leu Ala
1184

40 3553 GAT GGC GGC TCG CGC TAT GAA GGA GTA ACG GAA GCG ATT GCC ATC GGG
3600
1185 ~~Asp Gly~~ Gly Ser Arg Tyr Glu Gly Val Thr Glu Ala Ile Ala Ile Gly
1200

45 3601 TTA ATG GCT GCC GGA CAA GCC ACC AGC GTG GTG GCC GAG CGT CTG GCA
3648
1201 Leu Met Ala Ala Gly Gln Ala Thr Ser Val Val Ala Glu Arg Leu Ala
1216

50 3649 ACC ACG GAG AAT TAC CGC CGC CGC CGT GAA GAG TGG CAA ATC CAA TAC
3696
1217 Thr Thr Glu Asn Tyr Arg Arg Arg Arg Glu Glu Trp Gln Ile Gln Tyr
1232

55 3697 CAG CAG GCA CAG TCT GAG GTC GAC GCA TTA CAG AAA CAG TTG GAT GCG
3744
1233 Gln Gln Ala Gln Ser Glu Val Asp Ala Leu Gln Lys Gln Leu Asp Ala
1248

60 3744
1233
1248

65 3697 CAG CAG GCA CAG TCT GAG GTC GAC GCA TTA CAG AAA CAG TTG GAT GCG
3744
1233 Gln Gln Ala Gln Ser Glu Val Asp Ala Leu Gln Lys Gln Leu Asp Ala
1248

70

3745 CTG GCA GTG GAG AAA GCA GCT CAA ACT TCC CAA CAG GCG AAG
 3792
 1249 Leu Ala Val Arg Glu Lys Ala Ala Gln Thr Ser Leu Gln Gln Ala Lys
 1264
 5
 3793 GCA CAG CAG GTA CAA ATT CGG ACC ATG CTG ACT TAC TTA ACT ACT CGT
 3840
 1265 Ala Gln Gln Val Gln Ile Arg Thr Met Leu Thr Tyr Leu Thr Thr Arg
 1280
 10
 3841 TTC ACC CAG GCG ACT CTG TAC CAG TGG CTG AGT GGT CAA TTA TCC GCG
 3888
 1281 Phe Thr Gln Ala Thr Leu Tyr Gln Trp Leu Ser Gly Gln Leu Ser Ala
 1296
 15
 3889 TTG TAT TAT CAA GCG TAT GAT GCC GTG GTT GCT CTC TGC CTC TCC GCC
 3936
 1297 Leu Tyr Tyr Gln Ala Tyr Asp Ala Val Val Ala Leu Cys Leu Ser Ala
 1312
 20
 3937 CAA GCT TGC TGG CAG TAT GAA TTG GGT GAT TAC GCT ACC ACT TTT ATC
 3984
 1313 Gln Ala Cys Trp Gln Tyr Glu Leu Gly Asp Tyr Ala Thr Thr Phe Ile
 1328
 25
 3985 CAG ACC GGT ACC TGG AAC GAC CAT TAC CGT GGT TTG CAA GTG GGG GAG
 4032
 1329 Gln Thr Gly Thr Trp Asn Asp His Tyr Arg Gly Leu Gln Val Gly Glu
 1344
 30
 35
 4033 ACA CTG CAA CTC AAT TTG CAT CAG ATG GAA GCG GCC TAT TTA GTT CGT
 4080
 1345 Thr Leu Gln Leu Asn Leu His Gln Met Glu Ala Ala Tyr Leu Val Arg
 1360
 40
 4081 CAC GAA CGC CGT CTT AAT GTG ATC CGT ACT GTG TCG CTC AAA AGC CTA
 4128
 1361 His Glu Arg Arg Leu Asn Val Ile Arg Thr Val Ser Leu Lys Ser Leu
 1376
 45
 4129 TTG GGT GAT GAT GGT TTT GGT AAG TTA AAA ACC GAA GGC AAA GTC GAC
 4176
 1377 Leu Gly Asp Asp Gly Phe Gly Lys Leu Lys Thr Glu Gly Lys Val Asp
 1392
 50
 4177 TTT CCA TTA AGC GAA AAG CTG TTT GAC AAC GAC TAT CCG GGG CAC TAT
 4224
 1393 Phe Pro Leu Ser Glu Lys Leu Phe Asp Asn Asp Tyr Pro Gly His Tyr
 1408
 55
 4225 TTG CGC CAG ATT AAA ACT GTG TCA GTG ACG TTG CCG ACG TTA GTC GGG
 4272
 1409 Leu Arg Gln Ile Lys Thr Val Ser Val Thr Leu Pro Thr Leu Val Gly
 1424
 60
 65
 4273 CCG TAT CAA AAC GTG AAG GCA ACG CTC ACT CAG ACC AGC AGC AGT ATA
 4320
 1425 Pro Tyr Gln Asn Val Lys Ala Thr Leu Thr Gln Thr Ser Ser Ser Ile
 1440
 70

4321 TTG TTA GCA GCA GAT ATC AAT GGT GTT AAA CGT CTC AAT GAT CCG ACA
 4368
 1441 Leu Leu Ala Ala Asp Ile Asn Gly Val Lys Arg Leu Asn Asp Pro Thr
 1456
 5
 4369 GGT AAA GAG GGT GAT GCG ACG CAT ATT GTC ACC AAT CTG CGT GCC AGC
 4416
 10 1457 Gly Lys Glu Gly Asp Ala Thr His Ile Val Thr Asn Leu Arg Ala Ser
 1472
 4417 CAG CAG GTG GCG CTC TCT TCT GGC ATT AAT GAT GCC GGT AGC TTT GAG
 4464
 15 1473 Gln Gln Val Ala Leu Ser Ser Gly Ile Asn Asp Ala Gly Ser Phe Glu
 1488
 4465 TTG CGT TTG GAA GAT GAG CGC TAT CTA TCA TTT GAG GGG ACT GGA GCT
 4512
 20 1489 Leu Arg Leu Glu Asp Glu Arg Tyr Leu Ser Phe Glu Gly Thr Gly Ala
 1504
 25 4513 GTT TCC AAA TGG ACT CTT AAC TTC CCG CGT TCT GTG GAT GAG CAT ATT
 4560
 1505 Val Ser Lys Trp Thr Leu Asn Phe Pro Arg Ser Val Asp Glu His Ile
 1520
 30 4561 GAC GAT AAG ACA TTG AAA GCG GAT GAG ATG CAG GCC GCA CTG TTG GCG
 4608
 1521 Asp Asp Lys Thr Leu Lys Ala Asp Glu Met Gln Ala Ala Leu Leu Ala
 1536
 35 4609 AAT ATG GAT GAT GTG CTG GTG CAG GTG CAT TAT ACC GCC TGC GAC GGC
 4656
 40 1537 Asn Met Asp Asp Val Leu Val Gln Val His Tyr Thr Ala Cys Asp Gly
 1552
 4657 GGC GCC AGT TTC GCA AAC CAG GTC AAG AAA ACA CTC TCT TAA CATTAACTTT 4708
 45 1553 Gly Ala Ser Phe Ala Asn Gln Val Lys Lys Thr Leu Ser End 1565
 4709 TAACTAATCC CTCCCACTCT GTTCGCCAGA GTGGGAGAAG GTTTGTCATA TCTAAAATCA 4768
 50 4770 ATCTTGCGAT CTTTCTCCAT TTCATTGGAA GGGAAGCTGT AAAACAAATA AGGAATATGA 4828
 4829 TATG 4932
 55

(2) INFORMATION FOR SEQ ID NO:59

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1565 amino acids
 (B) TYPE: amino acid
 (C) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59 (TccB peptide)
 Features From To Description
 1 Met Leu Ser Thr Met Glu Lys Gln Leu Asn Glu Ser Gln Arg Asp Ala
 16

17 Leu Val Thr Gly Tyr Met Asn Phe Val Ala Pro Thr Leu Lys Gly Val
 32
 5 33 Ser Gly Gln Pro Val Thr Val Glu Asp Leu Tyr Glu Tyr Leu Leu Ile
 48
 49 Asp Pro Glu Val Ala Asp Glu Val Glu Thr Ser Arg Val Ala Gln Ala
 64
 10 65 Ile Ala Ser Ile Gln Gln Tyr Met Thr Arg Leu Val Asn Gly Ser Glu
 80
 81 Pro Gly Arg Gln Ala Met Glu Pro Ser Thr Ala Asn Glu Trp Arg Asp
 15 96
 97 Asn Asp Asn Gln Tyr Ala Ile Trp Ala Ala Gly Ala Glu Val Arg Asn
 112
 20 113 Tyr Ala Glu Asn Tyr Ile Ser Pro Ile Thr Arg Gln Glu Lys Ser His
 128
 129 Tyr Phe Ser Glu Leu Glu Thr Thr Leu Asn Gln Asn Arg Leu Asp Pro
 144
 25 145 Asp Arg Val Gln Asp Ala Val Leu Ala Tyr Leu Asn Glu Phe Glu Ala
 160
 161 Val Ser Asn Leu Tyr Val Leu Ser Gly Tyr Ile Asn Gln Asp Lys Phe
 30 176
 177 Asp Gln Ala Ile Tyr Tyr Phe Ile Gly Arg Thr Thr Thr Lys Pro Tyr
 192
 35 193 Arg Tyr Tyr Trp Arg Gln Met Asp Leu Ser Lys Asn Arg Gln Asp Pro
 208
 209 Ala Gly Asn Pro Val Thr Pro Asn Cys Trp Asn Asp Trp Gln Glu Ile
 224
 40 225 Thr Leu Pro Leu Ser Gly Asp Thr Val Leu Glu His Thr Val Arg Pro
 240
 241 Val Phe Tyr Asn Asp Arg Leu Tyr Val Ala Trp Val Glu Arg Asp Pro
 45 256
 257 Ala Val Gln Lys Asp Ala Asp Gly Lys Asn Ile Gly Lys Thr His Ala
 272
 50 273 Tyr Asn Ile Lys Phe Gly Tyr Lys Arg Tyr Asp Asp Thr Trp Thr Ala
 288
 289 Pro Asn Thr Thr Thr Leu Met Thr Gln Gln Ala Gly Glu Ser Ser Glu
 304
 55 305 Thr Gln Arg Ser Ser Leu Leu Ile Asp Glu Ser Ser Thr Thr Leu Arg
 320
 321 Gln Val Asn Leu Leu Ala Thr Thr Asp Phe Ser Ile Asp Pro Thr Glu
 60 336
 337 Glu Thr Asp Ser Asn Pro Tyr Gly Arg Leu Met Leu Gly Val Phe Val
 352
 65 353 Arg Gln Phe Glu Gly Asp Gly Ala Asn Arg Lys Asn Lys Pro Val Val
 368
 369 Tyr Gly Tyr Leu Tyr Cys Asp Ser Ala Phe Asn Arg His Val Leu Arg
 384
 70

385 Pro Leu Ser Lys Asn Phe Leu Phe Ser Thr Tyr Arg Asp Glu Thr Asp
 400
 5 401 Gly Gln Asn Ser Leu Gln Phe Ala Val Tyr Asp Lys Lys Tyr Val Ile
 416
 417 Thr Lys Val Val Thr Gly Ala Thr Glu Asp Pro Glu Asn Thr Gly Trp
 432
 10 433 Val Ser Lys Val Asp Asp Leu Lys Gln Gly Thr Thr Gly Ala Tyr Val
 448
 449 Tyr Ile Asp Gln Asp Gly Leu Thr Leu His Ile Gln Thr Thr Thr Asn
 464
 15 465 Gly Asp Phe Ile Asn Arg His Thr Phe Gly Tyr Asn Asp Leu Val Tyr
 480
 481 Asp Ser Lys Ser Gly Tyr Gly Phe Thr Trp Ser Gly Asn Glu Gly Phe
 496
 497 Tyr Leu Asp Tyr His Asp Gly Asn Tyr Tyr Thr Phe His Asn Ala Ile
 512
 25 513 Ile Asn Tyr Tyr Pro Ser Gly Tyr Gly Gly Gly Ser Val Pro Asn Gly
 528
 529 Thr Trp Ala Leu Glu Gln Arg Ile Asn Glu Gly Trp Ala Ile Ala Pro
 544
 30 545 Leu Leu Asp Thr Leu His Thr Val Thr Val Lys Gly Ser Tyr Ile Ala
 560
 561 Trp Glu Gly Glu Thr Pro Thr Gly Tyr Asn Leu Tyr Ile Pro Asp Gly
 576
 35 577 Thr Val Leu Leu Asp Trp Phe Asp Lys Ile Asn Phe Ala Ile Gly Leu
 592
 40 593 Asn Lys Leu Glu Ser Val Phe Thr Ser Pro Asp Trp Pro Thr Leu Thr
 608
 609 Thr Ile Lys Asn Phe Ser Lys Ile Ala Asp Asn Arg Lys Phe Tyr Gln
 624
 45 625 Glu Ile Asn Ala Glu Thr Ala Asp Gly Arg Asn Leu Phe Lys Arg Tyr
 640
 641 Ser Thr Gln Thr Phe Gly Leu Thr Ser Gly Ala Thr Tyr Ser Thr Thr
 656
 50 657 Tyr Thr Leu Ser Glu Ala Asp Phe Ser Thr Asp Pro Asp Lys Asn Tyr
 672
 55 673 Leu Gln Val Cys Leu Asn Val Val Trp Asp His Tyr Asp Arg Pro Ser
 688
 689 Gly Lys Lys Gly Ala Tyr Ser Trp Val Ser Lys Trp Phe Asn Val Tyr
 704
 60 705 Val Ala Leu Gln Asp Ser Lys Ala Pro Asp Ala Ile Pro Arg Leu Val
 720
 721 Ser Arg Tyr Asp Ser Lys Arg Gly Leu Val Gln Tyr Leu Asp Phe Trp
 736
 65 737 Thr Ser Ser Leu Pro Ala Lys Thr Arg Leu Asn Thr Thr Phe Val Arg
 752
 70 753 Thr Leu Ile Glu Leu Ala Asn Leu Gly Leu Asp Ser Leu Leu Asp Tyr
 768

769 Thr Leu Gln Ala Asp Pro Ser Leu Glu Ala Asp Leu Val Thr Asp Gly
 784
 5 785 Lys Ser Glu Pro Met Asp Phe Asn Gly Ser Asn Gly Leu Tyr Phe Trp
 800
 801 Glu Leu Phe Phe His Leu Pro Phe Leu Val Ala Thr Arg Phe Ala Asn
 816
 10 817 Glu Gln Gln Phe Ser Pro Ala Gln Lys Ser Leu His Tyr Ile Phe Asp
 832
 833 Pro Ala Met Lys Asn Lys Pro His Asn Ala Pro Ala Tyr Trp Asn Val
 15 848
 849 Arg Pro Leu Val Glu Gly Asn Ser Asp Leu Ser Arg His Leu Asp Asp
 864
 20 865 Ser Ile Asp Pro Asp Thr Gln Ala Tyr Ala His Pro Val Ile Tyr Gln
 880
 881 Lys Ala Val Phe Ile Ala Tyr Val Ser Asn Leu Ile Ala Gln Gly Asp
 896
 25 897 Met Trp Tyr Arg Gln Leu Thr Arg Asp Gly Leu Thr Gln Ala Arg Val
 912
 913 Tyr Tyr Asn Leu Ala Ala Glu Leu Leu Gly Pro Arg Pro Asp Val Ser
 30 928
 929 Leu Ser Ser Ile Trp Thr Pro Gln Thr Leu Asp Thr Leu Ala Ala Gly
 944
 35 945 Gln Lys Ala Val Leu Arg Asp Phe Glu His Gln Leu Ala Asn Ser Asp
 960
 961 Thr Ala Leu Pro Ala Leu Pro Gly Arg Asn Val Ser Tyr Leu Lys Leu
 40 976
 977 Ala Asp Asn Gly Tyr Phe Asn Glu Pro Leu Asn Val Leu Met Leu Ser
 992
 993 His Trp Asp Thr Leu Asp Ala Arg Leu Tyr Asn Leu Arg His Asn Leu
 45 1008
 1009 Thr Val Asp Gly Lys Pro Leu Ser Leu Pro Leu Tyr Ala Ala Pro Val
 1024
 50 1025 Asp Pro Val Ala Leu Leu Ala Gln Arg Ala Gln Ser Gly Thr Leu Thr
 1040
 1041 Asn Gly Val Ser Gly Ala Met Leu Thr Val Pro Pro Tyr Arg Phe Ser
 55 1056
 1057 Ala Met Leu Pro Arg Ala Tyr Ser Ala Val Gly Thr Leu Thr Ser Phe
 1072
 60 1073 Gly Gln Asn Leu Leu Ser Leu Leu Glu Arg Ser Glu Arg Ala Cys Gln
 1088
 1089 Glu Glu Leu Ala Gln Gln Gln Leu Leu Asp Met Ser Ser Tyr Ala Ile
 1104
 65 1105 Thr Leu Gln Gln Gln Ala Leu Asp Gly Leu Ala Ala Asp Arg Leu Ala
 1120
 1121 Leu Leu Ala Ser Gln Ala Thr Ala Gln Gln Arg His Asp His Tyr Tyr
 1136
 70

1137 Thr Leu Tyr Gln Asn Asn Ile Ser Ser Ala Glu Gln Leu Val Met Asp
 1152
 5 1153 Thr Gln Thr Ser Ala Gln Ser Leu Ile Ser Ser Ser Thr Gly Val Gln
 1168
 1169 Thr Ala Ser Gly Ala Leu Lys Val Ile Pro Asn Ile Phe Gly Leu Ala
 1184
 10 1185 Asp Gly Gly Ser Arg Tyr Glu Gly Val Thr Glu Ala Ile Ala Ile Gly
 1200
 1201 Leu Met Ala Ala Gly Gln Ala Thr Ser Val Val Ala Glu Arg Leu Ala
 1216
 15 1217 Thr Thr Glu Asn Tyr Arg Arg Arg Arg Glu Glu Trp Gln Ile Gln Tyr
 1232
 1233 Gln Gln Ala Gln Ser Glu Val Asp Ala Leu Gln Lys Gln Leu Asp Ala
 1248
 1249 Leu Ala Val Arg Glu Lys Ala Ala Gln Thr Ser Leu Gln Gln Ala Lys
 1264
 25 1265 Ala Gln Gln Val Gln Ile Arg Thr Met Leu Thr Tyr Leu Thr Thr Arg
 1280
 1281 Phe Thr Gln Ala Thr Leu Tyr Gln Trp Leu Ser Gly Gln Leu Ser Ala
 1296
 30 1297 Leu Tyr Tyr Gln Ala Tyr Asp Ala Val Val Ala Leu Cys Leu Ser Ala
 1312
 1313 Gln Ala Cys Trp Gln Tyr Glu Leu Gly Asp Tyr Ala Thr Thr Phe Ile
 1328
 35 1329 Gln Thr Gly Thr Trp Asn Asp His Tyr Arg Gly Leu Gln Val Gly Glu
 1344
 40 1345 Thr Leu Gln Leu Asn Leu His Gln Met Glu Ala Ala Tyr Leu Val Arg
 1360
 1361 His Glu Arg Arg Leu Asn Val Ile Arg Thr Val Ser Leu Lys Ser Leu
 1376
 45 1377 Leu Gly Asp Asp Gly Phe Gly Lys Leu Lys Thr Glu Gly Lys Val Asp
 1392
 1393 Phe Pro Leu Ser Glu Lys Leu Phe Asp Asn Asp Tyr Pro Gly His Tyr
 1408
 50 1409 Leu Arg Gln Ile Lys Thr Val Ser Val Thr Leu Pro Thr Leu Val Gly
 1424
 55 1425 Pro Tyr Gln Asn Val Lys Ala Thr Leu Thr Gln Thr Ser Ser Ser Ile
 1440
 1441 Leu Leu Ala Ala Asp Ile Asn Gly Val Lys Arg Leu Asn Asp Pro Thr
 1456
 60 1457 Gly Lys Glu Gly Asp Ala Thr His Ile Val Thr Asn Leu Arg Ala Ser
 1472
 1473 Gln Gln Val Ala Leu Ser Ser Gly Ile Asn Asp Ala Gly Ser Phe Glu
 1488
 65 1489 Leu Arg Leu Glu Asp Glu Arg Tyr Leu Ser Phe Glu Gly Thr Gly Ala
 1504
 70 1505 Val Ser Lys Trp Thr Leu Asn Phe Pro Arg Ser Val Asp Glu His Ile
 1520

1521 Asp Asp Lys Thr Leu Lys Ala Asp Glu Met Gln Ala Ala Leu Leu Ala
1536

5 1537 Asn Met Asp Asp Val Leu Val Gln Val His Tyr Thr Ala Cys Asp Gly
1552

1553 Gly Ala Ser Phe Ala Asn Gln Val Lys Lys Thr Leu Ser 1565

10

(2) INFORMATION FOR SEQ ID NO:60

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 3132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60 (tccc)

1 ATG AGT CCG TCT GAG ACT ACT CTT TAT ACT CAA ACC CCA ACA GTC AGC 48
1 Met Ser Pro Ser Glu Thr Thr Leu Tyr Thr Gln Thr Pro Thr Val Ser 16

25

49 GTG TTA GAT AAT CGC GGT CTG TCC ATT CGT GAT ATT GGT TTT CAC CGT 96
17 Val Leu Asp Asn Arg Gly Leu Ser Ile Arg Asp Ile Gly Phe His Arg 32

30

97 ATT GTA ATC GGG GGG GAT ACT GAC ACC CGC GTC ACC CGT CAC CAG TAT
144
33 Ile Val Ile Gly Gly Asp Thr Asp Thr Arg Val Thr Arg His Gln Tyr 48

35

145 GAT GCC CGT GGA CAC CTG AAC TAC AGT ATT GAC CCA CGC TTG TAT GAT
192
49 Asp Ala Arg Gly His Leu Asn Tyr Ser Ile Asp Pro Arg Leu Tyr Asp 64

40

193 GCA AAG CAG GCT GAT AAC TCA GTA AAG CCT AAT TTT GTC TGG CAG CAT
240
65 Ala Lys Gln Ala Asp Asn Ser Val Lys Pro Asn Phe Val Trp Gln His 80

45

241 GAT CTG GCC GGT CAT GCC CTG CGG ACA GAG AGT GTC GAT GCT GGT CGT
288
81 Asp Leu Ala Gly His Ala Leu Arg Thr Glu Ser Val Asp Ala Gly Arg 96

50

289 ACT GTT GCA TTG AAT GAT ATT GAA GGT CGT TCG GTA ATG ACA ATG AAT
336
97 Thr Val Ala Leu Asn Asp Ile Glu Gly Arg Ser Val Met Thr Met Asn
112

55

337 GCG ACC GGT GTT CGT CAG ACC CGT CGC TAT GAA GGC AAC ACC TTG CCC
384
113 Ala Thr Gly Val Arg Gln Thr Arg Arg Tyr Glu Gly Asn Thr Leu Pro
128

60

385 GGT CGC TTG TTA TCT GTG AGC GAG CAA GTT TTC AAC CAA GAG AGT GCT
432
129 Gly Arg Leu Leu Ser Val Ser Glu Gln Val Phe Asn Gln Glu Ser Ala
144

65

433 AAA GTG ACA GAG CGC TTT ATC TGG GCT GGG AAT ACA ACC TCG GAG AAA
480

145 Lys Val Thr Glu Arg Phe Ile Trp Ala Gly Asn Thr Thr Ser Glu Lys
 160
 5 481 GAG TAT AAC CTC TCC GGT CTG TGT ATA CGC CAC TAC GAC ACA GCG GGA
 528
 161 Glu Tyr Asn Leu Ser Gly Leu Cys Ile Arg His Tyr Asp Thr Ala Gly
 176
 10 529 GTG ACC CGG TTG ATG AGT CAG TCA CTG GCG GGC GCC ATG CTA TCC CAA
 576
 177 Val Thr Arg Leu Met Ser Gln Ser Leu Ala Gly Ala Met Leu Ser Gln
 192
 15 577 TCT CAC CAA TTG CTG GCG GAA GGG CAG GAG GCT AAC TGG AGC GGT GAC
 624
 193 Ser His Gln Leu Leu Ala Glu Gly Gln Glu Ala Asn Trp Ser Gly Asp
 208
 20 625 GAC GAA ACT GTC TGG CAG GGA ATG CTG GCA AGT GAG GTC TAT ACG ACA
 672
 209 Asp Glu Thr Val Trp Gln Gly Met Leu Ala Ser Glu Val Tyr Thr Thr
 224
 25 673 CAA AGT ACC ACT AAT GCC ATC GGG GCT TTA CTG ACC CAA ACC GAT GCG
 720
 225 Gln Ser Thr Thr Asn Ala Ile Gly Ala Leu Leu Thr Gln Thr Asp Ala
 240
 30 721 AAA GGC AAT ATT CAG CGT CTG GCT TAT GAC ATT GCC GGT CAG TTA AAA
 768
 241 Lys Gly Asn Ile Gln Arg Leu Ala Tyr Asp Ile Ala Gly Gln Leu Lys
 256
 35 769 GGG AGT TGG TTG ACG GTG AAA GGC CAG AGT GAA CAG GTG ATT GTT AAG
 816
 257 Gly Ser Trp Leu Thr Val Lys Gly Gln Ser Glu Gln Val Ile Val Lys
 272
 40 817 TCC CTG AGC TGG TCA GCC GCA GGT CAT AAA TTG CGT GAA GAG CAC GGT
 864
 273 Ser Leu Ser Trp Ser Ala Ala Gly His Lys Leu Arg Glu Glu His Gly
 288
 45 865 AAC GGC GTG GTT ACG GAG TAC AGT TAT GAG CCG GAA ACT CAA CGT CTG
 912
 289 Asn Gly Val Val Thr Glu Tyr Ser Tyr Glu Pro Glu Thr Gln Arg Leu
 304
 50 913 ATA GGT ATC ACC ACC CGG CGT GCC GAA GGG AGT CAA TCA GGA GCC AGA
 960
 305 Ile Gly Ile Thr Thr Arg Arg Ala Glu Gly Ser Gln Ser Gly Ala Arg
 320
 55 961 GTA TTG CAG GAT CTA CGC TAT AAG TAT GAT CCG GTG GGG AAT GTT ATC
 1008
 321 Val Leu Gln Asp Leu Arg Tyr Lys Tyr Asp Pro Val Gly Asn Val Ile 336
 60 1009 AGT ATC CAT AAT GAT GCC GAA GCT ACC CGC TTT TGG CGT AAT CAG AAA
 1056

337 Ser Ile His Asp Ala Glu Ala Thr Arg Phe Trp Asn Gln Lys 352

5 1057 GTG GAG CCG GAG AAT CGC TAT GTT TAT GAT TCT CTG TAT CAG CTT ATG
1104
353 Val Glu Pro Glu Asn Arg Tyr Val Tyr Asp Ser Leu Tyr Gln Leu Met 368

10 1105 AGT GCG ACA GGG CGT GAA ATG GCT AAT ATC GGT CAG CAA AGC AAC CAA
1152
369 Ser Ala Thr Gly Arg Glu Met Ala Asn Ile Gly Gln Gln Ser Asn Gln
384

15 1153 CTT CCC TCA CCC GTT ATA CCT GTT CCT ACT GAC GAC AGC ACT TAT ACC
1200
385 Leu Pro Ser Pro Val Ile Pro Val Pro Thr Asp Asp Ser Thr Tyr Thr 400

20 1201 AAT TAC CTT CGT ACC TAT ACT TAT GAC CGT GGC GGT AAT TTG GTT CAA
1248
401 Asn Tyr Leu Arg Thr Tyr Thr Tyr Asp Arg Gly Gly Asn Leu Val Gln 416

25 1249 ATC CGA CAC AGT TCA CCC GCG ACT CAA AAT AGT TAC ACC ACA GAT ATC
1296
417 Ile Arg His Ser Ser Pro Ala Thr Gln Asn Ser Tyr Thr Thr Asp Ile 432

30 1297 ACC GTT TCA AGC CGC AGT AAC CGG GCG GTA TTG AGT ACA TTA ACG ACA
1344
433 Thr Val Ser Ser Arg Ser Asn Arg Ala Val Leu Ser Thr Leu Thr Thr 448

35 1345 GAT CCA ACC CGA GTG GAT GCG CTA TTT GAT TCC GGC GGT CAT CAG AAG
1392
449 Asp Pro Thr Arg Val Asp Ala Leu Phe Asp Ser Gly Gly His Gln Lys 464

40 1393 ATG TTA ATA CCG GGG CAA AAT CTG GAT TGG AAT ATT CGG GGT GAA TTG
1440
465 Met Leu Ile Pro Gly Gln Asn Leu Asp Trp Asn Ile Arg Gly Glu Leu 480

45 1441 CAA CGA GTC ACA CCG GTG AGC CGT GAA AAT AGC AGT GAC AGT GAA TGG
1488
481 Gln Arg Val Thr Pro Val Ser Arg Glu Asn Ser Ser Asp Ser Glu Trp 496

50 1489 TAT CGC TAT AGC AGT GAT GGC ATG CGG CTG CTA AAA GTG AGT GAA CAG
1536
497 Tyr Arg Tyr Ser Ser Asp Gly Met Arg Leu Leu Lys Val Ser Glu Gln 512

55 1537 CAG ACG GGC AAC AGT ACT CAA GTA CAA CGG GTG ACT TAT CTG CCG GGA
1584
513 Gln Thr Gly Asn Ser Thr Gln Val Gln Arg Val Thr Tyr Leu Pro Gly 528

60 1585 TTA GAG CTA CGG ACA ACT GGG GTT GCA GAT AAA ACA ACC GAA GAT TTG
1632
529 Leu Glu Leu Arg Thr Thr Gly Val Ala Asp Lys Thr Thr Glu Asp Leu 544

65 1633 CAG GTG ATT ACG GTA GGT GAA GCG GGT CGC GCA CAG GTA AGG GTA TTG
1680
545 Gln Val Ile Thr Val Gly Glu Ala Gly Arg Ala Gln Val Arg Val Leu 560

70 1681 CAC TGG GAA AGT GGT AAG CCG ACA GAT ATT GAC AAC AAT CAG GTG CGC
1728

561 His Trp Glu Ser Gly Lys Pro Thr Asp Ile Asp Asn Asn Gln Val Arg 576

5 1729 TAC AGC TAC GAT AAT CTG CTT GGC TCC AGC CAG CTT GAA CTG GAT AGC
1776
577 Tyr Ser Tyr Asp Asn Leu Leu Gly Ser Ser Gln Leu Glu Leu Asp Ser 592

10 1777 GAA GGG CAG ATT CTC AGT CAG GAA GAG TAT TAT CCG TAT GGC GGT ACG
1824
593 Glu Gly Gln Ile Leu Ser Gln Glu Glu Tyr Tyr Pro Tyr Gly Gly Thr 608

15 1825 GCG ATA TGG GCG GCG AGA AAT CAG ACA GAA GCC AGC TAC AAA TTT ATT
1872
609 Ala Ile Trp Ala Ala Arg Asn Gln Thr Glu Ala Ser Tyr Lys Phe Ile 624

20 1873 CGT TAC TCC GGT AAA GAG CGG GAT GCC ACT GGA TTG TAT TAT TAC GGC
1920
625 Arg Tyr Ser Gly Lys Glu Arg Asp Ala Thr Gly Leu Tyr Tyr Tyr Gly 640

25 1921 TAC CGT TAT TAT CAA CCT TGG GTG GGT CGA TGG TTG AGT GCT GAT CCG
1968
641 Tyr Arg Tyr Tyr Gln Pro Trp Val Gly Arg Trp Leu Ser Ala Asp Pro 656

30 1969 GCG GGA ACC GTG GAT GGG CTG AAT TTG TAC CGA ATG GTG AGG AAT AAC
2016
657 Ala Gly Thr Val Asp Gly Leu Asn Leu Tyr Arg Met Val Arg Asn Asn 672

35 2017 CCC ATC ACA TTG ACT GAC CAT GAC GGA TTA GCA CCG TCT CCA AAT AGA
2064
673 Pro Ile Thr Leu Thr Asp His Asp Gly Leu Ala Pro Ser Pro Asn Arg 688

40 2065 AAT CGA AAT ACA TTT TGG TTT GCT TCA TTT TTG TTT CGT AAA CCT GAT
2112
689 Asn Arg Asn Thr Phe Trp Phe Ala Ser Phe Leu Phe Arg Lys Pro Asp 704

45 2113 GAG GGA ATG TCC GCG TCA ATG AGA CGG GGA CAA AAA ATT GGC AGA GCC
2160
705 Glu Gly Met Ser Ala Ser Met Arg Arg Gly Gln Lys Ile Gly Arg Ala 720

50 2161 ATT GCC GGC GGG ATT GCG ATT GGC GGT CTT GCG GCT ACC ATT GCC GCT
2208
721 Ile Ala Gly Gly Ile Ala Ile Gly Gly Leu Ala Ala Thr Ile Ala Ala 736

55 2209 ACG GCT GGC GCG GCT ATC CCC GTC ATT CTG GGG GTT GCG GCC GTA GGC
2256
737 Thr Ala Gly Ala Ala Ile Pro Val Ile Leu Gly Val Ala Ala Val Gly 752

60 2257 GCG GGG ATT GGC GCG TTG ATG GGA TAT AAC GTC GGT AGC CTG CTG GAA
2304
753 Ala Gly Ile Gly Ala Leu Met Gly Tyr Asn Val Gly Ser Leu Leu Glu 768

65 2305 AAA GGC GGG GCA TTA CTT GCT CGA CTC GTA CAG GGG AAA TCG ACG TTA
2352
769 Lys Gly Gly Ala Leu Leu Ala Arg Leu Val Gln Gly Lys Ser Thr Leu 784

70 2353 GTA CAG TCG GCG GCT GGC GCG GCT GCC GGA GCG AGT TCA GCC GCG GCT
2400
785 Val Gln Ser Ala Ala Gly Ala Ala Ala Gly Ala Ser Ser Ala Ala Ala 800

	2401	TAT GGC GCA CGG GCA CAA GGT GTC GGT GTT GCA TCA GCC GCC GGG GCG	
5	2448 801	Tyr Gly Ala Arg Ala Gln Gly Val Gly Val Ala Ser Ala Ala Gly Ala	816
	2449	GTA ACA GGG GCT GTG GGA TCA TGG ATA AAT AAT GCT GAT CGG GGG ATT	
10	2496 817	Val Thr Gly Ala Val Gly Ser Trp Ile Asn Asn Ala Asp Arg Gly Ile	832
	2497	GGC GGC GCT ATT GGG GCC GGG AGT GCG GTA GGC ACC ATT GAT ACT ATG	
15	2544 833	Gly Gly Ala Ile Gly Ala Gly Ser Ala Val Gly Thr Ile Asp Thr Met	848
	2545	TTA GGG ACT GCC TCT ACC CTT ACC CAT GAA GTC GGG GCA GCG GCG GGT	
20	2592 849	Leu Gly Thr Ala Ser Thr Leu Thr His Glu Val Gly Ala Ala Ala Gly	864
	2593	GGG GCG GCG GGT GGG ATG ATC ACC GGT ACG CAA GGG AGT ACT CGG GCA	
25	2640 865	Gly Ala Ala Gly Gly Met Ile Thr Gly Thr Gln Gly Ser Thr Arg Ala	880
	2641	GGT ATC CAT GCC GGT ATT GGC ACC TAT TAT GGC TCC TGG ATT GGT TTT	
30	2688 881	Gly Ile His Ala Gly Ile Gly Thr Tyr Tyr Gly Ser Trp Ile Gly Phe	896
	2689	GGT TTA GAT GTC GCT AGT AAC CCC GCC GGA CAT TTA GCG AAT TAC GCA	
35	2736 897	Gly Leu Asp Val Ala Ser Asn Pro Ala Gly His Leu Ala Asn Tyr Ala	912
	2737	GTG GGT TAT GCC GCT GGT TTG GGT GCT GAA ATG GCT GTC AAC AGA ATA	
40	2784 913	Val Gly Tyr Ala Ala Gly Leu Gly Ala Glu Met Ala Val Asn Arg Ile	928
	2785	ATG GGT GGT GGA TTT TTG AGT AGG CTC TTA GGC CGG GTT GTC AGC CCA	
45	2832 929	Met Gly Gly Gly Phe Leu Ser Arg Leu Leu Gly Arg Val Val Ser Pro	944
	2833	TAT GCC GCC GGT TTA GCC AGA CAA TTA GTA CAT TTC AGT GTC GCC AGA	
50	2880 945	Tyr Ala Ala Gly Leu Ala Arg Gln Leu Val His Phe Ser Val Ala Arg	960
	2881	CCT GTC TTT GAG CCG ATA TTT AGT GTT CTC GGC GGG CTT GTC GGT GGT	
55	2928 961	Pro Val Phe Glu Pro Ile Phe Ser Val Leu Gly Gly Leu Val Gly Gly	976
	2929	ATT GGA ACT GGC CTG CAC AGA GTG ATG GGA AGA GAG AGT TGG ATT TCC	
60	2976 977	Ile Gly Thr Gly Leu His Arg Val Met Gly Arg Glu Ser Trp Ile Ser	992
	2977	AGA GCG TTA AGT GCT GCC GGT AGT GGT ATA GAT CAT GTC GCT-GGC ATG	
65	3024 993 1008	Arg Ala Leu Ser Ala Ala Gly Ser Gly Ile Asp His Val Ala Gly Met	
	3025	ATT GGT AAT CAG ATC AGA GGC AGG GTC TTG ACC ACA ACC GGG ATC GCT	
70	3072		

1009 Ile Gly Asn Gln Ile Arg Gly Arg Val Leu Thr Thr Thr Gly Ile Ala
1024

5 3073 AAT GCG ATA GAC TAT GGC ACC AGT GCT GTG GGA GCC GCA CGA CGA GTT
3120
1025 Asn Ala Ile Asp Tyr Gly Thr Ser Ala Val Gly Ala Ala Arg Arg Val
1040

10 3121 TTT TCT TTG TAA 3132
1041 Phe Ser Leu End 1043

15 (2) INFORMATION FOR SEQ ID NO:61

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1043 amino acids

(B) TYPE: amino acid

20 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61 (Tccc peptide)

25 1 Met Ser Pro Ser Glu Thr Thr Leu Tyr Thr Gln Thr Pro Thr Val Ser 16
17 Val Leu Asp Asn Arg Gly Leu Ser Ile Arg Asp Ile Gly Phe His Arg 32
30 33 Ile Val Ile Gly Gly Asp Thr Asp Thr Arg Val Thr Arg His Gln Tyr 48
49 Asp Ala Arg Gly His Leu Asn Tyr Ser Ile Asp Pro Arg Leu Tyr Asp 64
35 65 Ala Lys Gln Ala Asp Asn Ser Val Lys Pro Asn Phe Val Trp Gln His 80
81 Asp Leu Ala Gly His Ala Leu Arg Thr Glu Ser Val Asp Ala Gly Arg 96
97 Thr Val Ala Leu Asn Asp Ile Glu Gly Arg Ser Val Met Thr Met Asn 112
40 113 Ala Thr Gly Val Arg Gln Thr Arg Arg Tyr Glu Gly Asn Thr Leu Pro 128
129 Gly Arg Leu Leu Ser Val Ser Glu Gln Val Phe Asn Gln Glu Ser Ala 144
145 Lys Val Thr Glu Arg Phe Ile Trp Ala Gly Asn Thr Thr Ser Glu Lys 160
45 161 Glu Tyr Asn Leu Ser Gly Leu Cys Ile Arg His Tyr Asp Thr Ala Gly 176
177 Val Thr Arg Leu Met Ser Gln Ser Leu Ala Gly Ala Met Leu Ser Gln 192
50 193 Ser His Gln Leu Leu Ala Glu Gly Gln Glu Ala Asn Trp Ser Gly Asp 208
209 Asp Glu Thr Val Trp Gln Gly Met Leu Ala Ser Glu Val Tyr Thr Thr 224
225 Gln Ser Thr Thr Asn Ala Ile Gly Ala Leu Leu Thr Gln Thr Asp Ala 240
55 241 Lys Gly Asn Ile Gln Arg Leu Ala Tyr Asp Ile Ala Gly Gln Leu Lys 256
257 Gly Ser Trp Leu Thr Val Lys Gly Gln Ser Glu Gln Val Ile Val Lys 272
60 273 Ser Leu Ser Trp Ser Ala Ala Gly His Lys Leu Arg Glu Glu His Gly 288
289 Asn Gly Val Val Thr Glu Tyr Ser Tyr Glu Pro Glu Thr Gln Arg Leu 304
305 Ile Gly Ile Thr Thr Arg Arg Ala Glu Gly Ser Gln Ser Gly Ala Arg 320
65 321 Val Leu Gln Asp Leu Arg Tyr Lys Tyr Asp Pro Val Gly Asn Val Ile 336
337 Ser Ile His Asn Asp Ala Glu Ala Thr Arg Phe Trp Arg Asn Gln Lys 352

	353	Val	Glu	Pro	G	sn	Arg	Tyr	Val	Tyr	Asp	Ser	Leu	Gln	Leu	Met	368	
	369	Ser	Ala	Thr	Gly	Arg	Glu	Met	Ala	Asn	Ile	Gly	Gln	Gln	Ser	Asn	Gln	384
5	385	Leu	Pro	Ser	Pro	Val	Ile	Pro	Val	Pro	Thr	Asp	Asp	Ser	Thr	Tyr	Thr	400
	401	Asn	Tyr	Leu	Arg	Thr	Tyr	Thr	Tyr	Asp	Arg	Gly	Gly	Asn	Leu	Val	Gln	416
10	417	Ile	Arg	His	Ser	Ser	Pro	Ala	Thr	Gln	Asn	Ser	Tyr	Thr	Thr	Asp	Ile	432
	433	Thr	Val	Ser	Ser	Arg	Ser	Asn	Arg	Ala	Val	Leu	Ser	Thr	Leu	Thr	Thr	448
	449	Asp	Pro	Thr	Arg	Val	Asp	Ala	Leu	Phe	Asp	Ser	Gly	Gly	His	Gln	Lys	464
15	465	Met	Leu	Ile	Pro	Gly	Gln	Asn	Leu	Asp	Trp	Asn	Ile	Arg	Gly	Glu	Leu	480
	481	Gln	Arg	Val	Thr	Pro	Val	Ser	Arg	Glu	Asn	Ser	Ser	Asp	Ser	Glu	Trp	496
20	497	Tyr	Arg	Tyr	Ser	Ser	Asp	Gly	Met	Arg	Leu	Leu	Lys	Val	Ser	Glu	Gln	512
	513	Gln	Thr	Gly	Asn	Ser	Thr	Gln	Val	Gln	Arg	Val	Thr	Tyr	Leu	Pro	Gly	528
	529	Leu	Glu	Leu	Arg	Thr	Thr	Gly	Val	Ala	Asp	Lys	Thr	Thr	Glu	Asp	Leu	544
25	545	Gln	Val	Ile	Thr	Val	Gly	Glu	Ala	Gly	Arg	Ala	Gln	Val	Arg	Val	Leu	560
	561	His	Trp	Glu	Ser	Gly	Lys	Pro	Thr	Asp	Ile	Asp	Asn	Asn	Gln	Val	Arg	576
30	577	Tyr	Ser	Tyr	Asp	Asn	Leu	Leu	Gly	Ser	Ser	Gln	Leu	Glu	Leu	Asp	Ser	592
	593	Glu	Gly	Gln	Ile	Leu	Ser	Gln	Glu	Glu	Tyr	Tyr	Pro	Tyr	Gly	Gly	Thr	608
	609	Ala	Ile	Trp	Ala	Ala	Arg	Asn	Gln	Thr	Glu	Ala	Ser	Tyr	Lys	Phe	Ile	624
35	625	Arg	Tyr	Ser	Gly	Lys	Glu	Arg	Asp	Ala	Thr	Gly	Leu	Tyr	Tyr	Tyr	Gly	640
	641	Tyr	Arg	Tyr	Tyr	Gln	Pro	Trp	Val	Gly	Arg	Trp	Leu	Ser	Ala	Asp	Pro	656
40	657	Ala	Gly	Thr	Val	Asp	Gly	Leu	Asn	Leu	Tyr	Arg	Met	Val	Arg	Asn	Asn	672
	673	Pro	Ile	Thr	Leu	Thr	Asp	His	Asp	Gly	Leu	Ala	Pro	Ser	Pro	Asn	Arg	688
	689	Asn	Arg	Asn	Thr	Phe	Trp	Phe	Ala	Ser	Phe	Leu	Phe	Arg	Lys	Pro	Asp	704
45	705	Glu	Gly	Met	Ser	Ala	Ser	Met	Arg	Arg	Gly	Gln	Lys	Ile	Gly	Arg	Ala	720
	721	Ile	Ala	Gly	Gly	Ile	Ala	Ile	Gly	Gly	Leu	Ala	Ala	Thr	Ile	Ala	Ala	736
50	737	Thr	Ala	Gly	Ala	Ala	Ile	Pro	Val	Ile	Leu	Gly	Val	Ala	Ala	Val	Gly	752
	753	Ala	Gly	Ile	Gly	Ala	Leu	Met	Gly	Tyr	Asn	Val	Gly	Ser	Leu	Leu	Glu	768
	769	Lys	Gly	Gly	Ala	Leu	Leu	Ala	Arg	Leu	Val	Gln	Gly	Lys	Ser	Thr	Leu	784
55	785	Val	Gln	Ser	Ala	Ala	Gly	Ala	Ala	Ala	Gly	Ala	Ser	Ser	Ala	Ala	Ala	800
	801	Tyr	Gly	Ala	Arg	Ala	Gln	Gly	Val	Gly	Val	Ala	Ser	Ala	Ala	Gly	Ala	816
60	817	Val	Thr	Gly	Ala	Val	Gly	Ser	Trp	Ile	Asn	Asn	Ala	Asp	Arg	Gly	Ile	832
	833	Gly	Gly	Ala	Ile	Gly	Ala	Gly	Ser	Ala	Val	Gly	Thr	Ile	Asp	Thr	Met	848
	849	Leu	Gly	Thr	Ala	Ser	Thr	Leu	Thr	His	Glu	Val	Gly	Ala	Ala	Ala	Gly	864
65	865	Gly	Ala	Ala	Gly	Gly	Met	Ile	Thr	Gly	Thr	Gln	Gly	Ser	Thr	Arg	Ala	880
	881	Gly	Ile	His	Ala	Gly	Ile	Gly	Thr	Tyr	Tyr	Gly	Ser	Trp	Ile	Gly	Phe	896
70	897	Gly	Leu	Asp	Val	Ala	Ser	Asn	Pro	Ala	Gly	His	Leu	Ala	Asn	Tyr	Ala	912
	913	Val	Gly	Tyr	Ala	Ala	Gly	Leu	Gly	Ala	Glu	Met	Ala	Val	Asn	Arg	Ile	928

5 929 Met Gly Gly Gly Phe Leu Ser Arg Leu Leu Gly Arg Val Val Ser Pro 944
 945 Tyr Ala Ala Gly Leu Ala Arg Gln Leu Val His Phe Ser Val Ala Arg 960
 961 Pro Val Phe Glu Pro Ile Phe Ser Val Leu Gly Gly Leu Val Gly Gly 976
 977 Ile Gly Thr Gly Leu His Arg Val Met Gly Arg Glu Ser Trp Ile Ser 992
 10 993 Arg Ala Leu Ser Ala Ala Gly Ser Gly Ile Asp His Val Ala Gly Met 1008
 1009 Ile Gly Asn Gln Ile Arg Gly Arg Val Leu Thr Thr Thr Gly Ile Ala 1024
 1025 Asn Ala Ile Asp Tyr Gly Thr Ser Ala Val Gly Ala Ala Arg Arg Val 1040
 15 1041 Phe Ser Leu 1043

(2) INFORMATION FOR SEQ ID NO:62: TcaA_{iv}

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 25 (ii) MOLECULAR TYPE: protein
 (v) FRAGMENT TYPE: internal

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62: TcaA_{iv}
 30 Asn Ile Gly Gly Asp
 1 5

(2) INFORMATION FOR SEQ ID NO:63: TcaA_{ii}-syn

35

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 40 (ii) MOLECULAR TYPE: protein
 (v) FRAGMENT TYPE: internal

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63: TcaA_{ii}-syn
 45 Cys Leu Arg Gly Asn Ser Pro Thr Asn Pro Asp Lys Asp Gly Ile
 1 5 10 15
 Phe Ala Gln Val Ala
 20

50

(2) INFORMATION FOR SEQ ID NO:64: TcaA_{iii}-syn

55

(i) SEQUENCE CHARACTERISTICS;
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULAR TYPE: protein
 60 (v) FRAGMENT TYPE: Internal

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64: TcaA_{iii}-syn

 Cys Tyr Thr Pro Asp Gln Thr Pro Ser Phe Tyr Glu Thr Ala Phe

1
Arg Ser Ala Asp Gly
20

10

15

5 (2) INFORMATION FOR SEQ ID NO:65: TcaB_i-syn

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: Internal

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65: TcaB_i-syn

His Gly Gln Ser Tyr Asn Asp Asn Asn Tyr Cys Asn Phe Thr Leu
1 5 10 15
Ser Ile Asn Thr
19

20

(2) INFORMATION FOR SEQ ID NO:66: TcaB_{ii}-syn

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(ii) MOLECULAR TYPE: protein

30

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66: TcaB_{ii}-syn

Cys Val Asp Pro Lys Thr Leu Gln Arg Gln Gln Ala Gly Gly Asp
1 5 10 15
Gly Thr Gly Ser Ser
20

35

(2) INFORMATION FOR SEQ ID NO:67: TcaC-syn

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45

(ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67: TcaC-syn

50

Cys Tyr Lys Ala Pro Gln Arg Gln Glu Asp Gly Asp Ser Asn Ala
1 5 10 15
Val Thr Tyr Asp Lys
20

55

(2) INFORMATION FOR SEQ ID NO:68: TcbA_{ii}-syn

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68: TcbA_{ii}-syn

Cys	Tyr	Asn	Glu	Asn	Pro	Ser	Ser	Glu	Asp	Lys	Lys	Trp	Tyr	Phe
1				5					10					15
Ser	Ser	Lys	Asp	Asp										
				20										

(2) INFORMATION FOR SEQ ID NO:69: TcbA_{iii}-syn

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69: TcbA_{iii}-syn

Cys	Phe	Asp	Ser	Tyr	Ser	Gln	Leu	Tyr	Glu	Glu	Asn	Ile	Asn	Ala
1				5					10					15
Gly	Glu	Gln	Arg	Ala										
				20										

(2) INFORMATION FOR SEQ ID NO:70: TcdA_{ii}-syn

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70: TcdA_{ii}-syn

Cys	Asn	Pro	Asn	Asn	Ser	Ser	Asn	Lys	Leu	Met	Phe	Tyr	Pro	Val
1				5					10					15
Tyr	Gln	Tyr	Ser	Gly	Asn	Thr								
				20										

(2) INFORMATION FOR SEQ ID NO:71: TcdA_{iii}-syn

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71: TcdA_{iii}-syn

Val Ser Gln Gly Ser Gly Ser Ala Gly Ser Gly Asn Asn Asn Leu
 1 5 10 15
 Ala Phe Gly Ala Gly
 20

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULAR TYPE: protein
 (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72: 160 kDa - Hb

Met Gln Asp Ser Pro Glu Val Ala Ile Thr Thr Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULAR TYPE: protein
 (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73: 170 kDa - WIR

Met Gln Arg Ser Ser Glu Val Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULAR TYPE: protein
 (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74: 180 kDa - H9

Met Gln Asp Ile Pro Glu Val Gln Leu Asn
 1 5 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75: 170 kDa - Hm(2)
 INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULAR TYPE: protein
 (v) FRAGMENT TYPE: N-terminal

Met Gln Asp Ser Pro Glu Val Ser Val Thr Gln Asn

1

5

10

(2) INFORMATION FOR SEQ ID NO:76:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

- (ii) MOLECULAR TYPE: protein
- (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76: 74 kDa - H9

15

Ser Glu Ser Leu Phe Thr Gln Ser Leu Lys Glu Ala Arg Arg Asp
 1 5 10 15

20 (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25

- (ii) MOLECULAR TYPE: protein
- (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77: 71 kDa - Hb

30

Met Asn Leu Ile Glu Ala Lys Leu Gln Glu Asn Arg Asp Ala
 1 5 10

35

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

40

- (ii) MOLECULAR TYPE: protein
- (v) FRAGMENT TYPE: N-terminal

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78: 170 kDa - H9

Met Leu Ser Thr Met Glu Lys Gln Leu Asn Glu Ser Gln Arg Asp
 1 5 10 15

50

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

55

- (ii) MOLECULAR TYPE: protein
- (v) FRAGMENT TYPE: N-terminal

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79: 109 kDa - Hm

Met Leu Asp Ile Met Glu Lys Gln Leu Asn Glu Ser Glu Arg Asp
 1 5 10 15

65

(2) INFORMATION FOR SEQ ID NO:80:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 10 (ii) MOLECULAR TYPE: protein
 (v) FRAGMENT TYPE: N-terminal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80: 170 kDa - WX-1
 15 Met Gln Asp Ser Arg Glu Val Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:81:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear
 (ii) MOLECULAR TYPE: protein
 (v) FRAGMENT TYPE: N-terminal
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81: 69 kDa - H9
 30 Leu Arg Ser Ala Xxx Ser Ala Leu Thr Thr Leu Leu
 1 5 10

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 40 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULAR TYPE: protein
 (v) FRAGMENT TYPE: N-terminal
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82: 64 kDa - HP88
 Leu Lys Leu Ala Asp Asn Gly Tyr Phe Asn Glu Pro Leu Asn Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 55 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULAR TYPE: protein
 (v) FRAGMENT TYPE: N-terminal
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83: 70 kDa - NC-1
 Leu Lys Leu Ala Asp Asn Ser Tyr Phe Asn Glu Pro Leu Asn
 1 5 10 15
 65

(2) INFORMATION FOR SEQ ID NO:84:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
10 (ii) MOLECULAR TYPE: protein
(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84: 60 kDa - WIR
15 Ser Lys Asp Glu Ser Lys Ala Asp Ser Gln Leu Val Tyr His Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:85:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
25 (ii) MOLECULAR TYPE: protein
(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85: 58 kDa - NC-1
30 Met Lys Lys Arg Gly Leu Thr Thr Asn Ala Gly Ala Pro Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:86:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
40 (D) TOPOLOGY: linear
(ii) MOLECULAR TYPE: protein
(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86: 60 kDa - WX-12
45 Met Leu Asn Pro Ile Val Arg Lys Phe Glu Tyr Gly Glu His Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:87:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULAR TYPE: protein
(v) FRAGMENT TYPE: N-terminal

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87: 60 kDa - Hm
Ala Glu Ile Tyr Asn Lys Asp Gly Asn Lys Leu Asp Leu Tyr Gly
1 5 10 15

65

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: protein

- (v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88: 140 kDa - Hm

Asn Leu Ile Glu Ala Thr Leu Glu Gln Asn Leu Arg Asp Ala
1 5 10 15

We claim:

1. A composition, comprising an effective amount of a *Photorhabdus* protein toxin that has functional activity
5 against an insect.

2. The composition of Claim 1, wherein the *Photorhabdus* toxin is produced by a purified culture of *Photorhabdus*, a
10 transgenic plant, baculovirus, or heterologous microbial host.

3. The composition of Claim 2, wherein the *Photorhabdus* toxin produced by a purified culture of *Photorhabdus luminescens*.

4. The composition of Claim 2, wherein the toxin is
15 produced from a purified culture of *Photorhabdus luminescens* strain designated ATCC 55397.

5. The composition of Claim 2, wherein the toxin is
20 produced by a purified culture of *Photorhabdus luminescens* strain designated W-14.

6. The composition of Claim 1, wherein the toxin is
produced by a purified culture of *Photorhabdus* strain
25 designated WX-1, WX-2, WX-3, WX-4, WX-5, WX6, WX-7, WX-8, WX-9, WX-10, WX-11, WX-12, WX-14, WX-15, H9, Hb, Hm, HP88, NC-1, W30, WIR, B2, ATCC# 43948, ATCC# 43949, ATCC# 43950, ATCC# 43951, ATCC# 43952, DEP1, DEP2, DEP3, *P. zealandrica*, *P. hepialus*, HB-Arg, HB Oswego, HB Oswego, HB Lewiston, K-122,
30 HMGD, Indicus, GD, PWH-5, Megidis, HF-85, A. Cows, MP1, MP2, MP3, MP4, MP5, GL98, GL101, GL138, GL55, GL217, or GL257.

7. The composition of Claim 2, wherein the toxin is
produced from a purified culture of *Photorhabdus luminescens*
35 strain designated WX-1, WX-2, WX-3, WX-4, WX-5, WX-6, WX-7, WX-8, WX-9, WX-10, WX-11, WX-12, WX-14, WX-15, H9, Hb, Hm, HP88, NC-1, W30, WIR, B2, ATCC# 43948, ATCC# 43949, ATCC# 43950, ATCC# 43951, ATCC# 43952, DEP1, DEP2, DEP3, *P. zealandrica*, *P. hepialus*, HB-Arg, HB Oswego, HB Oswego, HB
40 Lewiston, K-122, HMGD, Indicus, GD, PWH-5, Megidis, HF-85, A. Cows, MP1, MP2, MP3, MP4, MP5, GL98, GL101, GL138, GL55, GL217, or GL257.

8. The composition of Claim 1, wherein the toxin is represented by amino acid sequence is SEQ ID NO:12.

5 9. The composition of Claim 6, wherein the composition is a mixture of one or more toxins produced from purified cultures of *Photorhabdus*.

10 10. The composition of Claim 1 or 6, wherein the insect is of the order *Lepidoptera*, *Coleoptera*, *Hymenoptera*, *Diptera*, *Dictyoptera*, *Acarina* or *Homoptera*.

15 11. The composition of Claim 1 or 6, wherein the insect species is from order *Coleoptera* and is Southern Corn Rootworm, Western Corn Rootworm, Colorado Potato Beetle, Mealworm, Boll Weevil or Turf Grub.

20 12. The composition of Claim 1 or 6, wherein the insect species is from order *Lepidoptera* and is Beet Armyworm, Black Cutworm, Cabbage Looper, Codling Moth, Corn Earworm, European Corn Borer, Tobacco Hornworm, or Tobacco Budworm.

25 13. The composition of Claim 1 or 6, wherein the toxin is formulated as a sprayable insecticide.

14. The composition of Claim 1 or Claim 6, wherein the toxin is formulated as a bait matrix and delivered in an above ground or below ground bait station.

30 15. A method of controlling an insect, comprising orally delivering to an insect an effective amount of a protein toxin that has functional activity against an insect, wherein the protein is produced by a purified bacterial culture of the genus *Photorhabdus*.

35 16. The method of Claim 15, wherein the bacterium is a purified culture of *Photorhabdus luminescens*.

40 17. The method of Claim 15, wherein the toxin is produced from a purified culture of *Photorhabdus luminescens* strain designated ATCC 55397.

18. The method of Claim 16, wherein the toxin is produced from a purified culture of *Photorhabdus luminescens* strain designated W-14.

5 19. The method of Claim 15, wherein the toxin is produced from a purified culture of *Photorhabdus* strains designated WX-1, WX-2, WX-3, WX-4, WX-5, WX-6, WX-7, WX-8, WX-9, WX-10, WX-11, WX-12, WX-14, WX-15, H9, Hb, Hm, HP88, NC-1, W30, WIR, B2, ATCC# 43948, ATCC# 43949, ATCC# 43950, ATCC#
10 43951, ATCC# 43952, DEP1, DEP2, DEP3, *P. zealandrica*, *P. hepialus*, HB-Arg, HB Oswego, HB Oswego, HB Lewiston, K-122, HMGD, Indicus, GD, PWH-5, Megidis, HF-85, A. Cows, MP1, MP2, MP3, MP4, MP5, GL98, GL101, GL138, GL155, GL217, or GL257.

15 20. The method of Claim 15, wherein the toxin is produced from a purified culture of *Photorhabdus luminescens* strains designated WX-1, WX-2, WX-3, WX-4, WX-5, WX-6, WX-7, WX-8, WX-9, WX-10, WX-11, WX-12, WX-14, WX-15, H9, Hb, Hm, HP88, NC-1, W30, WIR, B2, ATCC# 43948, ATCC# 43949, ATCC#
20 43950, ATCC# 43951, ATCC# 43952, DEP1, DEP2, DEP3, *P. zealandrica*, *P. hepialus*, HB-Arg, HB Oswego, HB Oswego, HB Lewiston, K-122, HMGD, Indicus, GD, PWH-5, Megidis, HF-85, A. Cows, MP1, MP2, MP3, MP4, MP5, GL98, GL101, GL138, GL155,
25 GL217, or GL257.

21. The method of Claim 19, wherein a mixture of one or more toxins is produced from a purified culture of *Photorhabdus* and said toxins are orally delivered to an
30 insect.

22. The method of Claim 15, wherein the toxin is produced by a prokaryotic host transformed with a gene encoding the toxin.

35 23. The method of Claim 15, wherein the toxin is produced by a eukaryotic host transformed with a gene encoding the toxin.

40 24. The method of Claim 23, wherein the eukaryotic host is baculovirus.

25. The method of Claim 15 or 19, wherein insect is of the order *Lepidoptera*, *Coleoptera*, *Hymenoptera*, *Diptera*, *Dictyoptera*, *Acarina* or *Homoptera*.

26. The method of Claim 15 or 19, wherein the insect species is from order *Coleoptera* and is Southern Corn Rootworm, Western Corn Rootworm, Colorado Potato Beetle, Mealworm, Boll Weevil or Turf Grub.

27. The method of Claim 15 or 19, wherein the insect species is from order *Lepidoptera* and is Beet Armyworm, Black Cutworm, Cabbage Looper, Codling Moth, Corn Earworm, European Corn Borer, Tobacco Hornworm, or Tobacco Budworm.

28. The method of Claim 15 or 19, wherein the toxin is formulated as a sprayable insecticide.

29. The method of Claim 15 or Claim 19, wherein the toxin is formulated as a bait matrix and delivered in an above ground or below ground bait station.

30. A method of isolating a gene coding for a protein subunit, comprising the steps of: constructing at least one RNA or DNA oligonucleotide molecule that corresponds to at least a part of a DNA coding region of an amino acid sequence selected from a group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:62, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, and SEQ ID NO:88, wherein the nucleotide molecule is used to isolate genetic material from *Photobacterium* or *Photobacterium luminescens*.

31. A method for expressing a protein produced by a purified bacterial culture of the genus *Photobacterium* in a prokaryotic or eukaryotic host in an effective amount so that

the protein has functional activity against an insect, wherein the method comprises: constructing a chimeric DNA construct having 5' to 3' a promoter, a DNA sequence encoding a protein, a transcription terminator, and then transferring the chimeric
5 DNA construct into the host.

32. The method of Claim 31, wherein the protein has functional activity against insects selected from a group consisting of *Coleoptera*, *Lepidoptera*, *Diptera*, *Homoptera*,
10 *Hymenoptera*, *Dictyoptera*, and *Acarina*.

33. The method of Claim 31, wherein the protein encoded by the DNA sequence has an N-terminal amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID
15 NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:36, SEQ ID NO:37,
20 SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:62, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID
25 NO:87, and SEQ ID NO:88.

34. The method of Claim 31, wherein the protein encoded by the DNA sequence includes the amino acid sequence selected from the group consisting of SEQ ID NO:12, SEQ ID NO:26, SEQ
30 ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, and SEQ ID NO:61.

35. A chimeric DNA construct, adapted for expression in a prokaryotic or eukaryotic host comprising, 5' to 3' a transcriptional promoter active in the host; a DNA sequence encoding a *Photorhabdus* protein that has functional activity against an insect; and a transcriptional terminator.

40 36. A chimeric DNA construct of Claim 35, wherein the protein encoded by the DNA sequence has an N-terminal amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ

ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10,
SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ
ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID
NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:36,
5 SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID
NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:62, SEQ ID NO:72,
SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID
NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81,
SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID
10 NO:86, SEQ ID NO:87, and SEQ ID NO:88.

37. The chimeric DNA construct of Claim 35, wherein the
protein encoded by the DNA sequence has an amino acid sequence
selected from the group consisting of SEQ ID NO:12, SEQ ID
15 NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34,
SEQ ID NO:35, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID
NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, and SEQ ID
NO:61.

20 38. The chimeric DNA construct of Claim 35, wherein the
DNA sequence encoding the *Photobacterium luminescens* protein is
selected from the group comprising SEQ ID NO:11, SEQ ID NO:25,
SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID
NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54,
25 SEQ ID NO:56, SEQ ID NO:58, and SEQ ID NO:60.

39. The chimeric DNA construct of Claim 35, wherein the
host is baculovirus or a plant cell.

30 40. An isolated and substantially purified preparation
comprising, a DNA molecule capable of encoding an effective
amount of a protein that is produced by a bacterium of the
genus *Photobacterium* and that has functional activity against an
insect.

35 41. The preparation of Claim 40, wherein the bacterium
is *Photobacterium luminescens*.

40 42. A purified preparation comprising, a protein
produced by *Photobacterium* or *Photobacterium luminescens* having an
N-terminal amino acid sequence selected from the group
consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID
NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ

ID NO:9, SEQ ID NO:10, SEQ ID NO: 13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:62, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, and SEQ ID NO:88.

10

43. A purified protein preparation comprising, a protein that has an N-terminal amino acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, and SEQ ID NO:10, SEQ ID NO: 13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:62, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, and SEQ ID NO:88.

25

44. A purified protein preparation comprising, a protein selected from the group of SEQ ID NO:12, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, and SEQ ID NO:61.

30

45. A purified DNA preparation comprising, a DNA sequence selected from the group consisting of SEQ ID NO:11, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58 and SEQ ID NO:60, wherein the DNA sequence is isolated from its native host.

35

46. A purified protein preparation comprising, a *Photorhabdus luminescens* protein with at least one subunit having an approximate molecular weight between 18 kDa to about 230 kDa; between about 160 kDa to about 230 kDa; 100 kDa to

40

160 kDa; about 80 kDa to about 100 kDa; or about 50 kDa to about 80 kDa.

47. A purified protein preparation comprising, a
5 *Photobacterium luminescens* protein with at least one subunit having an approximate molecular weight of about 280 kDa.

48. A substantially pure microorganism culture comprising, ATCC 55397.

49. The culture of Claim 48, wherein the culture is a derivative of ATCC 55397 that produces a protein toxin that has functional activity against an insect.

50. A transgenic plant comprising in its genome, a chimeric artificial gene construction imbuing the plant with an ability to express an effective amount of a *Photobacterium* protein that has functional activity against an insect.

51. The transgenic plant of Claim 50, wherein the plant is transformed using acceleration of genetic material coated onto microparticles directly into cells, *Agrobacteria*, whiskers, or electroporation techniques

52. The transgenic plant of Claim 50, wherein the selectable marker is selected from the group consisting of kanamycin, neomycin, glyphosate, hygromycin, methotrexate, phosphinothricin (bialophos), chlorosulfuron, bromoxynil, dalapon and the like.

53. The transgenic plant of Claim 50, wherein the promoter is selected from the group consisting of octopine synthase, nopaline synthase, mannopine synthase, 35S, 19S, 35T, ribulose-1,6-bisphosphate (RUBP) carboxylase small subunit (ssu), beta-conglycinin, phaseolin, alcohol dehydrogenase (ADH), heat-shock, ubiquitin, zein, oleosin, napin, or acyl carrier protein (ACP).

54. The transgenic plant of Claim 50, wherein embryogenic tissue, callus tissue type I or II, hypocotyl, meristem, or plant tissue during dedifferentiation is used in preparing the transgenic plant.

55. The transgenic plant of Claim 50, wherein the chimeric gene is a DNA sequence which encodes a *Photorhabdus* protein that has functional activity against an insect and at least one codon of the gene has been modified so that the codon is a plant preferred codon.

56. A method of controlling an insect comprising orally delivering to an insect an effective amount of a protein toxin, wherein the protein is produced by a transgenic plant, which said insect feeds.

57. A composition of matter, comprising a purified DNA sequence from a purified bacterial culture from the genus *Photorhabdus*.

58. A substantially pure microorganism culture comprising, H9.

59. A substantially pure microorganism culture comprising, Hb.

60. A substantially pure microorganism culture comprising, Hm.

61. A substantially pure microorganism culture comprising, HP88.

62. A substantially pure microorganism culture comprising, NC-1.

63. A substantially pure microorganism culture comprising, W30.

64. A substantially pure microorganism culture comprising,

WIR.

65. A substantially pure microorganism culture comprising,

5 B2.

66. A substantially pure microorganism culture comprising, *P. zealandrica*.

10 67. A substantially pure microorganism culture comprising, *P. hepialus*.

68. A substantially pure microorganism culture comprising, HB-Arg.

15

69. A substantially pure microorganism culture comprising, HB Oswego.

70. A substantially pure microorganism culture comprising, HB Lewiston.

20

71. A substantially pure microorganism culture comprising, K-122.

72. A substantially pure microorganism culture comprising, HMGD.

25

73. A substantially pure microorganism culture comprising, Indicus.

30

74. A substantially pure microorganism culture comprising, GD.

75. A substantially pure microorganism culture comprising, PWH-5.

35

76. A substantially pure microorganism culture comprising, Megidis.

77. A substantially pure microorganism culture comprising, HF-85.

40

78. A substantially pure microorganism culture comprising, A. Cows.

5 79. A substantially pure microorganism culture comprising, MP1.

80. A substantially pure microorganism culture comprising, MP2.

10 81. A substantially pure microorganism culture comprising, MP3.

15 82. A substantially pure microorganism culture comprising, MP4.

83. A substantially pure microorganism culture comprising, MP5.

20 84. A substantially pure microorganism culture comprising, GL98.

85. A substantially pure microorganism culture comprising, GL155.

25 86. A substantially pure microorganism culture comprising, GL101.

30 87. A substantially pure microorganism culture comprising, GL138.

88. A substantially pure microorganism culture comprising, GL217.

35 89. A substantially pure microorganism culture comprising, GL257.

40 90. A method of making an antibody against a protein fragment that is part of a protein having functional activity, where the protein is produced by bacteria of the *Enterobacteraceae* family, wherein the method comprises:

a) isolating a fragment of the protein, where the protein fragment is at least six amino acids;

b) immunizing a mammalian species with the protein fragment; and

5 c) harvesting serum containing antibody or antibody from the spleen of the mammalian species, where the antibody harvested is antibody to the protein fragment having functional activity.

10 91. The method of Claim 1, wherein the protein fragment is selected from the group consisting of SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, and SEQ ID NO:71.

15 92. The method of Claim 90, wherein the bacteria is from the genus *Photothabdus*.

93. The method of Claim 90, wherein the bacteria is from the genus *Photothabdus luminescens*.

20 94. A method of selecting a DNA fragment which encodes a portion of a protein that has functional activity, where the protein is produced from a bacteria of the *Enterobacteraceae* family, wherein the method comprises:

25 a) isolating a fragment of the DNA sequence having at least 30 nucleotides;

30 b) tagging the DNA fragment with a radioactive or chemical agent;

c) hybridizing the DNA fragment to a DNA library, where the DNA library is an *Enterobacteraceae* cDNA or *Enterobacteraceae* genomic library; and.

35 d) selecting the fragment that is hybridized to the DNA in the library that encodes for the protein that has functional activity.

40 95. The method of Claim 94, wherein the bacteria is from the genus *Photothabdus*.

96. The method of Claim 95, wherein the bacteria is from the genus *Photorhabdus luminescens*.

5 97. A method of selecting a DNA fragment which encodes a portion of a protein that has functional activity, where the protein is produced from a bacteria of the *Enterobacteraceae* family, wherein the method comprises:

10 a) isolating at least two primers, where a primer is a fragment of DNA having at least twelve nucleotides;

b) using the primers from step a), amplifying a DNA fragment from *Enterobacteraceae* by using primers with polymerase chain reaction technology and purifying the DNA
15 fragment;

c) tagging the purified DNA fragment with a radioactive or chemical agent;

20 d) hybridizing the purified DNA fragment to a DNA library, where the DNA library is an *Enterobacteraceae* cDNA or *Enterobacteraceae* genomic library;.and

25 e) selecting a DNA fragment that is equal or larger in size to the purified DNA fragment from the library, where the selected DNA fragment or portion thereof encodes for a protein that has functional activity.

30 98. The method of Claim 97, wherein the bacteria is from the genus *Photorhabdus*.

99. The method of Claim 98, wherein the bacteria is from the genus *Photorhabdus luminescens*.

35

1 ATG CAG GAT TGT CCG GAA GTA TCG ATT ACA ACG CTG TCA CTT CCG AAA GGT GGC GGT
 TAC GTC CTA ACA GGC CTT CAT AGC TAA TGT TGC GAC AGT GAA GCG TTT CCA CCG CCA
 1 Met Gln Asp Cys Pro Glu Val Ser Ile Thr Thr Leu Ser Leu Pro Lys Gly Gly Gly
 P2Psh
 58 GCT ATC AAT GGC ATG GGA GAA GCA CTG AAT GCT GGC GGC OCT GAT GGA ATG GGC TOC
 CGA TAG TTA CCG TAC OCT CTT CGT GAC TTA CGA CCG CCG GGA CTA OCT TAC CCG AGG
 20 Ala Ile Asn Gly Met Gly Glu Ala Leu Asn Ala Ala Gly Pro Asp Gly Met Ala Ser
 115 CTA TCT CTG CCA TTA CCG CTT TCG AOC GGC AGA GGG ACG OCT CCT GGA TTA TOG CTG
 GAT AGA GAC GGT AAT GGG GAA AGC TGG CCG TCT CCG TGC CGA GGA OCT AAT AGC GAC
 39 Leu Ser Leu Pro Leu Pro Leu Ser Thr Gly Arg Gly Thr Ala Pro Gly Leu Ser Leu
 172 ATT TAC AGC AAC AGT GCA GGT AAT GGG CTT TTC GGC ATC GGC TGG CAA TGC GGT GTT
 TAA ATG TCG TTG TCA CGT CCA TTA CCG GGA AGC CCG TAG CCG AOC GTT ACG CCA CAA
 58 Ile Tyr Ser Asn Ser Ala Gly Asn Gly Pro Phe Gly Ile Gly Trp Gln Cys Gly Val
 229 ATG TOC ATT AGC CGA CCG ACC CAA CAT GGC CTT CAA CAT TGA CGA CGT
 TAC AGG TAA TCG GCT CCG TGG GTT GTA CCG GAA GTT GTA ACT GCT GCA
 77 Met Ser Ile Ser Arg Arg Thr Gln His Gly Leu Gln His ... Arg Arg
 P2.3.5R

FIG. 1

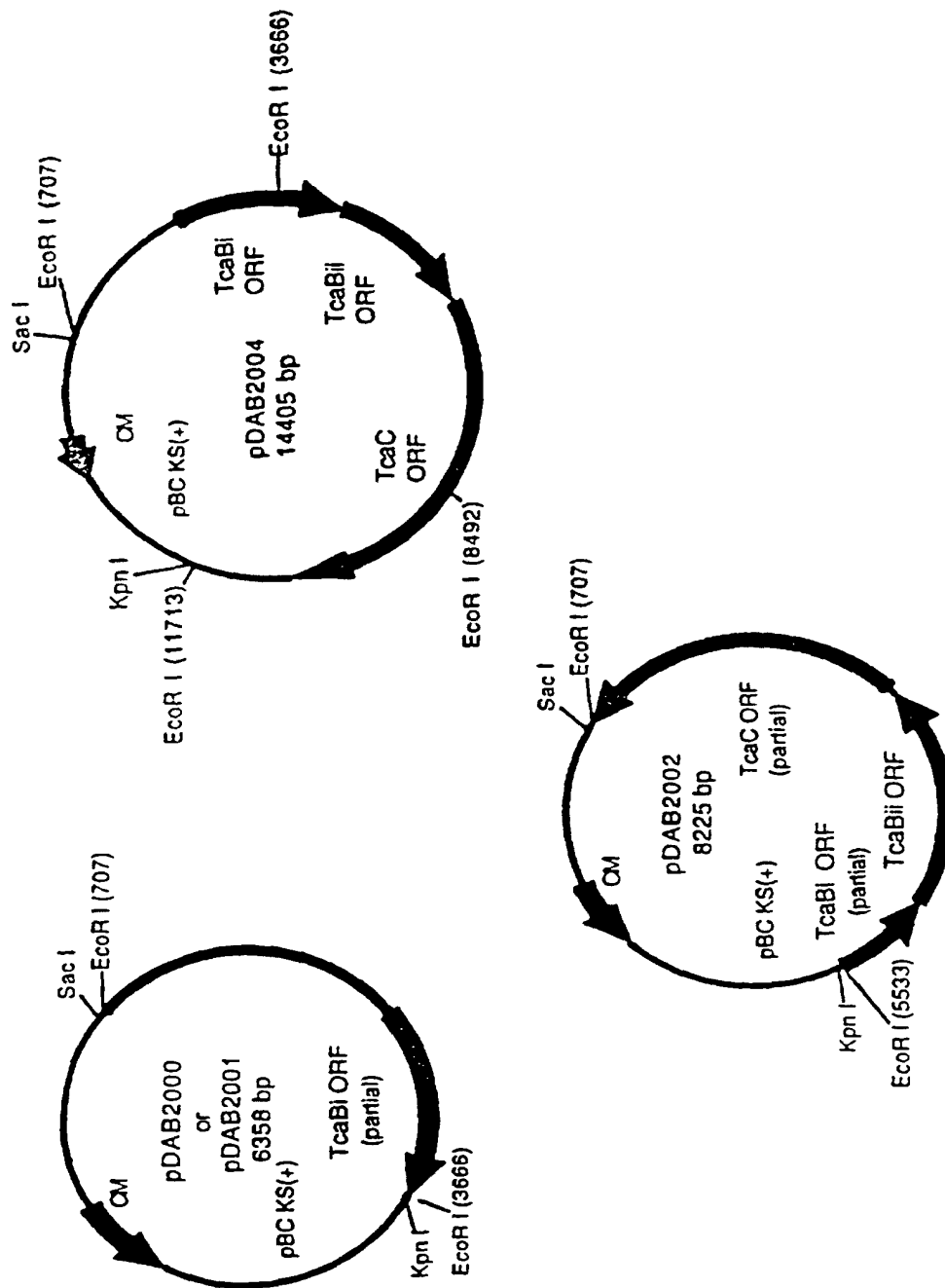


FIG. 2 Plasmids used in sequencing the *tca* locus. CM = Chloramphenicol resistance gene.
ORF = Open Reading Frame

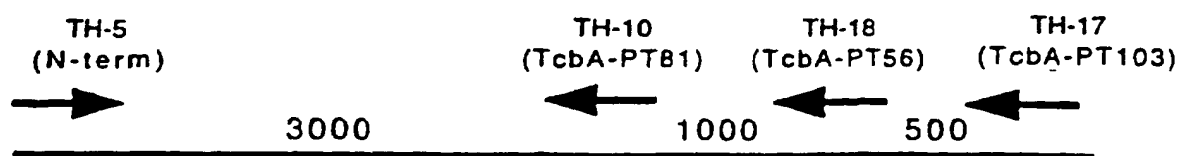


FIG. 3 Physical Map of DNA fragments of *tcb* locus.
Estimated distance between fragments given in nucleotides.

TcbA	1740	1750	1760	1770	1780
	SSAQALKND	EPMDFSGANA	LYFWELFYTT	PMMMAHRLLO	EQNFDAAHWH
TcaBi	gS	nPvDFSGpyg	iYlWEiFfhi	PflvtvRmqt	EQryedAdtw>
	~	~	~	~	~
TcbA	1790	1800	1810	1820	1830
	FRYVWSPSGY	IVDGKIAIYH	WVVRPLEEDT	SWNAQQLDST	DPDAVAQDDP
TcaBi	rdangql	ImDGskprY-	WNVmPLqldT	awdttQpatT	DPDviAmaDP>
	~	~	~	~	~
TcbA	1840	1850	1860	1870	1880
	MHYKVATFMA	TLDLLMARGD	AAYRQLERDT	LAEAKMWYTO	ALNLLGDEPO
TcaBi	540	550	560	570	580
	MHYKlaiflh	TLDLLiARGD	sAYRQLERDT	LvEAKMyYiQ	AqqLLGprPd>
	~	~	~	~	~
TcbA	1890	1900	1910	1920	1930
	VMLSTTWANP	TLGNAASKTT	QQVRQQVLTO	LRLNSRVKTP	LLGTANSLTA
TcaBi	ihctnTWpNP	TLsk>			
	~	~			
TcbA	1940	1950	1960	1970	1980
	LFLPQENSKL	KGYWRTLAQR	MFNLRHNLST	DGQPLSLPLY	AKPADPKALL
TcaBii	20	30	40	50	60
	_FLPpyNdvL	lGYWdkLeIR	lyNLRHNLST	DGQPLnLPLY	AtPvDPKtLq>
	~	~	~	~	~
TcbA	1990	2000	2010	2020	2030
	SAAVSASQGG	ADLPKAPLTI	HRFPQMLEGA	RGLVNQLIQF	GSSLLGYSER
TcaBii	70	80	90	100	110
	rqqaggdgtG	sspaggqgsV	qRyPlivErA	RsaVslLtQF	GnSLgttLEh>
	~	~	~	~	~
TcbA	2040	2050	2060	2070	2080
	QDAEAMSQLL	QTOASELILT	SIRMQDNQLA	ELDSEKTALQ	VSLAGVQORF
TcaBii	120	130	140	150	160
	QDnEkMtill	QTOqeailkh	ghdiQgNnLk	gLqhsLTALQ	aSrdGdtlRq>
	~	~	~	~	~

FIG. 4A

FIG. 4B

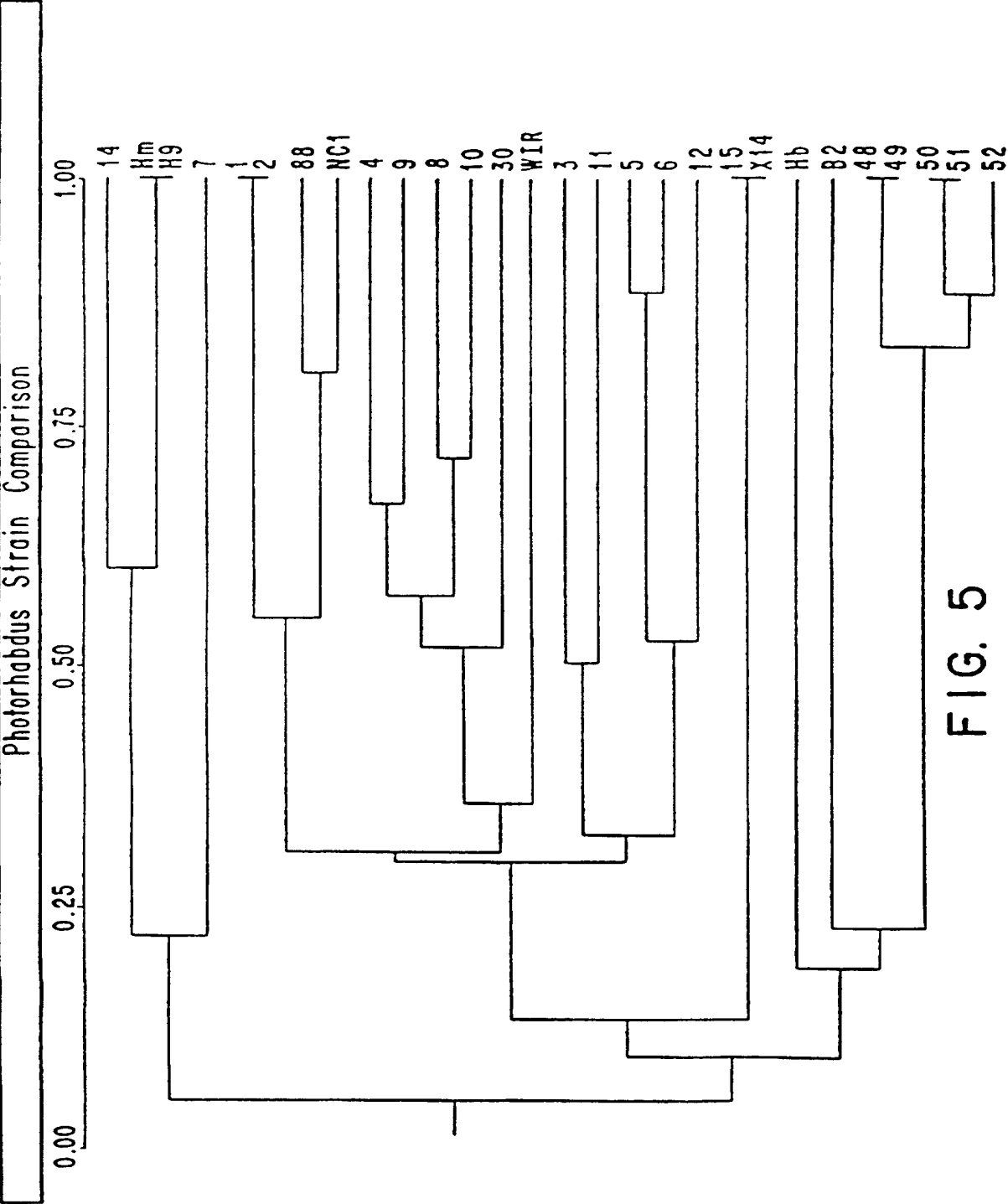


FIG. 5

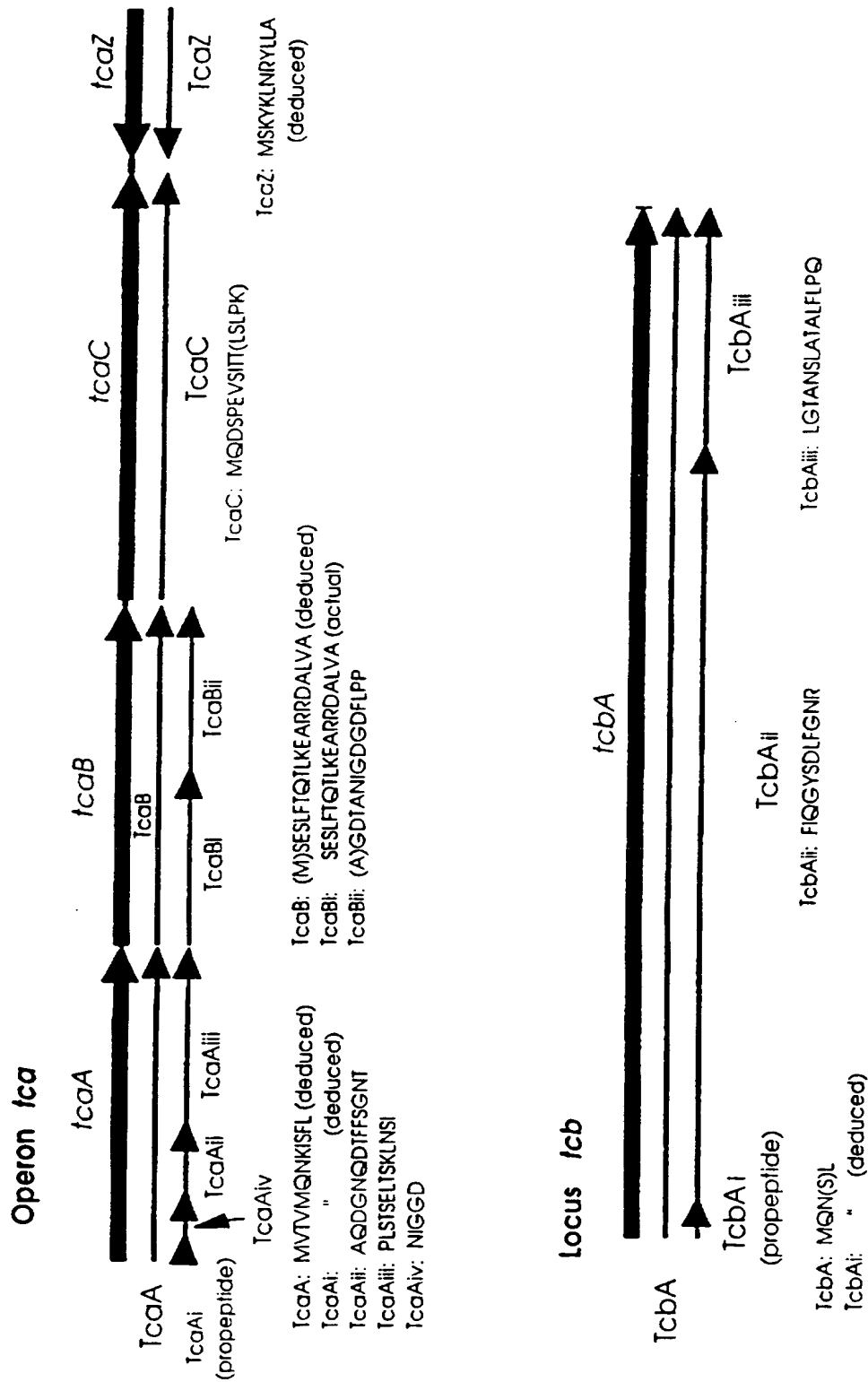
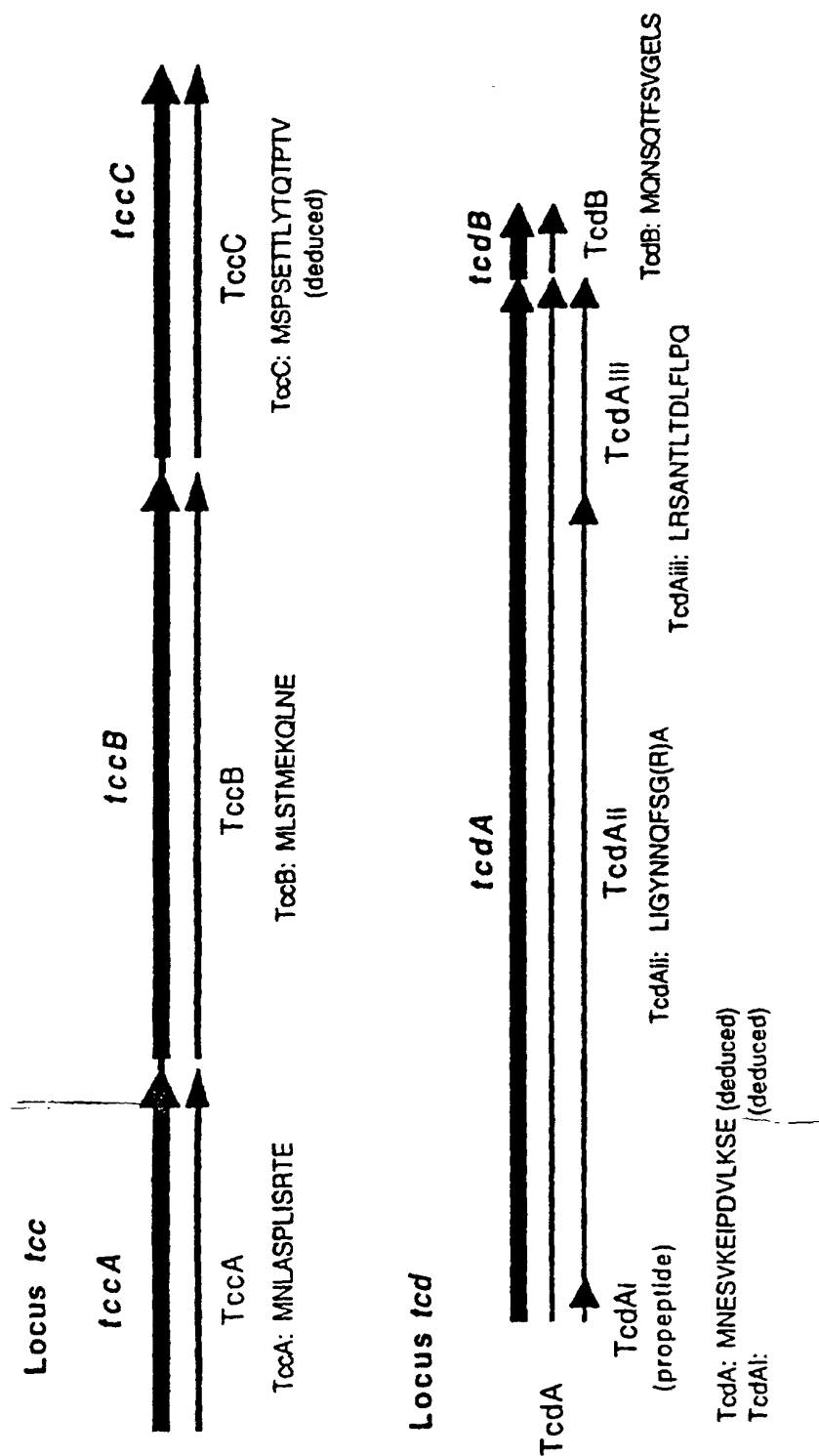


FIG.6A loci *tca* and *tcb*, primary gene products, and derived peptides

FIG. 6B Loci *tcc* and *tcd*, primary gene products, and derived peptides.

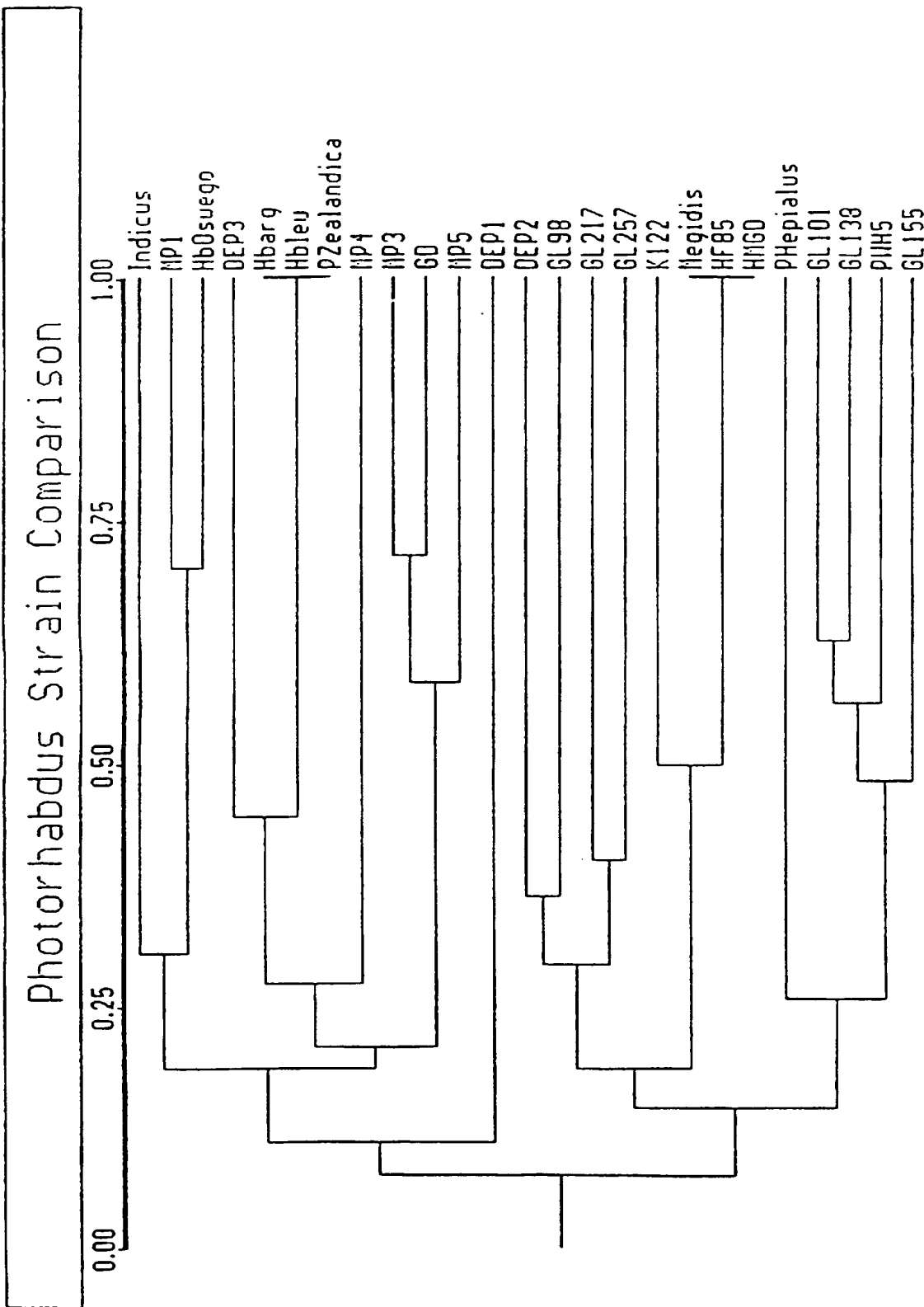


FIG. 7

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/07657**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) :Please See Extra Sheet.

US CL :Please See Extra Sheet.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.1, 172.1, 172.3, 243, 252.3, 320.1, 419; 530/350, 536/23.7, 24.1; 800/205, 250

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, CABA, CAPLUS, BIOSIS, MEDLINE, GENBANK, SCISEARCH

search terms: insecticide, protein, photorhabdus, xenorhabdus, transgenic, transformed, plant

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WILSON et al. Laboratory tests of the potential of entopathogenic nematodes for the control of field slugs. Journal of invertebrate Pathology. 1994, Vol. 64, pages 182-187.	1-99
Y	CLARKE et al. Virulence mechanisms of Photorhabdus sp. strain K122 toward wax moth larvae. Journal of Invertebrate Pathology. 1995, Vol. 66, pages 149-155.	1-99
Y	VAECK et al. Transgenic plants protected from insect attack. Nature. July 1987, vol. 328, pages 33-37.	1-99

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X*	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y*	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Z*	document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means		
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

15 AUGUST 1997

Date of mailing of the international search report

03 SEP 1997

Name and mailing address of the ISA/US
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Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.

PCT/7/07657

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6):

C12N 1/00, 1/20, 15/00, 15/09, 15/10, 15/29, 15/31, 15/82; A01G 13/00; A01H 1/00, 3/00, 4/00, 5/00

A. CLASSIFICATION OF SUBJECT MATTER:

US CL :

435/69.1, 172.1, 172.3, 243, 252.3, 320.1, 419; 530/350, 536/23.7, 24.1; 800/205, 250

1 ATG CAG GAT TGT CCG GAA GTA TCG ATT ACA ACG CTG TCA CTT CCG AAA GGT GGC GGT
 TAC GTC CTA ACA GGC CTT CAT ACC TAA TGT TCC GAC AGT GAA GCG TTT CCA CCG CCA
 1 Met Gln Asp Cys Pro Glu Val Ser Ile Thr Thr Leu Ser Leu Pro Lys Gly Gly Gly
 P2Psh
 58 GCT ATC AAT GGC ATG GGA GAA GCA CTG AAT GCT GGC GGC CTT GAT GGA ATG GGC TCC
 CGA TAG TTA CCG TAC CCT CTT CGT GAC TTA CGA CCG CCG GGA CTA CTT TAC CCG AGG
 20 Ala Ile Asn Gly Met Gly Glu Ala Leu Asn Ala Ala Gly Pro Asp Gly Met Ala Ser
 115 CTA TGT CTG CCA TTA CTT CCG ACG GGC ACG GGC CTT CTT GGA TTA TCG CTG
 GAT ACG GAC GGT AAT GCG GAA AGC TGG CCG TCT CTT CCG GGA CTT AAT AGC GAC
 39 Leu Ser Leu Pro Leu Pro Leu Ser Thr Gly Arg Gly Thr Ala Pro Gly Leu Ser Leu
 172 ATT TAC AGC AAC AGT GCA GGT AAT GCG CTT TTC GGC ATC GGC TGG CAA TGC GGT GGT
 TAA ATG TCG TTG TCA GGT CCA TTA CCG GAA AAG CCG TAG CCG ACC GTT ACG CCA CAA
 58 Ile Tyr Ser Asn Ser Ala Gly Asn Gly Pro Phe Gly Ile Gly Tyr Gln Cys Gly Val
 229 ATG TCC ATT AGC CGA CCG ACC CAA CAT GGC CTT CAA CAT TGA CCA CGT
 TAC AGG TAA TCG GCT GCG TGG GGT GTA CCG GAA GTT GTA ACT GCT GCA
 77 Met Ser Ile Ser Arg Arg Thr Gln His Gly Leu Gln His ... Arg Arg
 P2.3.5R

FIG. 1

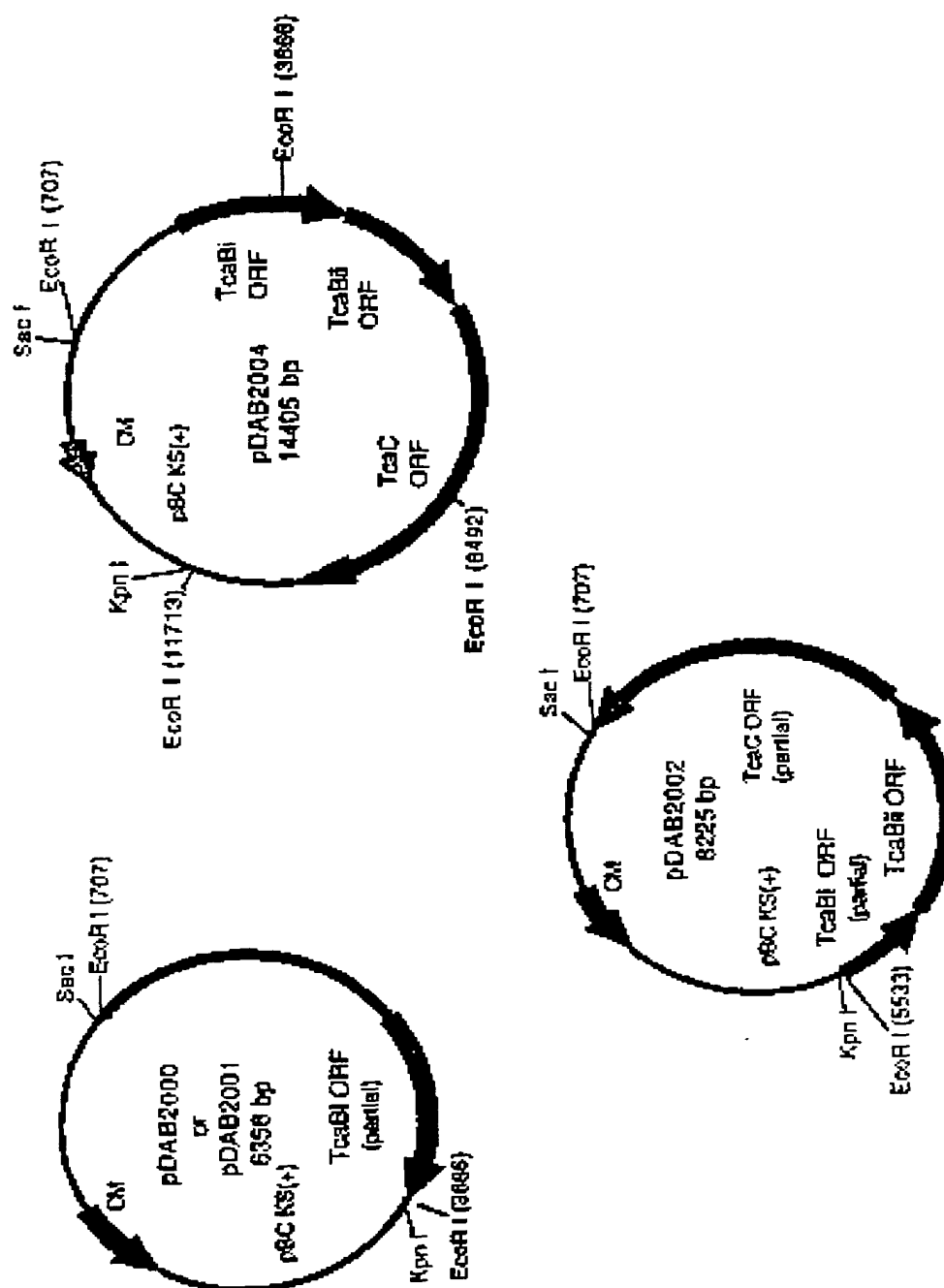


FIG. 2 Plasmids used in sequencing the *tca* locus. CM = Chloramphenicol resistance gene.
ORF = Open Reading Frame

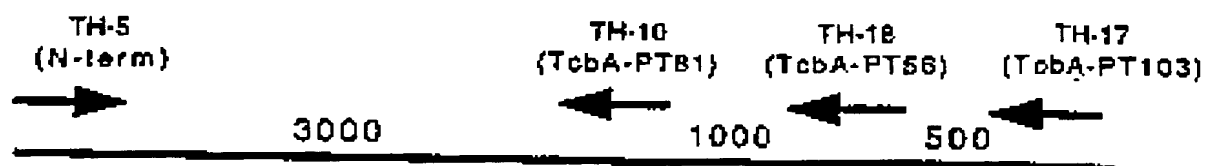


FIG. 3 Physical Map of DNA fragments of *fcb* locus.
Estimated distance between fragments given in nucleotides.

FIG. 4A

TcbA	2090	2100	2110	2120	2130
	DSYSQLYERN	INAGEQRALA	LRSESAIESQ	GAQISRMAGA	GVDNAPNIPG
TcaBii	170	180	190	200	210
	khYSdLingg	lsAAElaqLt	LRStamI-tn	Gvatglliaq	GinavPNvFG>
	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
TcbA	2140	2150	2160	2170	2180
	LADGGHFTGA	IAYALADGIE	LSASANKVDA	EKVAOSEIYR	RRRQEMKIQR
TcaBii	220	230	240	250	260
	LANGGsewGA	pligsqgqtq	vgAgIqqtSA	gisevtagYq	RRqeSWalQR>
	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
TcbA	2190	2200	2210	2220	2230
	DNAQAEINQL	NAQLESLSIR	REAAEMOKEY	LKTQQAQAQA	QLTFLRSKFS
TcaBii	270	280	290	300	310
	DiAdnEItQL	daQiqSLgeg	itmAgkQitl	seTeQAnAQA	iydlqttrFE>
	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
TcbA	2240	2250	2260	2270	2280
	NQALYSWLRG	RLSGIYTFQY	DLAVERCLMA	EDSYQWEAND	NSISFVKPGA
TcaBii	320	330	340	350	360
	gQALYmWmag	RLSalkYQmY	DstlpiCLqp	kaalvqEgek	eSdSlfgvpr>
	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
TcbA	2290	2300	2310	2320	2330
	WQTYAGLLC	GEALIQNLAQ	MEEAYLKWES	RALEVERTVS	LAWVYNLEG
TcaBii	370	380	390	400	410
	WndlwqGLia	GEglsaelqk	ldaiwLargg	igLEaiRTVS	Ldtlfgt--Q>
	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
TcbA	2340	2350	2360	2370	2380
	NDRFNLAEOI	PALLDKGGGT	AGYNNKGLSL	ANAILSASVK	LSDLKLCTDY
TcaBii	420	430	440	450	
	----ELaEmI	nkyLn-GEtv	spaggtlLaL	tgdlfgatld	LSgIgLdneY>
	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
TcbA	2390	2400	2410	2420	2430
	PDSIVGSKKV	RRIKQISVEL	PAZVGPYQDV	QAMLSYGCST	QLPKGCsAIA
TcaBii	460	470	480	490	500
	-n--lGneKk	RRIKrlaVEL	PeLIgFYQDI	eatLvtQaea	alshGvndgg>
	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
TcbA	2440	2450	2460	2470	
	VSHGTNDSCQ	FQLDPNDGKY	LPFEGIALDD	QGTLMLOFPN	
TcaBii	510	520	530		
	rfvtdfnder	F-LpF-eGrd	attgtleln>		
	~~~~~	~~~~~	~~~~~		

FIG. 4B

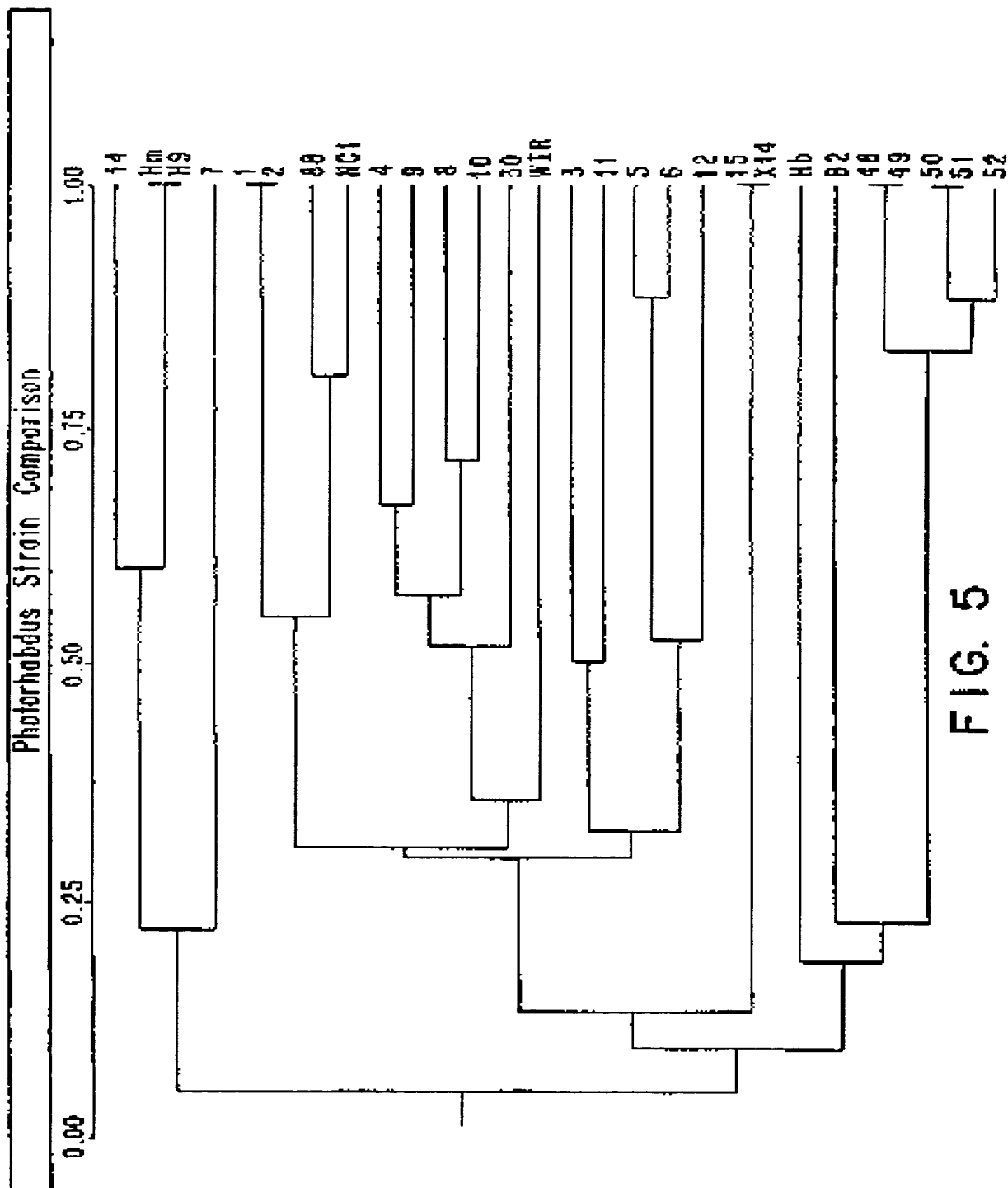


FIG. 5

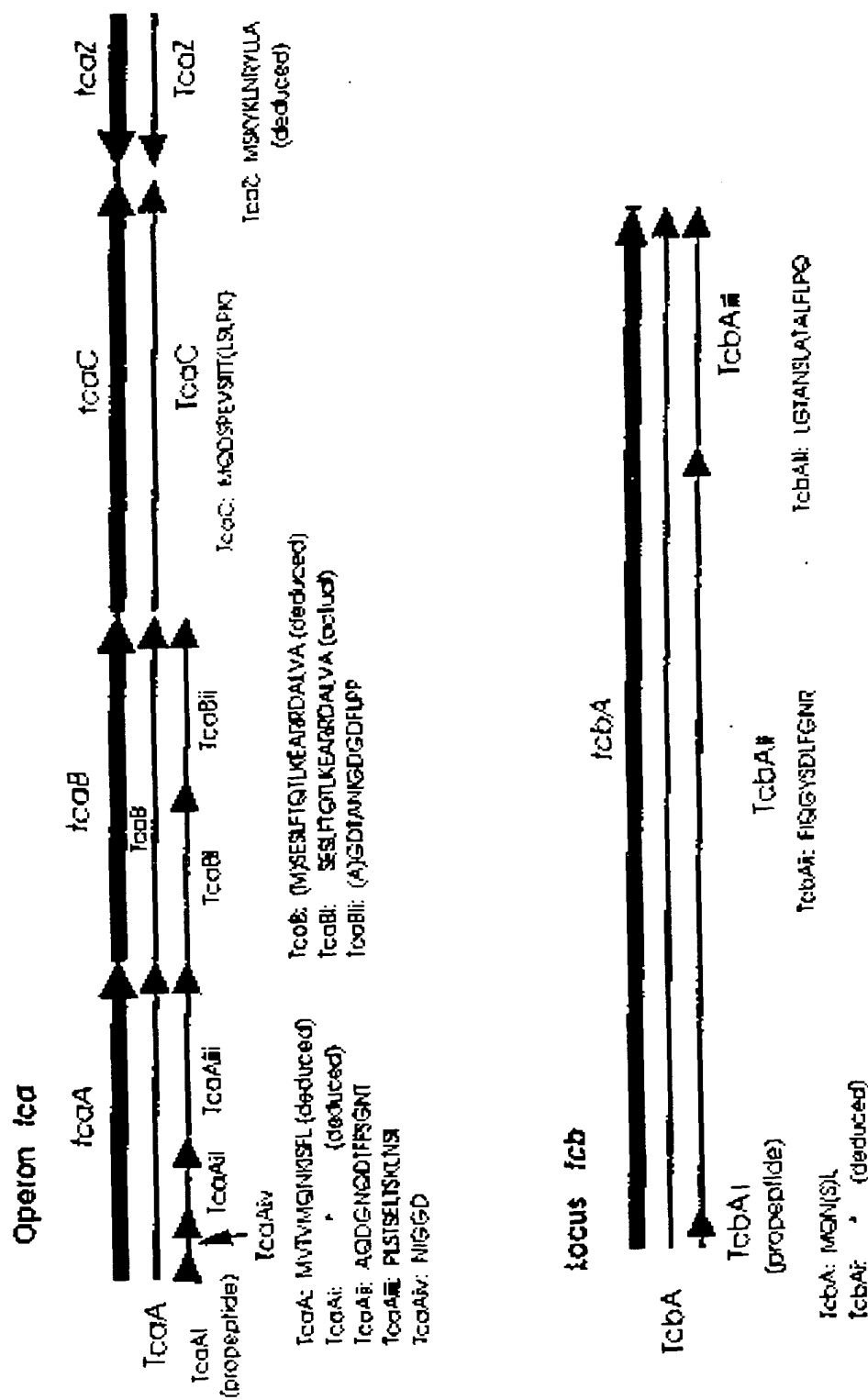


FIG.6A loci *tca* and *tcb*, primary gene products, and derived peptides

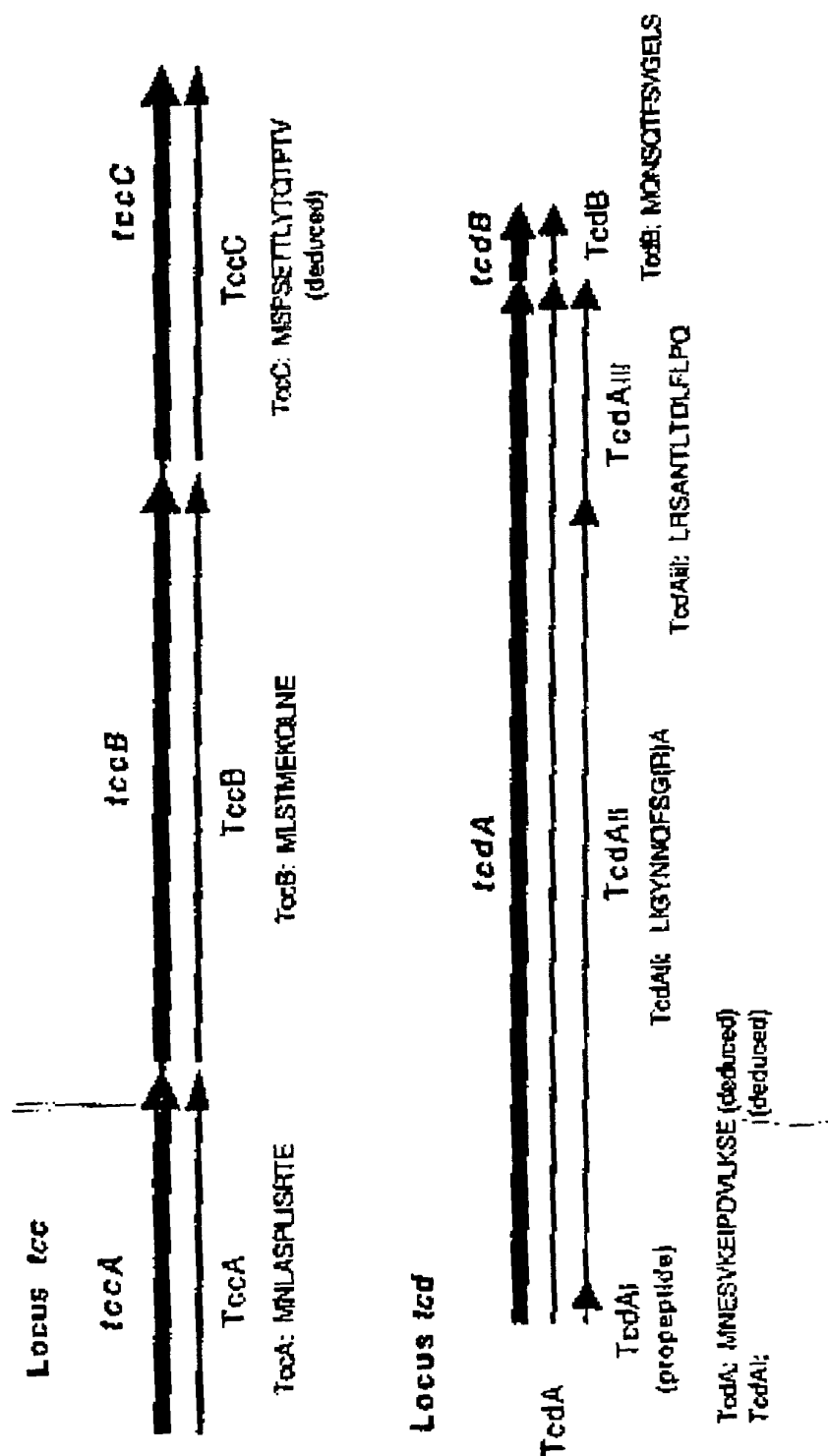


FIG. 6B Loci *tcc* and *tcd*, primary gene products, and derived peptides.

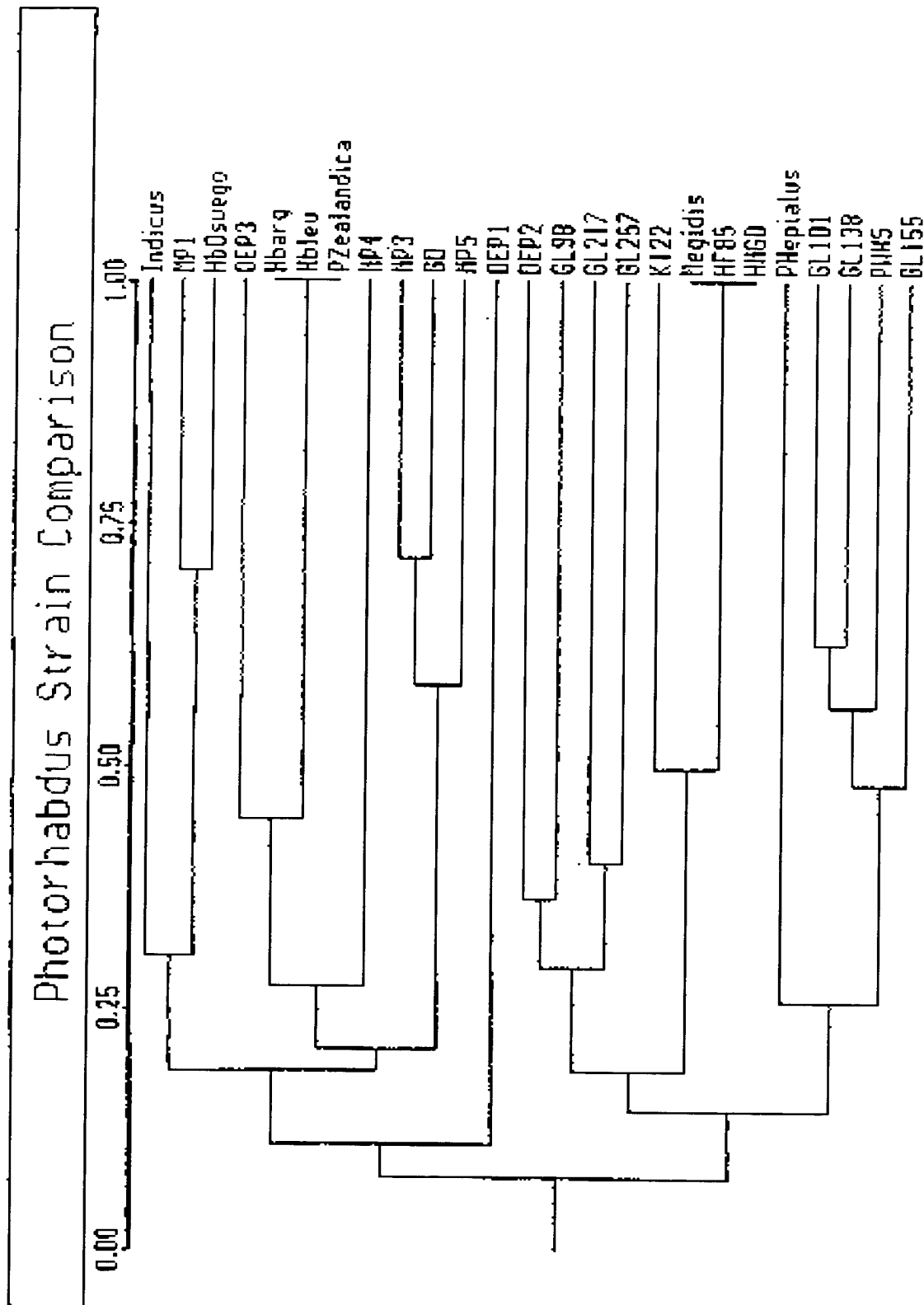


FIG. 7

